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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 20:59:06 ; Search time 72.1262 Seconds  
(without alignments)  
468.258 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19  
Sequence: 1 cccttgatgcggctaatc 19

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : Issued Patents NA:  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	100.0	27	3	US-09-724-678D-9 ✓
2	19	100.0	628	2	US-08-387-845-5
3	19	100.0	628	2	US-08-778-275-5
4	19	100.0	628	3	US-08-867-352-5
5	19	100.0	1220	3	US-09-116-032-2
6	19	100.0	1560	3	US-09-724-678D-16
7	19	100.0	2320	3	US-09-202-904A-10
8	19	100.0	7400	3	US-09-116-032-1
9	19	100.0	7441	3	US-09-284-349B-1
10	18	94.7	25	3	US-09-311-260-105
11	18	94.7	25	3	US-09-061-273-9
12	18	94.7	25	3	US-09-313-221A-114
13	18	94.7	7432	2	US-07-852-260-1
14	18	94.7	7432	2	US-08-461-503-1
15	18	94.7	7432	2	US-08-465-250-1
16	17.4	91.6	627	2	US-08-221-816B-31
17	17.4	91.6	627	3	US-10-112-547-31
18	17.4	91.6	627	3	US-10-112-241-31
19	17.4	91.6	627	3	US-10-104-611-31
20	17.4	91.6	627	3	US-10-109-368-31
21	17.4	91.6	627	3	US-09-724-380-31
22	16.4	85.3	32	2	US-08-246-373-1
23	15.8	83.2	250	3	US-07-113-1
24	15.4	81.1	1269	3	US-09-489-039A-5242

25	15.4	81.1	199945	3	US-09-949-016-15436	Sequence 15436, A
26	15	78.9	35	2	US-08-361-337-36	Sequence 36, Appl
27	15	78.9	35	2	US-08-361-337-38	Sequence 38, Appl
28	14.8	77.9	601	3	US-09-949-016-34646	Sequence 34646, A
c 29	14.8	77.9	601	3	US-09-949-016-146512	Sequence 146512,
c 30	14.8	77.9	601	3	US-09-949-016-170260	Sequence 170260,
c 31	14.8	77.9	678	3	US-09-270-767-13998	Sequence 13998, A
c 32	14.8	77.9	960	3	US-09-270-767-13244	Sequence 13244, A
c 33	14.8	77.9	9057	3	US-09-453-702B-178	Sequence 478, App
c 34	14.8	77.9	9057	3	US-10-114-170-194	Sequence 194, App
c 35	14.8	77.9	12537	2	US-08-611-280-4	Sequence 4, Appli
c 36	14.8	77.9	12537	3	US-09-195-940-4	Sequence 4, Appli
c 37	14.8	77.9	12537	3	US-09-562-466-4	Sequence 4, Appli
c 38	14.8	77.9	16083	3	US-09-949-016-17245	Sequence 17245, A
c 39	14.8	77.9	25235	3	US-10-164-230-2	Sequence 2, Appli
c 40	14.8	77.9	25235	3	US-09-949-016-16549	Sequence 16549, A
c 41	14.8	77.9	47555	3	US-09-949-016-12598	Sequence 12598, A
c 42	14.8	77.9	49673	3	US-09-949-016-17433	Sequence 17433, A
c 43	14.8	77.9	101349	3	US-09-949-016-13765	Sequence 13765, A
c 44	14.8	77.9	128470	3	US-09-949-016-15890	Sequence 15890, A
c 45	14.8	77.9	144922	3	US-09-949-016-15858	Sequence 15858, A
c 46	14.8	77.9	145320	3	US-09-103-840A-2	Sequence 2, Appli
c 47	14.8	77.9	4403765	3	US-09-103-840A-1	Sequence 1, Appli
c 48	14.8	77.9	4411529	3	US-09-702-705-1724	Sequence 1724, Ap
c 49	14.4	75.8	145	3	US-09-736-457-1724	Sequence 1724, Ap
50	14.4	75.8	145	3	US-09-671-325-1724	Sequence 1724, Ap
51	14.4	75.8	145	3	US-09-658-824-1724	Sequence 1724, Ap
52	14.4	75.8	145	3	US-10-017-754-1724	Sequence 1724, Ap
53	14.4	75.8	145	3	US-09-270-767-27427	Sequence 27427, A
54	14.4	75.8	671	3	US-09-902-540-8469	Sequence 8469, Ap
55	14.4	75.8	1494	3	US-09-221-017B-461	Sequence 461, App
c 56	14.4	75.8	1660	3	US-09-902-540-891	Sequence 11790, A
c 57	14.4	75.8	2058	3	US-09-524-101D-18	Sequence 18, Appl
58	14.4	75.8	6380	3	US-09-949-016-12008	Sequence 12008, A
59	14.4	75.8	27425	3	US-09-949-016-17056	Sequence 17056, A
c 60	14.4	75.8	331814	3	US-09-513-999C-30496	Sequence 30496, A
c 61	14.4	75.8	331814	3	US-09-949-016-185399	Sequence 185399,
c 62	14.2	74.7	403	3	US-09-949-016-185400	Sequence 185400,
c 63	14.2	74.7	601	3	US-09-949-016-185401	Sequence 185401,
c 64	14.2	74.7	601	3	US-09-949-016-185402	Sequence 185402,
c 65	14.2	74.7	601	3	US-09-949-016-185402	Sequence 185402,
c 66	14.2	74.7	601	3	US-09-949-016-185402	Sequence 185402,
c 67	14.2	74.7	1020	3	US-09-533-559-1622	Sequence 1622, Ap
c 68	14.2	74.7	1020	3	US-09-489-039A-5060	Sequence 5060, Ap
c 69	14.2	74.7	1218	3	US-10-029-180-61	Sequence 61, Appl
c 70	14.2	74.7	1218	3	US-09-602-777A-393	Sequence 393, App
c 71	14.2	74.7	3344	2	US-08-426-236-1	Sequence 1, Appli
c 72	14.2	74.7	3344	3	US-09-220-132-73	Sequence 73, Appl
c 73	14.2	74.7	3344	3	US-09-949-016-4054	Sequence 4054, Ap
c 74	14.2	74.7	3505	3	US-09-566-921-63	Sequence 63, Appl
c 75	14.2	74.7	8165	3	US-09-949-016-16816	Sequence 16816, A
c 76	14.2	74.7	9962	3	US-09-949-016-13284	Sequence 13284, A
c 77	14.2	74.7	23105	3	US-09-949-016-13659	Sequence 13659, A
c 78	14.2	74.7	23108	3	US-09-949-016-12582	Sequence 12582, A
c 79	14.2	74.7	36033	3	US-08-311-731A-124	Sequence 124, App
c 80	14.2	74.7	49407	3	US-09-949-016-12532	Sequence 12532, A
c 81	14.2	74.7	49408	3	US-09-949-016-17045	Sequence 17045, A
c 82	14.2	74.7	79578	3	US-09-949-016-16339	Sequence 16339, A
c 83	14.2	74.7	129908	3	US-09-585-858-1	Sequence 1, Appli
c 84	14.2	74.7	129908	3	US-10-270-878-1	Sequence 1, Appli
c 85	14.2	74.7	141560	3	US-09-949-016-16476	Sequence 16476, A
c 86	14.2	74.7	374159	3	US-09-949-016-15868	Sequence 15868, A
c 87	14	73.7	11823	3	US-08-956-171E-136	Sequence 136, App
c 88	14	73.7	11823	3	US-08-781-986A-136	Sequence 136, App
c 89	13.8	72.6	300	3	US-09-270-767-8260	Sequence 8260, Ap
c 90	13.8	72.6	300	3	US-09-270-767-23542	Sequence 23542, A
c 91	13.8	72.6	506	3	US-09-270-767-5089	Sequence 5089, Ap
c 92	13.8	72.6	506	3	US-09-270-767-20371	Sequence 20371, A
c 93	13.8	72.6	521	3	US-07-998-289B-2	Sequence 2, Appli
c 94	13.8	72.6	567	3	US-07-998-289B-2	Sequence 2, Appli
c 95	13.8	72.6	601	3	US-09-949-016-25349	Sequence 25349, A
c 96	13.8	72.6	601	3	US-09-949-016-69732	Sequence 69732, A
c 97	13.8	72.6	642	3	US-09-902-540-3264	Sequence 3264, Ap

c 98	13.8	72.6	672	3	US-09-533-559-6637	Sequence 6637, Ap	171	13.4	70.5	1607	3	US-09-099-932-50	Sequence 50, Appl
c 99	13.8	72.6	738	3	US-09-134-000C-3216	Sequence 3216, Ap	172	13.4	70.5	1607	3	US-10-392-970-50	Sequence 50, Appl
c 100	13.8	72.6	1302	3	US-08-945-038-5	Sequence 5, Appli	c 173	13.4	70.5	2078	3	US-09-212-609B-14	Sequence 14, Appl
c 101	13.8	72.6	1425	3	US-09-489-039A-4673	Sequence 4673, Ap	c 174	13.4	70.5	2232	3	US-09-212-609B-19	Sequence 19, Appl
c 102	13.8	72.6	1431	3	US-09-489-039A-1316	Sequence 1, Appli	c 175	13.4	70.5	2271	3	US-09-506-286B-105	Sequence 105, App
c 103	13.8	72.6	1435	3	US-10-019-817D-11	Sequence 1, Appli	c 176	13.4	70.5	2271	3	US-09-506-286B-108	Sequence 108, App
c 104	13.8	72.6	1451	3	US-09-693-746-19	Sequence 19, Appl	c 177	13.4	70.5	2271	3	US-10-065-133A-105	Sequence 105, App
c 105	13.8	72.6	2451	3	US-09-489-039A-3349	Sequence 3349, Ap	c 178	13.4	70.5	2271	3	US-10-065-133A-108	Sequence 108, App
c 106	13.8	72.6	2523	3	US-09-489-039A-3473	Sequence 3473, Ap	c 179	13.4	70.5	2341	3	US-09-506-286B-103	Sequence 103, App
c 107	13.8	72.6	3112	3	US-09-774-528-261	Sequence 261, App	c 180	13.4	70.5	2341	3	US-09-506-286B-106	Sequence 106, App
c 108	13.8	72.6	3112	3	US-10-120-988-261	Sequence 261, App	c 181	13.4	70.5	2341	3	US-10-065-133A-103	Sequence 103, App
c 109	13.8	72.6	3117	2	US-08-747-536-1	Sequence 1, Appli	c 182	13.4	70.5	2341	3	US-10-065-133A-106	Sequence 106, App
c 110	13.8	72.6	3159	3	US-09-134-000C-3215	Sequence 3215, Ap	c 183	13.4	70.5	2535	3	US-09-614-221A-415	Sequence 415, App
c 111	13.8	72.6	18107	3	US-09-949-016-13674	Sequence 13674, A	c 184	13.4	70.5	3097	3	US-09-282-147-36	Sequence 36, Appl
c 112	13.8	72.6	18954	3	US-09-902-540-1150	Sequence 1150, Ap	c 185	13.4	70.5	3171	3	US-09-016-434-1348	Sequence 1348, Ap
c 113	13.8	72.6	40000	3	US-09-780-049-18	Sequence 18, Appl	c 186	13.4	70.5	3219	3	US-09-895-652A-17	Sequence 17, Appl
c 114	13.8	72.6	51043	3	US-09-949-016-12739	Sequence 12739, A	c 187	13.4	70.5	3582	3	US-09-620-312D-552	Sequence 552, App
c 115	13.8	72.6	51046	3	US-09-949-016-13946	Sequence 13946, A	c 188	13.4	70.5	5128	3	US-09-264-512B-1	Sequence 1, Appli
c 116	13.8	72.6	72455	3	US-09-949-016-13793	Sequence 13793, A	c 189	13.4	70.5	8345	3	US-09-949-016-16833	Sequence 16833, A
c 117	13.8	72.6	87563	3	US-09-453-702B-57	Sequence 57, Appl	c 190	13.4	70.5	15101	2	US-08-799-464A-14	Sequence 14, Appl
c 118	13.8	72.6	87563	3	US-10-114-170-57	Sequence 57, Appl	c 191	13.4	70.5	15101	6	PCT-US95-08927-14	Sequence 14, Appl
c 119	13.8	72.6	90776	3	US-09-949-016-17230	Sequence 17230, A	c 192	13.4	70.5	15108	2	US-08-157-005-1	Sequence 1, Appli
c 120	13.8	72.6	104475	3	US-09-949-016-12115	Sequence 12115, A	c 193	13.4	70.5	15108	3	US-08-747-863-1	Sequence 1, Appli
c 121	13.8	72.6	111282	3	US-09-754-250-3	Sequence 3, Appli	c 194	13.4	70.5	15108	3	US-09-565-864-1	Sequence 1, Appli
c 122	13.8	72.6	111282	3	US-10-094-989-3	Sequence 3, Appli	c 195	13.4	70.5	15108	3	US-10-226-065-1	Sequence 1, Appli
c 123	13.8	72.6	183112	3	US-09-949-016-14184	Sequence 14184, A	c 196	13.4	70.5	25321	3	US-09-949-016-12355	Sequence 12355, A
c 124	13.8	72.6	636591	3	US-09-949-016-11808	Sequence 11808, A	c 197	13.4	70.5	25321	3	US-09-949-016-14039	Sequence 14039, A
c 125	13.8	72.6	636591	3	US-09-949-016-13388	Sequence 13388, A	c 198	13.4	70.5	26729	3	US-10-283-247-6	Sequence 6, Appli
c 126	13.4	70.5	335	3	US-09-621-976-18860	Sequence 18860, A	c 199	13.4	70.5	32675	3	US-08-976-063B-1	Sequence 1, Appli
c 127	13.4	70.5	451	3	US-09-643-597-211	Sequence 211, App	c 200	13.4	70.5	36759	3	US-09-949-016-16994	Sequence 16994, A
c 128	13.4	70.5	451	3	US-09-480-884A-211	Sequence 211, App	c 201	13.4	70.5	38059	3	US-09-328-925-4	Sequence 4, Appli
c 129	13.4	70.5	451	3	US-09-542-615A-211	Sequence 211, App	c 202	13.4	70.5	38155	3	US-09-453-702B-79	Sequence 79, Appl
c 130	13.4	70.5	451	3	US-09-606-421B-211	Sequence 211, App	c 203	13.4	70.5	38155	3	US-10-114-170-79	Sequence 79, Appl
c 131	13.4	70.5	451	3	US-09-466-396A-211	Sequence 211, App	c 204	13.4	70.5	49795	3	US-09-453-702B-60	Sequence 60, Appl
c 132	13.4	70.5	451	3	US-09-476-496A-211	Sequence 211, App	c 205	13.4	70.5	49795	3	US-10-114-170-60	Sequence 60, Appl
c 133	13.4	70.5	451	3	US-09-630-940B-211	Sequence 211, App	c 206	13.4	70.5	56702	3	US-09-949-016-12568	Sequence 12568, A
c 134	13.4	70.5	451	3	US-10-007-700-211	Sequence 211, App	c 207	13.4	70.5	56702	3	US-09-949-016-15423	Sequence 15423, A
c 135	13.4	70.5	601	3	US-09-949-016-29841	Sequence 29841, A	c 208	13.4	70.5	61158	3	US-09-949-016-15041	Sequence 15041, A
c 136	13.4	70.5	601	3	US-09-949-016-57836	Sequence 57836, A	c 209	13.4	70.5	70383	3	US-10-283-247-3	Sequence 3, Appli
c 137	13.4	70.5	601	3	US-09-949-016-57838	Sequence 57838, A	c 210	13.4	70.5	75431	3	US-09-949-016-15122	Sequence 15122, A
c 138	13.4	70.5	601	3	US-09-949-016-57839	Sequence 57839, A	c 211	13.4	70.5	87752	3	US-09-949-016-16807	Sequence 16807, A
c 139	13.4	70.5	601	3	US-09-949-016-57839	Sequence 57839, A	c 212	13.4	70.5	87752	3	US-09-949-016-12756	Sequence 12756, A
c 140	13.4	70.5	623	3	US-09-492-709A-466	Sequence 466, App	c 213	13.4	70.5	136264	3	US-09-949-016-12756	Sequence 13001, A
c 141	13.4	70.5	623	3	US-09-446-301A-2	Sequence 2, Appli	c 214	13.4	70.5	136265	3	US-09-949-016-13001	Sequence 13418, A
c 142	13.4	70.5	636	3	US-09-446-301A-2	Sequence 2, Appli	c 215	13.4	70.5	23674	3	US-09-949-016-13418	Sequence 13418, A
c 143	13.4	70.5	636	3	US-09-099-932-2	Sequence 2, Appli	c 216	13.4	70.5	23674	3	US-09-949-016-16101	Sequence 16101, A
c 144	13.4	70.5	636	3	US-10-392-970-2	Sequence 2, Appli	c 217	13.4	70.5	256176	3	US-09-949-016-12822	Sequence 12822, A
c 145	13.4	70.5	1133	3	US-09-533-559-309	Sequence 309, App	c 218	13.2	69.5	34	3	US-09-182-859-18	Sequence 18, Appl
c 146	13.4	70.5	1140	3	US-09-252-991A-15122	Sequence 15122, A	c 219	13.2	69.5	34	3	US-09-537-168-17	Sequence 17, Appl
c 147	13.4	70.5	1188	3	US-09-506-286B-87	Sequence 87, Appl	c 220	13.2	69.5	34	3	US-09-672-459-18	Sequence 18, Appl
c 148	13.4	70.5	1188	3	US-09-506-286B-90	Sequence 90, Appl	c 221	13.2	69.5	34	3	US-10-186-042-18	Sequence 18, Appl
c 149	13.4	70.5	1188	3	US-09-506-286B-93	Sequence 93, Appl	c 222	13.2	69.5	41	3	US-09-025-769B-111	Sequence 111, App
c 150	13.4	70.5	1188	3	US-09-506-286B-96	Sequence 96, Appl	c 223	13.2	69.5	41	3	US-09-490-070A-111	Sequence 111, App
c 151	13.4	70.5	1188	3	US-10-065-133A-87	Sequence 87, Appl	c 224	13.2	69.5	41	3	US-09-490-153-111	Sequence 111, App
c 152	13.4	70.5	1188	3	US-10-065-133A-90	Sequence 90, Appl	c 225	13.2	69.5	41	3	US-09-490-324-111	Sequence 111, App
c 153	13.4	70.5	1188	3	US-10-065-133A-93	Sequence 93, Appl	c 226	13.2	69.5	66	3	US-09-173-941-115	Sequence 115, App
c 154	13.4	70.5	1188	3	US-10-065-133A-96	Sequence 96, Appl	c 227	13.2	69.5	66	3	US-09-494-190-115	Sequence 115, App
c 155	13.4	70.5	1234	3	US-09-506-286B-85	Sequence 85, Appl	c 228	13.2	69.5	192	2	US-08-485-450D-74	Sequence 74, Appl
c 156	13.4	70.5	1234	3	US-10-065-133A-85	Sequence 85, Appl	c 229	13.2	69.5	192	2	US-08-482-130C-74	Sequence 74, Appl
c 157	13.4	70.5	1240	3	US-09-506-286B-88	Sequence 88, Appl	c 230	13.2	69.5	192	2	US-08-484-211C-74	Sequence 74, Appl
c 158	13.4	70.5	1240	3	US-10-065-133A-88	Sequence 88, Appl	c 231	13.2	69.5	192	3	US-08-906-769-74	Sequence 74, Appl
c 159	13.4	70.5	1241	3	US-09-506-286B-91	Sequence 91, Appl	c 232	13.2	69.5	192	3	US-08-906-616-74	Sequence 74, Appl
c 160	13.4	70.5	1241	3	US-09-506-286B-94	Sequence 94, Appl	c 233	13.2	69.5	192	3	US-08-817-795-74	Sequence 74, Appl
c 161	13.4	70.5	1241	3	US-10-065-133A-91	Sequence 91, Appl	c 234	13.2	69.5	192	3	US-08-485-443B-74	Sequence 74, Appl
c 162	13.4	70.5	1281	3	US-10-065-133A-94	Sequence 94, Appl	c 235	13.2	69.5	192	3	US-08-639-075A-74	Sequence 74, Appl
c 163	13.4	70.5	1425	3	US-09-489-039A-3180	Sequence 3180, Ap	c 236	13.2	69.5	192	3	US-09-012-431-74	Sequence 74, Appl
c 164	13.4	70.5	1425	3	US-09-538-414-7	Sequence 7, Appli	c 237	13.2	69.5	192	3	US-09-012-692-74	Sequence 74, Appl
c 165	13.4	70.5	1425	3	US-10-074-279-7	Sequence 7, Appli	c 238	13.2	69.5	192	3	US-08-906-613-74	Sequence 74, Appl
c 166	13.4	70.5	1440	3	US-09-891-641-47	Sequence 47, Appl	c 239	13.2	69.5	192	6	PCT-US95-14442A-74	Sequence 74, Appl
c 167	13.4	70.5	1444	3	US-09-958-969-1	Sequence 1, Appli	c 240	13.2	69.5	201	3	US-09-248-796A-8933	Sequence 8933, Ap
c 168	13.4	70.5	1458	3	US-09-252-991A-14865	Sequence 14865, A	c 241	13.2	69.5	213	3	US-09-513-999C-432	Sequence 432, App
c 169	13.4	70.5	1596	3	US-08-976-063E-33	Sequence 33, Appl	c 242	13.2	69.5	215	3	US-09-270-767-1960	Sequence 1960, Ap
c 170	13.4	70.5	1607	3	US-09-446-301A-16	Sequence 16, Appl	c 243	13.2	69.5	215	3	US-09-270-767-17242	Sequence 17242, A



C 244	13.2	69.5	215	3	US-09-513-999C-27894	Sequence 27894, A	C 317	13.2	69.5	636	3	US-10-017-754-1530	Sequence 1530, Ap
C 245	13.2	69.5	234	3	US-08-956-171E-4590	Sequence 4590, Ap	C 318	13.2	69.5	636	3	US-09-651-563-1530	Sequence 1530, Ap
C 246	13.2	69.5	234	3	US-08-781-986A-4590	Sequence 4590, Ap	C 319	13.2	69.5	672	3	US-08-485-453D-16	Sequence 16, Appl
C 247	13.2	69.5	237	3	US-09-976-594-408	Sequence 408, Ap	C 320	13.2	69.5	672	2	US-08-482-130C-16	Sequence 16, Appl
C 248	13.2	69.5	242	3	US-08-956-171E-4540	Sequence 4540, Ap	C 321	13.2	69.5	672	2	US-08-484-211C-16	Sequence 16, Appl
C 249	13.2	69.5	242	3	US-08-781-986A-4540	Sequence 4540, Ap	C 322	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 250	13.2	69.5	252	3	US-09-513-999C-31381	Sequence 31381, A	C 323	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 251	13.2	69.5	264	3	US-08-956-171E-4483	Sequence 4483, Ap	C 324	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 252	13.2	69.5	264	3	US-08-781-986A-4483	Sequence 4483, Ap	C 325	13.2	69.5	672	3	US-08-817-795-16	Sequence 16, Appl
C 253	13.2	69.5	265	3	US-09-919-039-181	Sequence 181, Ap	C 326	13.2	69.5	672	3	US-08-485-443B-16	Sequence 16, Appl
C 254	13.2	69.5	278	3	US-09-313-294A-6858	Sequence 6858, Ap	C 327	13.2	69.5	672	3	US-08-639-075A-16	Sequence 16, Appl
C 255	13.2	69.5	279	3	US-08-956-171E-4455	Sequence 4455, Ap	C 328	13.2	69.5	672	3	US-09-012-632-16	Sequence 16, Appl
C 256	13.2	69.5	279	3	US-08-781-986A-4455	Sequence 4455, Ap	C 329	13.2	69.5	672	3	US-09-012-632-16	Sequence 16, Appl
C 257	13.2	69.5	321	3	US-09-025-769B-54	Sequence 54, Appl	C 330	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 258	13.2	69.5	321	3	US-09-490-070A-54	Sequence 54, Appl	C 331	13.2	69.5	672	3	US-08-906-769-16	Sequence 16, Appl
C 259	13.2	69.5	321	3	US-09-490-153-54	Sequence 54, Appl	C 332	13.2	69.5	672	3	PCT-US95-14442A-16	Sequence 16, Appl
C 260	13.2	69.5	321	3	US-09-490-324-54	Sequence 54, Appl	C 333	13.2	69.5	672	3	US-07-998-636-1	Sequence 1, Appl
C 261	13.2	69.5	324	3	US-08-956-171E-4279	Sequence 4279, Ap	C 334	13.2	69.5	884	3	US-09-774-639-23	Sequence 23, Appl
C 262	13.2	69.5	324	3	US-08-781-986A-4279	Sequence 4279, Ap	C 335	13.2	69.5	891	3	US-09-602-787A-273	Sequence 273, Appl
C 263	13.2	69.5	372	3	US-09-270-767-1879	Sequence 1879, Ap	C 336	13.2	69.5	891	4	US-09-605-703B-945	Sequence 945, Appl
C 264	13.2	69.5	372	3	US-08-956-171E-17161	Sequence 17161, A	C 337	13.2	69.5	891	4	US-09-605-703B-947	Sequence 947, Appl
C 265	13.2	69.5	400	3	US-08-956-171E-3899	Sequence 3899, Ap	C 338	13.2	69.5	975	3	US-09-252-991A-5370	Sequence 5370, Ap
C 266	13.2	69.5	400	3	US-08-956-171E-3901	Sequence 3901, Ap	C 339	13.2	69.5	989	3	US-09-906-391A-19	Sequence 19, Appl
C 267	13.2	69.5	400	3	US-08-956-171E-4429	Sequence 4429, Ap	C 340	13.2	69.5	990	3	US-09-976-594-565	Sequence 565, Appl
C 268	13.2	69.5	400	3	US-08-781-986A-3899	Sequence 3899, Ap	C 341	13.2	69.5	990	3	US-09-919-039-324	Sequence 324, Appl
C 269	13.2	69.5	400	3	US-08-781-986A-3901	Sequence 3901, Ap	C 342	13.2	69.5	1008	3	US-08-235-836C-130	Sequence 130, Appl
C 270	13.2	69.5	400	3	US-08-781-986A-4429	Sequence 4429, Ap	C 343	13.2	69.5	1011	3	US-08-235-836C-131	Sequence 131, Appl
C 271	13.2	69.5	402	3	US-09-118-554-28	Sequence 28, Appl	C 344	13.2	69.5	1086	3	US-08-235-836C-51	Sequence 51, Appl
C 272	13.2	69.5	402	3	US-09-118-627-28	Sequence 28, Appl	C 345	13.2	69.5	1182	3	US-09-328-352-99	Sequence 99, Appl
C 273	13.2	69.5	402	3	US-09-602-877A-28	Sequence 28, Appl	C 346	13.2	69.5	1182	3	US-09-489-039A-4766	Sequence 4766, Ap
C 274	13.2	69.5	426	3	US-09-252-991A-5382	Sequence 5382, Ap	C 347	13.2	69.5	1200	3	US-08-712-363-18	Sequence 18, Appl
C 275	13.2	69.5	439	3	US-09-513-999C-1208	Sequence 1208, Ap	C 348	13.2	69.5	1236	3	US-09-252-991A-5386	Sequence 5386, Ap
C 276	13.2	69.5	455	3	US-09-621-976-12457	Sequence 12457, A	C 349	13.2	69.5	1248	3	US-09-758-759-50	Sequence 50, Appl
C 277	13.2	69.5	458	3	US-08-956-171E-1219	Sequence 1219, A	C 350	13.2	69.5	1283	3	US-09-614-221A-439	Sequence 439, Appl
C 278	13.2	69.5	458	3	US-08-781-986A-1219	Sequence 1219, Ap	C 351	13.2	69.5	1283	3	US-08-976-259-72	Sequence 72, Appl
C 279	13.2	69.5	490	3	US-09-533-559-2377	Sequence 2377, A	C 352	13.2	69.5	1283	3	US-09-956-004-72	Sequence 72, Appl
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C 281	13.2	69.5	528	3	US-08-781-986A-3684	Sequence 3684, Ap	C 354	13.2	69.5	1413	3	US-09-252-991A-12131	Sequence 12131, A
C 282	13.2	69.5	564	3	US-09-252-991A-6135	Sequence 6135, Ap	C 355	13.2	69.5	1482	3	US-09-613-303-18	Sequence 18, Appl
C 283	13.2	69.5	601	3	US-09-949-016-19024	Sequence 19024, A	C 356	13.2	69.5	1517	3	US-10-267-311-18	Sequence 18, Appl
C 284	13.2	69.5	601	3	US-09-949-016-27784	Sequence 27784, A	C 357	13.2	69.5	1517	3	US-09-270-767-12029	Sequence 12029, A
C 285	13.2	69.5	601	3	US-09-949-016-27785	Sequence 27785, A	C 358	13.2	69.5	1653	3	US-09-270-767-28978	Sequence 28978, A
C 286	13.2	69.5	601	3	US-09-949-016-27786	Sequence 27786, A	C 359	13.2	69.5	1805	3	US-09-016-434-1086	Sequence 1086, Ap
C 287	13.2	69.5	601	3	US-09-949-016-27787	Sequence 27787, A	C 360	13.2	69.5	1805	3	US-09-949-016-851	Sequence 851, Ap
C 288	13.2	69.5	601	3	US-09-949-016-43042	Sequence 43042, A	C 361	13.2	69.5	1805	3	US-09-949-016-3817	Sequence 3817, Ap
C 289	13.2	69.5	601	3	US-09-949-016-44369	Sequence 44369, A	C 362	13.2	69.5	2034	3	US-09-489-847-83	Sequence 83, Appl
C 290	13.2	69.5	601	3	US-09-949-016-47104	Sequence 47104, A	C 363	13.2	69.5	2055	3	US-09-583-110-2594	Sequence 2594, Ap
C 291	13.2	69.5	601	3	US-09-949-016-54403	Sequence 54403, A	C 364	13.2	69.5	2076	3	US-09-107-433-1657	Sequence 1657, Ap
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C 293	13.2	69.5	601	3	US-09-949-016-104751	Sequence 104751, A	C 366	13.2	69.5	2185	3	US-09-270-767-13085	Sequence 13085, A
C 294	13.2	69.5	601	3	US-09-949-016-104752	Sequence 104752, A	C 367	13.2	69.5	2412	3	US-09-620-312D-1023	Sequence 1023, Ap
C 295	13.2	69.5	601	3	US-09-949-016-107955	Sequence 107955, A	C 368	13.2	69.5	2493	3	US-09-252-991A-12390	Sequence 12390, A
C 296	13.2	69.5	601	3	US-09-949-016-107956	Sequence 107956, A	C 369	13.2	69.5	2682	3	US-09-489-039A-6956	Sequence 6956, Ap
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C 298	13.2	69.5	601	3	US-09-949-016-129193	Sequence 129193, A	C 371	13.2	69.5	3024	3	US-09-252-991A-12202	Sequence 12202, A
C 299	13.2	69.5	601	3	US-09-949-016-129194	Sequence 129194, A	C 372	13.2	69.5	3270	3	US-09-614-221A-311	Sequence 311, Appl
C 300	13.2	69.5	601	3	US-09-949-016-129195	Sequence 129195, A	C 373	13.2	69.5	3397	3	US-09-345-236B-145	Sequence 145, Appl
C 301	13.2	69.5	601	3	US-09-949-016-131028	Sequence 131028, A	C 374	13.2	69.5	3997	3	US-09-345-236B-146	Sequence 146, Appl
C 302	13.2	69.5	601	3	US-09-949-016-140363	Sequence 140363, A	C 375	13.2	69.5	4029	3	US-08-956-171E-301	Sequence 301, Appl
C 303	13.2	69.5	601	3	US-09-949-016-172153	Sequence 172153, A	C 376	13.2	69.5	4308	3	US-08-781-986A-301	Sequence 301, Appl
C 304	13.2	69.5	601	3	US-09-949-016-172154	Sequence 172154, A	C 377	13.2	69.5	4308	3	US-09-634-238-182	Sequence 182, Appl
C 305	13.2	69.5	601	3	US-09-949-016-202288	Sequence 202288, A	C 378	13.2	69.5	4415	3	US-09-614-221A-599	Sequence 599, Appl
C 306	13.2	69.5	601	3	US-09-949-016-202289	Sequence 202289, A	C 379	13.2	69.5	4415	3	US-09-486-580A-1	Sequence 1, Appl
C 307	13.2	69.5	601	3	US-09-949-016-202290	Sequence 202290, A	C 380	13.2	69.5	5037	3	US-10-013-770A-1	Sequence 1, Appl
C 308	13.2	69.5	601	3	US-09-949-016-202291	Sequence 202291, A	C 381	13.2	69.5	5805	3	US-09-976-594-202	Sequence 202, Appl
C 309	13.2	69.5	601	3	US-09-949-002-2054	Sequence 2054, Ap	C 382	13.2	69.5	5806	3	US-09-949-016-12593	Sequence 12593, A
C 310	13.2	69.5	601	3	US-09-949-002-2055	Sequence 2055, Ap	C 383	13.2	69.5	5838	2	US-09-949-016-15559	Sequence 15559, A
C 311	13.2	69.5	636	3	US-09-949-002-8811	Sequence 8811, Ap	C 384	13.2	69.5	5838	2	US-08-578-096A-1	Sequence 1, Appl
C 312	13.2	69.5	636	3	US-09-702-705-1530	Sequence 1530, Ap	C 385	13.2	69.5	6439	3	US-09-240-426-1	Sequence 1, Appl
C 313	13.2	69.5	636	3	US-09-736-457-1530	Sequence 1530, Ap	C 386	13.2	69.5	7585	3	US-09-902-540-813	Sequence 813, Appl
C 314	13.2	69.5	636	3	US-09-614-124B-1530	Sequence 1530, Ap	C 387	13.2	69.5	8158	3	US-09-949-016-14641	Sequence 14641, A
C 315	13.2	69.5	636	3	US-09-671-325-1530	Sequence 1530, Ap	C 388	13.2	69.5	8654	3	US-09-949-016-13387	Sequence 13387, A
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C 495 13 68.4 4411529 3 US-09-103-840A-1 Sequence 1, Appli  
C 496 12.8 67.4 18 3 US-09-422-978-8815 Sequence 8815, Ap  
C 497 12.8 67.4 20 3 US-07-998-289B-18 Sequence 18, Appl  
C 498 12.8 67.4 25 3 US-09-396-196G-38020 Sequence 38020, A  
C 499 12.8 67.4 25 3 US-09-396-196G-38021 Sequence 38021, A  
500 12.8 67.4 25 3 US-09-396-196G-38022 Sequence 38022, A

ALIGNMENTS

RESULT 1

US-09-724-678D-9  
; Sequence 9, Application US/09724678D  
; Patent No. 6818397

GENERAL INFORMATION:

; APPLICANT: Lee, Kang-Hung  
; APPLICANT: Bair, Chi-Hong  
; APPLICANT: Tseng, Yang-Yuan  
; APPLICANT: Wang, Yih-Weng  
; APPLICANT: Wang, Shing-Hwan  
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the p  
; TITLE OF INVENTION: and Probes Therefor  
; FILE REFERENCE: TAI 3L6  
; CURRENT APPLICATION NUMBER: US/09/724,678D  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 9  
; LENGTH: 27  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Artificial Sequence is Synthesized  
; Patent No. 6818397

Query Match 100.0%; Score 19; DB 3; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.71;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 9 CCCCTGAATGCGGCTAATC 27

## RESULT 2

US-08-387-845-5  
; Sequence 5, Application US/08387845  
; Patent No. 5685567  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a  
; TITLE OF INVENTION: bicistronic vector system in mammalian cells  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/387,845  
; FILING DATE:  
; CLASSIFICATION: 435  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 628 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)  
; IMMEDIATE SOURCE:  
; CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..628 /note= "shown are the first  
; OTHER INFORMATION: 628 nt of the 5' non-translated region of  
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 610 /note= "non-authentic sequence  
; OTHER INFORMATION: due to a base pair substitution from C to G  
; OTHER INFORMATION: at position 610"  
; PUBLICATION INFORMATION:  
; AUTHORS: Sarnow, P.  
; JOURNAL: J. Virol.  
; VOLUME: 63  
; PAGES: 467-470  
; DATE: 1989  
US-08-387-845-5

Query Match 100.0%; Score 19; DB 2; Length 628;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 451 CCCCTGAATGCGGCTAATC 469

## RESULT 3

US-08-778-275-5  
; Sequence 5, Application US/08778275  
; Patent No. 5935819  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a  
; TITLE OF INVENTION: bicistronic vector system in mammalian cells  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,275  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,845  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 628 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORIGINAL SOURCE:  
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)  
; IMMEDIATE SOURCE:  
; CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 1..628 /note= "shown are the first  
; OTHER INFORMATION: 628 nt of the 5' non-translated region of  
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"  
; FEATURE:  
; NAME/KEY: -  
; LOCATION: 610 /note= "non-authentic sequence  
; OTHER INFORMATION: due to a base pair substitution from C to G  
; OTHER INFORMATION: at position 610"  
; PUBLICATION INFORMATION:  
; AUTHORS: Sarnow, P.  
; JOURNAL: J. Virol.  
; VOLUME: 63  
; PAGES: 467-470  
; DATE: 1989  
US-08-778-275-5

Query Match 100.0%; Score 19; DB 2; Length 628;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 451 CCCCTGAATGCGGCTAATC 469

## RESULT 4

US-08-867-352-5  
; Sequence 5, Application US/08867352  
; Patent No. 6060273  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: Multicistronic expression units and their use  
; NUMBER OF SEQUENCES: 25  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,352  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,847  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 628 base pairs  
; TYPE: nucleic acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-S-Polio (M) (4708 bp), (Sarnow, 1989)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..628 /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at Location 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
; US-08-867-352-5

Query Match 100.0%; Score 19; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 451 CCCCTGAATGGCGCTAATC 469

RESULT 5
US-09-116-032-2
; Sequence 2, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
; APPLICANT: CHANG, EDWARD L.
; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND
; TITLE OF INVENTION: PREPARATION PROCESS AND USE THEREOF
; FILE REFERENCE: 9751.79US01
; CURRENT APPLICATION NUMBER: US/09/116,032
; CURRENT FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: CHINA 86105814
; EARLIER FILING DATE: 1997-05-01
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1220
; TYPE: DNA
; ORGANISM: SWINE VESICULAR DISEASE VIRUS
US-09-116-032-2

Query Match 100.0%; Score 19; DB 3; Length 1220;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 454 CCCCTGAATGGCGCTAATC 472

RESULT 6
US-09-724-678D-16
; Sequence 16, Application US/09724678D
```

```
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the
; TITLE OF INVENTION: and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 16
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-09-724-678D-16

Query Match 100.0%; Score 19; DB 3; Length 1560;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 456 CCCCTGAATGGCGCTAATC 474

RESULT 7
US-09-202-904A-10
; Sequence 10, Application US/09202904A
; Patent No. 6395471
; GENERAL INFORMATION:
; APPLICANT: Kang, Sung Key
; APPLICANT: Hahn, Bumsuk
; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant
; TITLE OF INVENTION: Gene and a Use Thereof
; FILE REFERENCE: A32210-PCT-USA 072944.0104
; CURRENT APPLICATION NUMBER: US/09/202,904A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/KR97/00120
; PRIOR FILING DATE: 1997-06-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genetically engineered virus derived from
; OTHER INFORMATION: poliovirus and hepatitis C virus
US-09-202-904A-10

Query Match 100.0%; Score 19; DB 3; Length 2320;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
Db 451 CCCCTGAATGGCGCTAATC 469

RESULT 8
US-09-116-032-1
; Sequence 1, Application US/09116032
; Patent No. 6200576
; GENERAL INFORMATION:
; APPLICANT: HWONG, CHING LONG
; APPLICANT: LO, CHENG-KAI
; APPLICANT: YANG, YING-CHUAN
; APPLICANT: JENG, KING-SONG
```

APPLICANT: CHANG, EDWARD L.  
; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY  
; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND  
; FILE REFERENCE: 9751.79US01  
; CURRENT APPLICATION NUMBER: US/09/116,032  
; EARLIER FILING DATE: 1998-07-15  
; EARLIER APPLICATION NUMBER: CHINA 86105814  
; NUMBER OF SEQ ID NOS: 39  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1  
; LENGTH: 7400  
; TYPE: DNA  
; ORGANISM: SWINE VESICULAR DISEASE VIRUS  
US-09-116-032-1

Query Match 100.0%; Score 19; DB 3; Length 7400;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 454 CCCCTGAATGCGGCTAATC 472

RESULT 9  
US-09-284-349B-1  
; Sequence 1, Application US/09284349B  
; Patent No. 6696289  
; GENERAL INFORMATION:  
; APPLICANT: Yong Soo, Bae  
; APPLICANT: Jung, Hye Rhan  
; TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain  
; FILE REFERENCE: Docket No. 6696289; 4220-109 US  
; CURRENT APPLICATION NUMBER: US/09/284,349B  
; CURRENT FILING DATE: 1999-06-04  
; PRIOR APPLICATION NUMBER: PCT/KR98/00242  
; PRIOR FILING DATE: 1998-07-08  
; PRIOR APPLICATION NUMBER: KR 97/37812  
; PRIOR FILING DATE: 1997-07-08  
; NUMBER OF SEQ ID NOS: 30  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 7441  
; TYPE: DNA  
; ORGANISM: Human poliovirus 1  
US-09-284-349B-1

Query Match 100.0%; Score 19; DB 3; Length 7441;  
Best Local Similarity 100.0%; Pred. No. 1.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 451 CCCCTGAATGCGGCTAATC 469

RESULT 10  
US-09-311-260-105  
; Sequence 105, Application US/09311260  
; Patent No. 6214555  
; GENERAL INFORMATION:  
; APPLICANT: Leushner, James  
; APPLICANT: Hui, May  
; APPLICANT: Dunn, James M.  
; APPLICANT: Lacroix, Jean-Michel  
; TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR DETECTION OF  
; TITLE OF INVENTION: MICROORGANISMS AND BI-DIRECTIONAL SEQUENCING OF NUCLEIC ACID  
; TITLE OF INVENTION: POLYMERS  
; NUMBER OF SEQUENCES: 189  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Oppedahl & Larson LLP

STREET: P.O. Box 5270  
CITY: Frisco  
STATE: CO  
COUNTRY: US  
ZIP: 80443-5270  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/311,260  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-058-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 668-2050  
TELEFAX: (970) 668-2082  
TELEX:  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: yes  
FRAGMENT TYPE: internal  
US-09-311-260-105

Query Match 94.7%; Score 18; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18  
Db 8 CCCCTGAATGCGGCTAAT 25

RESULT 11  
US-09-061-273-9  
; Sequence 9, Application US/09061273  
; Patent No. 6258570  
; GENERAL INFORMATION:  
; APPLICANT: Glustein, Joseph Z.  
; APPLICANT: Ehrlich, Garth D.  
; APPLICANT: Zhang, Yingze  
; TITLE OF INVENTION: PCR Assay For Bacterial and  
; TITLE OF INVENTION: Viral Meningitis  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: University of Pittsburgh  
STREET: Office of Technology Transfer  
STREET: 911 William Pitt Union  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15260  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" high density diskette  
COMPUTER: IBM PC or compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/061,273  
FILING DATE: 17-APR-1998

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: No. 6258570 applicable
; FILING DATE: No. 6258570 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary-Elizabeth Buckles
; REGISTRATION NUMBER: 31,907
; REFERENCE/DOCKET NUMBER: 017917/20132
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/414-3267
; TELEFAX: 202/414/9299
; TELEX: 64711
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: synthetic DNA
US-09-061-273-9

Query Match          94.7%; Score 18; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 8 CCCCTGAATCGGCTAAT 25

RESULT 12
US-09-313-221A-114
; Sequence 114, Application US/09313221A
; Patent No. 6468743
; GENERAL INFORMATION:
; APPLICANT: Thomas L. Romick (Inventor)
; APPLICANT: Mark S. Fraser (Inventor)
; TITLE OF INVENTION: PCR TECHNIQUES FOR DETECTING MICROBIAL
; TITLE OF INVENTION: AND VIRAL CONTAMINANTS IN FOODSTUFFS
; FILE REFERENCE: HUNT-042784
; CURRENT APPLICATION NUMBER: US/09/313.221A
; CURRENT FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: US 60/086,025
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 114
; LENGTH: 44
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Related to Entoviruses
US-09-313-221A-114

Query Match          94.7%; Score 18; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 8 CCCCTGAATCGGCTAAT 25

RESULT 13
US-07-852-260-1
; Sequence 1, Application US/07852260
; Patent No. 5525715
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
```

```
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/852,260
; FILING DATE: 19920619
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-07-852-260-1

Query Match          94.7%; Score 18; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAAT 18
   |||||
Db 454 CCCCTGAATCGGCTAAT 471

RESULT 14
US-08-461-503-1
; Sequence 1, Application US/08461503
; Patent No. 5834302
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
; TITLE OF INVENTION: FROM CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
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;; FILING DATE: 5-JUN-1995  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: White, John P.  
;; REGISTRATION NUMBER: 28,678  
;; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (212) 278-0400  
;; TELEFAX: (212) 391-0525  
;; INFORMATION FOR SEQ ID NO: 1:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7432 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 743..7361  
US-08-461-503-1

Query Match 94.7%; Score 18; DB 2; Length 7432;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAAT 18  
|||||  
DB 454 CCCCTGAATGGCGCTAAT 471

RESULT 15  
US-08-465-250-1  
; Sequence 1, Application US/08465250  
; Patent No. 6136570  
; GENERAL INFORMATION:  
; APPLICANT: Racaniello, Vincent  
; APPLICANT: Tatem, Joanne M.  
; APPLICANT: Weeks-Levy, Carolyn L.  
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM  
; TITLE OF INVENTION: CDNA  
; NUMBER OF SEQUENCES: 9  
; CORRESPONDENCE ADDRESS:  
; STREET: Cooper & Dunham LLP  
; CITY: New York  
; STATE: New York  
; COUNTRY: U.S.A.  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release 1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/465,250  
; FILING DATE: 6-JUN-1995  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 36607-E-PCT-US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 278-0400  
; TELEFAX: (212) 391-0525  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7432 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single

;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 743..7361  
US-08-465-250-1

Query Match 94.7%; Score 18; DB 3; Length 7432;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAAT 18  
|||||  
DB 454 CCCCTGAATGGCGCTAAT 471

RESULT 16  
US-08-221-816B-31  
; Sequence 31, Application US/08221816B  
; Patent No. 5738985  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; APPLICANT: Mathews, Michael B.  
; APPLICANT: Katze, Michael G.  
; APPLICANT: Witherell, Gary  
; APPLICANT: Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; TITLE OF INVENTION: OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; STREET: Pennie & Edmonds  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,816B  
; FILING DATE: 01-APR-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7960-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 627 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
US-08-221-816B-31

Query Match 91.6%; Score 17.4; DB 2; Length 627;  
Best Local Similarity 78.9%; Pred. No. 7.8;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19  
|||||  
DB 457 CCCUGAUGCGCUAAC 475



## RESULT 17

US-10-112-547-31  
; Sequence 31, Application US/10112547  
; Patent No. 6579674  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/112,547  
; FILING DATE: 28-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,816B  
; FILING DATE: 01-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7960-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 627 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-112-547-31  
  
Query Match 91.6%; Score 17.4; DB 3; Length 627;  
Best Local Similarity 78.9%; Pred. No. 7.8;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | : | | | | | : | |  
Db 457 CCCUGAUGCGCUAAC 475  
  
RESULT 18  
US-10-112-241-31  
; Sequence 31, Application US/10112241  
; Patent No. 6623961  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/112,241  
; FILING DATE: 28-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,816B  
; FILING DATE: 01-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7960-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 627 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-112-241-31  
  
Query Match 91.6%; Score 17.4; DB 3; Length 627;  
Best Local Similarity 78.9%; Pred. No. 7.8;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | : | | | | | : | |  
Db 457 CCCUGAUGCGCUAAC 475  
  
RESULT 19  
US-10-104-611-31  
; Sequence 31, Application US/10104611  
; Patent No. 6667152  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/104,611  
; FILING DATE: 22-Mar-2002

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;
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816B
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||:||||:||||:|
Db 457 CCCUGAAGCGGCUAAC 475

RESULT 20
US-10-109-368-31
; Sequence 31, Application US/10109368
; Patent No. 677179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||:||||:||||:|
Db 457 CCCUGAAGCGGCUAAC 475

RESULT 20
US-10-109-368-31
; Sequence 31, Application US/10109368
; Patent No. 677179
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-104-611-31
```

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;
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||:||||:||||:|
Db 457 CCCUGAAGCGGCUAAC 475

RESULT 21
US-09-724-380-31
; Sequence 31, Application US/09724380
; Patent No. 6824976
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/724,380
; FILING DATE: 01-APR-1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-09-724-380-31

Query Match          91.6%; Score 17.4; DB 3; Length 627;
Best Local Similarity 78.9%; Pred. No. 7.8;
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||:||||:||||:|
```

```
Db 457 CCCUGAUGCGGCUAACC 475

RESULT 22
US-08-246-373-1
; Sequence 1, Application US/08246373
; Patent No. 5550018
; GENERAL INFORMATION:
; APPLICANT: LEVENBOOK, Inessa
; APPLICANT: CHUMAKOV, Konstantin
; APPLICANT: POWERS, Laurie
; APPLICANT: RONINSON, Igor
; TITLE OF INVENTION: "TEST FOR VIRULENT REVERTANTS IN
; TITLE OF INVENTION: ATTENUATED LIVE VACCINES"
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH
; STREET: 301 No. 5550018th Washington Street
; CITY: Falls Church
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22040-0747
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/246.373
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/607,742
; FILING DATE: No. 5550018ember 6, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Gerald M. Murphy, Jr.
; REGISTRATION NUMBER: 28,977
; REFERENCE/DOCKET NUMBER: 1173-234P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 241-1300
; TELEFAX: (703) 241-0369
; TELEX: 248345
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: sense strand PCR primer
; ANTI-SENSE: (N)
; US-08-246-373-1

Query Match 86.3%; Score 16.4; DB 2; Length 32;
Best Local Similarity 94.4%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18
| | | | | | | | | | | | | | | |
Db 15 CCCCTGAATGCGGCTGAT 32
| | | | | | | | | | | | | | | |

RESULT 23
5340713-1
; Patent No. 5340713
; APPLICANT: TORGENSEN, HELGE; SKERN, TIMOTHY; BLAAS, DIETER
; TITLE OF INVENTION: PROCESS FOR THE CHARACTERIZATION OF
; HUMAN RHINOVIRUSES
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/541,907
; FILING DATE: 22-JUN-1990
; SEQ ID NO: 1:

; LENGTH: 250
5340713-1

Query Match 83.2%; Score 15.8; DB 9; Length 250;
Best Local Similarity 89.5%; Pred. No. 52;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 202 CCCTGAATGCGCTAACC 220
| | | | | | | | | | | | | | | |

RESULT 24
US-09-489-039A-5242
; Sequence 5242, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 5242
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-5242

Query Match 81.1%; Score 15.4; DB 3; Length 1269;
Best Local Similarity 94.1%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
| | | | | | | | | | | | | | | |
Db 1067 CGCTGAATGCGGCTAAT 1083
| | | | | | | | | | | | | | | |

RESULT 25
US-09-949-016-15436
; Sequence 15436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15436
; LENGTH: 199945
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15436

Query Match 81.1%; Score 15.4; DB 3; Length 199945;
Best Local Similarity 94.1%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
| | | | | | | | | | | | | | | |
Db 168571 CCCTGAATGCGGCTAAT 168587
| | | | | | | | | | | | | | | |
```

RESULT 26  
US-08-361-337-36  
; Sequence 36, Application US/08361337  
; Patent No. 5728519  
; GENERAL INFORMATION:  
; APPLICANT: Levenbook, Inessa S.  
; APPLICANT: Chumakov, Konstantin M.  
; APPLICANT: No. 5728519wood, Laurie P.  
; APPLICANT: Roninson, Igor  
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NEEDLE & ROSENBERG, P.C.  
; STREET: 127 Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/361.337  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 1414.634  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 36:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
US-08-361-337-36  
Query Match 78.9%; Score 15; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCT 15  
Db 21 CCCCTGAATGCGGCT 35

RESULT 27  
US-08-361-337-38  
; Sequence 38, Application US/08361337  
; Patent No. 5728519  
; GENERAL INFORMATION:  
; APPLICANT: Levenbook, Inessa S.  
; APPLICANT: Chumakov, Konstantin M.  
; APPLICANT: No. 5728519wood, Laurie P.  
; APPLICANT: Roninson, Igor  
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF  
; NUMBER OF SEQUENCES: 77  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: NEEDLE & ROSENBERG, P.C.  
; STREET: 127 Peachtree Street, N.E.  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA

; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; FILING DATE: US/08/361.337  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Perryman, David G.  
; REGISTRATION NUMBER: 33,438  
; REFERENCE/DOCKET NUMBER: 1414.634  
; TELEPHONE: (404) 688-0770  
; TELEFAX: (404) 688-9880  
; INFORMATION FOR SEQ ID NO: 38:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 35 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Other nucleic acid  
US-08-361-337-38

Query Match 78.9%; Score 15; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19  
Db 1 TGAATGCGGCTAATC 15

RESULT 28  
US-09-949-016-34646  
; Sequence 34646, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949.016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 34646  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-34646

Query Match 77.9%; Score 14.8; DB 3; Length 601;  
Best Local Similarity 88.9%; Pred. No. 2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
Db 393 CCCTGAATGCGGCTGATC 410

RESULT 29  
US-09-949-016-146512/c  
; Sequence 146512, Application US/09949016  
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 146512
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-146512

Query Match          77.9%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18
   |||||
Db 580 CCCCTGAATGCAACTAAT 563

RESULT 30
US-09-949-016-170260
; Sequence 170260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 170260
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-170260

Query Match          77.9%; Score 14.8; DB 3; Length 601;
Best Local Similarity 88.9%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
   |||||
Db 393 CCCTGAATGCGGCTAATC 410

RESULT 31
US-09-270-767-13998/c
; Sequence 13998, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
```

```
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13998
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13998

Query Match          77.9%; Score 14.8; DB 3; Length 678;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
   |||||
Db 299 CTCTGAATGTGGCTAATC 282

RESULT 32
US-09-270-767-13244
; Sequence 13244, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13244
; LENGTH: 960
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-13244

Query Match          77.9%; Score 14.8; DB 3; Length 960;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
   |||||
Db 689 CTCTGAATGTGGCTAATC 706

RESULT 33
US-09-614-221A-478/c
; Sequence 478, Application US/09614221A
; Patent No. 6723837
; GENERAL INFORMATION:
; APPLICANT: Karunanandaa, Balasulojini
; APPLICANT: Yu, Jaehyuk
; APPLICANT: Kishore, Ganesh M.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED
; TITLE OF INVENTION: WITH STEROL SYNTHESIS AND METABOLISM
; FILE REFERENCE: 16516.075
; CURRENT APPLICATION NUMBER: US/09/614,221A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/142,981
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 626
; SEQ ID NO 478
; LENGTH: 4086
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-614-221A-478

Query Match          77.9%; Score 14.8; DB 3; Length 4086;
Best Local Similarity 88.9%; Pred. No. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
   |||||
```

Db 408 CCTGATCGCGCAGATC 391

## RESULT 34

US-09-453-702B-194  
; Sequence 194, Application US/09453702B  
; Patent No. 6365723

## GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.  
Burland, Valerie  
Perna, Nicole T.  
Plunkett, Guy  
Welch, Rod

TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI

COUNTRY: US

ZIP: 53701-2113

## COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Word Perfect 8.0

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/453,702B

FILING DATE: 03-Dec-1999

CLASSIFICATION: <Unknown>

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/110,955

FILING DATE: 04-DEC-1998

## ATTORNEY/AGENT INFORMATION:

NAME: Seay, Nicholas J.

REGISTRATION NUMBER: 27386

REFERENCE/DOCKET NUMBER: 960296.95017

TELECOMMUNICATION INFORMATION:

TELEPHONE: (608) 251-5000

TELEFAX: (608) 251-9166

## INFORMATION FOR SEQ ID NO: 194:

SEQUENCE CHARACTERISTICS:

LENGTH: 9057

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 194:

US-09-453-702B-194

Query Match 77.9%; Score 14.8; DB 3; Length 9057;  
Best Local Similarity 88.9%; Pred. No. 2.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGATCGCGCTAATC 19

Db 4504 CACTGATCGCGCTAATC 4521

## RESULT 35

US-10-114-170-194

; Sequence 194, Application US/10114170

; Patent No. 6855814

## GENERAL INFORMATION:

APPLICANT: Blattner, Frederick R.  
Burland, Valerie  
Perna, Nicole T.  
Plunkett, Guy  
Welch, Rod

TITLE OF INVENTION: No. 6855814el Sequences of E. coli 0157

NUMBER OF SEQUENCES: 265

CORRESPONDENCE ADDRESS:

ADDRESSEE: Quarles & Brady  
STREET: 1 South Pinckney Street  
CITY: Madison  
STATE: WI  
COUNTRY: US  
ZIP: 53701-2113  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 8.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/114,170  
FILING DATE: 01-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/453,702  
FILING DATE: 03-DEC-1999  
APPLICATION NUMBER: 60/110,955  
FILING DATE: 04-DEC-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Seay, Nicholas J.  
REGISTRATION NUMBER: 27386  
REFERENCE/DOCKET NUMBER: 960296.95017  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (608) 251-5000  
TELEFAX: (608) 251-9166  
INFORMATION FOR SEQ ID NO: 194:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 9057  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 194:  
US-10-114-170-194

Query Match 77.9%; Score 14.8; DB 3; Length 9057;  
Best Local Similarity 88.9%; Pred. No. 2.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGATCGCGCTAATC 19

Db 4504 CACTGATCGCGCTAATC 4521

## RESULT 36

US-08-611-280-4/c

; Sequence 4, Application US/08611280

; Patent No. 5891666

## GENERAL INFORMATION:

APPLICANT: Matsuyama, Toshifumi

APPLICANT: Grossman, Alex

APPLICANT: Richardson, Christopher D.

TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:

ADDRESSEE: Amgen Canada Inc.

STREET: 6733 Mississauga Road, Suite 303

CITY: Mississauga

STATE: Ontario

COUNTRY: Canada

ZIP: L5N 6J8

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

## CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/611,280

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oleski, Nancy A.  
REGISTRATION NUMBER: 34,688  
REFERENCE/DOCKET NUMBER: A-338A  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12537 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-611-280-4

Query Match 77.9%; Score 14.8; DB 2; Length 12537;  
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19  
|||||  
Db 1565 CCCTGAATGCTGCTAACC 1548

## RESULT 37

US-09-195-940-4/c  
Sequence 4, Application US/09195940  
Patent No. 6258935

GENERAL INFORMATION:  
APPLICANT: Matsuyama, Toshifumi  
APPLICANT: Grossman, Alex  
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Canada Inc.  
STREET: 6733 Mississauga Road, Suite 303  
CITY: Mississauga  
STATE: Ontario  
COUNTRY: Canada  
ZIP: L5N 6J8

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/195,940  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/611,280  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Oleski, Nancy A.  
REGISTRATION NUMBER: 34,688  
REFERENCE/DOCKET NUMBER: A-338A  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12537 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-195-940-4

Query Match 77.9%; Score 14.8; DB 3; Length 12537;  
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19  
|||||  
Db 1565 CCCTGAATGCTGCTAACC 1548

## RESULT 38

US-09-562-466-4/c  
Sequence 4, Application US/09562466  
Patent No. 6369202

GENERAL INFORMATION:  
APPLICANT: Matsuyama, Toshifumi  
APPLICANT: Grossman, Alex  
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Canada Inc.  
STREET: 6733 Mississauga Road, Suite 303  
CITY: Mississauga  
STATE: Ontario  
COUNTRY: Canada  
ZIP: L5N 6J8

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/562,466  
FILING DATE: 01-May-2000  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/195,940  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Oleski, Nancy A.  
REGISTRATION NUMBER: 34,688  
REFERENCE/DOCKET NUMBER: A-338A  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 12537 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-562-466-4  
Query Match 77.9%; Score 14.8; DB 3; Length 12537;  
Best Local Similarity 88.9%; Pred. No. 3e+02; Indels 0; Gaps 0;  
Matches 16; Conservative 0; Mismatches 2;

Qy 2 CCCTGAATGCGGCTAATC 19  
|||||  
Db 1565 CCCTGAATGCTGCTAACC 1548

## RESULT 39

US-09-949-016-17245/c  
Sequence 17245, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 17245  
LENGTH: 16083  
TYPE: DNA



ORGANISM: Human  
US-09-949-016-17245

Query Match 77.9%; Score 14.8; DB 3; Length 16083;  
Best Local Similarity 88.9%; Pred. No. 3.1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAAT 18  
Db 15339 CCCCTGAATGGCGCGAAT 15322

RESULT 40

US-10-164-230-2/c  
; Sequence 2, Application US/10164230  
; Patent No. 6933118  
; GENERAL INFORMATION:  
; APPLICANT: Inoko, Hidetoshi  
; APPLICANT: Tamiya, Gen  
; TITLE OF INVENTION: METHOD OF TESTING FOR PSORIASIS VULGARIS  
; FILE REFERENCE: 06501-112US1  
; CURRENT APPLICATION NUMBER: US/10/164,230  
; PRIOR FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: PCT/JP00/08624  
; PRIOR FILING DATE: 2000-12-06  
; PRIOR APPLICATION NUMBER: JP 11/346867  
; PRIOR FILING DATE: 1999-12-06  
; NUMBER OF SEQ ID NOS: 63  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 25235  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: exon  
; LOCATION: (1)....(420)  
; NAME/KEY: exon  
; LOCATION: (1282)....(1405)  
; NAME/KEY: exon  
; LOCATION: (1602)....(1702)  
; NAME/KEY: exon  
; LOCATION: (1602)....(1631)  
; NAME/KEY: exon  
; LOCATION: (2352)....(2364)  
; NAME/KEY: exon  
; LOCATION: (6287)....(6509)  
; NAME/KEY: exon  
; LOCATION: (10417)....(10493)  
; NAME/KEY: exon  
; LOCATION: (14244)....(14407)  
; NAME/KEY: exon  
; LOCATION: (14244)....(14344)  
; NAME/KEY: exon  
; LOCATION: (25190)....(25235)

Query Match 77.9%; Score 14.8; DB 3; Length 25235;  
Best Local Similarity 88.9%; Pred. No. 3.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAAT 18  
Db 18057 CCCCTGAATGGCGCTAAT 18040

RESULT 41

US-09-949-016-16549  
; Sequence 16549, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16549  
; LENGTH: 47555  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-16549

Query Match 77.9%; Score 14.8; DB 3; Length 47555;  
Best Local Similarity 88.9%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAATC 19  
Db 30940 CCCTGAATGGCGCTGATC 30957

RESULT 42

US-09-949-016-12598  
; Sequence 12598, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12598  
; LENGTH: 49673  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-12598

Query Match 77.9%; Score 14.8; DB 3; Length 49673;  
Best Local Similarity 88.9%; Pred. No. 3.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAATC 19  
Db 30940 CCCTGAATGGCGCTGATC 30957

RESULT 43

US-09-949-016-17433/c  
; Sequence 17433, Application US/09949016  
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17433
; LENGTH: 101349
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17433

Query Match          77.9%; Score 14.8; DB 3; Length 101349;
Best Local Similarity 88.9%; Pred. No. 3.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
Db 79405 CCCTGAAGGCGAGCTAATC 79388

RESULT 44
US-09-949-016-13765
; Sequence 13765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13765
; LENGTH: 128470
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13765

Query Match          77.9%; Score 14.8; DB 3; Length 128470;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
Db 6099 CCCTGAATGCTTCTAATC 6116

RESULT 45
US-09-949-016-15890/c
; Sequence 15890, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
```

```
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15890
; LENGTH: 144922
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15890

Query Match          77.9%; Score 14.8; DB 3; Length 144922;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
Db 70425 CCCTGAATGCGTCAATC 70408

RESULT 46
US-09-949-016-15858
; Sequence 15858, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 15858
; LENGTH: 145320
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15858

Query Match          77.9%; Score 14.8; DB 3; Length 145320;
Best Local Similarity 88.9%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAAT 18
Db 30228 CCCTGAATGCACTAAT 30245

RESULT 47
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
```

```
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          77.9%; Score 14.8; DB 3; Length 4403765;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
    |||||
Db 1547708 CCTGAATGCGGGAATC 1547691

RESULT 48
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          77.9%; Score 14.8; DB 3; Length 4411529;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
    |||||
Db 1547869 CCTGAATGCGGGAATC 1547852

RESULT 49
US-09-702-705-1724
; Sequence 1724, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121-478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833

; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          77.9%; Score 14.8; DB 3; Length 4403765;
Best Local Similarity 88.9%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
    |||||
Db 1547708 CCTGAATGCGGGAATC 1547691

RESULT 48
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          77.9%; Score 14.8; DB 3; Length 4411529;
Best Local Similarity 88.9%; Pred. No. 3.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAATC 19
    |||||
Db 1547869 CCTGAATGCGGGAATC 1547852

RESULT 49
US-09-702-705-1724
; Sequence 1724, Application US/09702705
; Patent No. 6504010
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121-478C14
; CURRENT APPLICATION NUMBER: US/09/702,705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-702-705-1724

Query Match          75.8%; Score 14.4; DB 3; Length 145;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAAT 18
    |||||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 50
US-09-736-457-1724
; Sequence 1724, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121-478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1724
; LENGTH: 145
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(145)
; OTHER INFORMATION: n = A,T,C or G
US-09-736-457-1724

Query Match          75.8%; Score 14.4; DB 3; Length 145;
Best Local Similarity 88.2%; Pred. No. 2.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCTGAATGCGGCTAAT 18
    |||||
Db 116 CCATGNATGCGGCTAAT 132

RESULT 51
US-09-671-325-1724
; Sequence 1724, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
```

; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C12  
; CURRENT APPLICATION NUMBER: US/09/671,325  
; CURRENT FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 1825  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1724  
; LENGTH: 145  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(145)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-671-325-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18  
||| ||||| ||||| |||||  
Db 116 CCATGNATGCGGCTAAT 132

RESULT 52  
US-09-658-824-1724

; Sequence 1724, Application US/09658824  
; Patent No. 6746846  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.478C11  
; CURRENT APPLICATION NUMBER: US/09/658,824  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 1788  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1724  
; LENGTH: 145  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(145)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-658-824-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18  
||| ||||| ||||| |||||  
Db 116 CCATGNATGCGGCTAAT 132

RESULT 53  
US-10-017-754-1724

; Sequence 1724, Application US/10017754  
; Patent No. 6858204  
; GENERAL INFORMATION:  
; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Carter, Darrick  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedvick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; FILE REFERENCE: 210121.478C18  
; CURRENT APPLICATION NUMBER: US/10/017,754  
; CURRENT FILING DATE: 2001-10-29  
; NUMBER OF SEQ ID NOS: 2004  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1724  
; LENGTH: 145  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 4, 12, 27, 32, 45, 47, 48, 59, 61, 65, 93, 98, 103, 121  
; OTHER INFORMATION: n = A,T,C or G  
US-10-017-754-1724

Query Match 75.8%; Score 14.4; DB 3; Length 145;  
Best Local Similarity 88.2%; Pred. No. 2.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18  
||| ||||| ||||| |||||  
Db 116 CCATGNATGCGGCTAAT 132

RESULT 54

US-09-270-767-27427  
; Sequence 27427, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 27427  
; LENGTH: 671  
; TYPE: DNA  
; ORGANISM: *Drosophila melanogaster*  
; FEATURE:  
; OTHER INFORMATION: n means any nucleotide  
US-09-270-767-27427

Query Match 75.8%; Score 14.4; DB 3; Length 671;  
Best Local Similarity 93.8%; Pred. No. 3.4e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19  
||| ||||| ||||| |||||  
Db 79 CTGAATGCGGCTAATC 94

RESULT 55

US-09-902-540-8469  
; Sequence 8469, Application US/09902540  
; Patent No. 6833447  
; GENERAL INFORMATION:  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.

```

; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8469
; LENGTH: 1494
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-8469

Query Match      75.8%; Score 14.4; DB 3; Length 1494;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTA 16
DB 535 CCCCTGAATGGCGGTA 550

RESULT 56
US-09-221-017B-461/c
; Sequence 461, Application US/09221017B
; Patent No. 6444799
; GENERAL INFORMATION:
; APPLICANT: Ross, Bruce C.
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF
; NUMBER OF SEQUENCES: 1120
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/221,017B
; FILING DATE: 23-DEC-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1182
; FILING DATE: 31-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP1546
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PP2911
; FILING DATE: 09-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU98/01023
; FILING DATE: 10-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Montoy, Gladys H
; REGISTRATION NUMBER: 32,430
; REFERENCE/DOCKET NUMBER: 27340-20021.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-813-5600
; TELEFAX: 650-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 461:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1660 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double

```

```

; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: UNKNOWN
; ORIGINAL SOURCE:
; ORGANISM: PORYPHYROMONAS GINGIVALIS
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1...1660
US-09-221-017B-461

Query Match      75.8%; Score 14.4; DB 3; Length 1660;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGAATGGCGCTAATC 19
DB 327 CTGAATGGCGCTAAGC 312

RESULT 57
US-09-270-767-11790
; Sequence 11790, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11790
; LENGTH: 2058
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: n means any nucleotide
US-09-270-767-11790

Query Match      75.8%; Score 14.4; DB 3; Length 2058;
Best Local Similarity 93.8%; Pred. No. 3.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 CTGAATGGCGCTAATC 19
DB 79 CTGAATGGCGATAATC 94

RESULT 58
US-09-902-540-891
; Sequence 891, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 891
; LENGTH: 6380
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-891

Query Match      75.8%; Score 14.4; DB 3; Length 6380;
Best Local Similarity 93.8%; Pred. No. 4.5e+02;

```

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTA 16  
 |||||  
 Db 1168 CCCCTGAATCGGCTA 1183

RESULT 59

US-09-524-101D-18  
 ; Sequence 18, Application US/09524101D  
 ; Patent No. 6762291  
 ; GENERAL INFORMATION:  
 ; APPLICANT: EXELIXIS, INC.  
 ; TITLE OF INVENTION: INSECT P53 TUMOR SUPPRESSOR GENES AND PROTEINS  
 ; FILE REFERENCE: EX00015C FIRST AMENDMENT  
 ; CURRENT APPLICATION NUMBER: US/09/524,101D  
 ; CURRENT FILING DATE: 2000-03-13  
 ; PRIOR APPLICATION NUMBER: US 09/268,969  
 ; PRIOR FILING DATE: 1999-03-16  
 ; PRIOR APPLICATION NUMBER: US 60/184,373  
 ; PRIOR FILING DATE: 2000-02-23  
 ; NUMBER OF SEQ ID NOS: 35  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 18  
 ; LENGTH: 27425  
 ; TYPE: DNA  
 ; ORGANISM: Drosophila melanogaster  
 US-09-524-101D-18

Query Match 75.8%; Score 14.4; DB 3; Length 27425;  
 Best Local Similarity 93.8%; Pred. No. 5.4e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATCGGCTAATC 19  
 |||||  
 Db 3535 CTGAATCGGCTAATC 3550

RESULT 60

US-09-949-016-12008/c  
 ; Sequence 12008, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 12008  
 ; LENGTH: 331814  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(331814)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-12008

Query Match 75.8%; Score 14.4; DB 3; Length 331814;  
 Best Local Similarity 93.8%; Pred. No. 6.9e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTGAATCGGCTAAT 18  
 |||||

Db 79048 CCTTAATCGGCTAAT 79033

RESULT 61

US-09-949-016-17056/c  
 ; Sequence 17056, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 17056  
 ; LENGTH: 331814  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)...(331814)  
 ; OTHER INFORMATION: n = A,T,C or G  
 US-09-949-016-17056

Query Match 75.8%; Score 14.4; DB 3; Length 331814;  
 Best Local Similarity 93.8%; Pred. No. 6.9e+02;  
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 CCTGAATCGGCTAAT 18  
 |||||

Db 79048 CCTTAATCGGCTAAT 79033

RESULT 62

US-09-513-999C-30496  
 ; Sequence 30496, Application US/09513999C  
 ; Patent No. 6783961  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dumas Milne Edwards, J.B.  
 ; APPLICANT: Duclert, A.  
 ; APPLICANT: Giordano, J.Y.  
 ; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 ; FILE REFERENCE: 59.US2.REG  
 ; CURRENT APPLICATION NUMBER: US/09/513,999C  
 ; CURRENT FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/122,487  
 ; PRIOR FILING DATE: 1999-02-26  
 ; NUMBER OF SEQ ID NOS: 36681  
 ; SOFTWARE: Patent.Pm  
 ; SEQ ID NO 30496  
 ; LENGTH: 403  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: 371  
 ; OTHER INFORMATION: n=a, g, c or t  
 US-09-513-999C-30496

Query Match 74.7%; Score 14.2; DB 3; Length 403;  
 Best Local Similarity 84.2%; Pred. No. 4.1e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19





; APPLICANT: Michael W. Rev  
 ; APPLICANT: Jeffrey R. Shuster  
 ; APPLICANT: Sakari Kauppinen  
 ; APPLICANT: Ib Groth Clausen  
 ; APPLICANT: Peter Bjørke Olsen  
 ; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
 ; FILE REFERENCE: 5849.200-US  
 ; CURRENT APPLICATION NUMBER: US/09/533,559  
 ; EARLIER FILING DATE: 2000-03-22  
 ; EARLIER FILING DATE: 1999-03-22  
 ; NUMBER OF SEQ ID NOS: 7860  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1622  
 ; LENGTH: 608  
 ; TYPE: DNA  
 ; ORGANISM: Fusarium venenatum  
 ; FEATURE:  
 ; NAME/KEY: misc.feature  
 ; LOCATION: (1)...(608)  
 ; OTHER INFORMATION: n = A,T,C or G  
 ; US-09-533-559-1622

Query Match 74.7%; Score 14.2; DB 3; Length 608;  
 Best Local Similarity 84.2%; Pred. No. 4.3e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 ||| ||||| ||||| |||||  
 Db 208 CCCAAGAATCGGCCAATC 226

RESULT 68  
 US-09-489-039A-5060  
 ; Sequence 5060, Application US/09489039A  
 ; Patent No. 6610836  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gary Breton et. al  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
 ; FILE REFERENCE: 2709.2004001  
 ; CURRENT APPLICATION NUMBER: US/09/489,039A  
 ; CURRENT FILING DATE: 2000-01-27  
 ; PRIOR APPLICATION NUMBER: US 60/117,747  
 ; PRIOR FILING DATE: 1999-01-29  
 ; NUMBER OF SEQ ID NOS: 14342  
 ; SEQ ID NO 5060  
 ; LENGTH: 1020  
 ; TYPE: DNA  
 ; ORGANISM: Klebsiella pneumoniae  
 ; US-09-489-039A-5060

Query Match 74.7%; Score 14.2; DB 3; Length 1020;  
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 ||| ||||| ||||| |||||  
 Db 508 CCGCTGATTGAGGCTAATC 526

RESULT 69  
 US-10-029-180-61/c  
 ; Sequence 61, Application US/10029180  
 ; Patent No. 6806082  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cali, Brian M.  
 ; APPLICANT: Holtzman, Doug  
 ; APPLICANT: Madden, Kevin T.  
 ; APPLICANT: Milna, G. Todd  
 ; APPLICANT: Sherman, Amir  
 ; APPLICANT: Silva, Jeffrey C.

; APPLICANT: Trueheart, Josh  
 ; APPLICANT: Zhang, Lixin  
 ; TITLE OF INVENTION: No. 6806082el Regulators of Fungal Gene Expression  
 ; FILE REFERENCE: MIC-004  
 ; CURRENT APPLICATION NUMBER: US/10/029,180  
 ; CURRENT FILING DATE: 2001-12-22  
 ; PRIOR APPLICATION NUMBER: US 60/257,431  
 ; PRIOR FILING DATE: 2000-12-22  
 ; NUMBER OF SEQ ID NOS: 138  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 61  
 ; LENGTH: 1095  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: fungal gene  
 ; US-10-029-180-61

Query Match 74.7%; Score 14.2; DB 3; Length 1095;  
 Best Local Similarity 84.2%; Pred. No. 4.6e+02;  
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 ||| ||||| ||||| |||||  
 Db 418 CCTCTGAATACGGCTCATC 400

RESULT 70  
 US-09-602-777A-393/c  
 ; Sequence 393, Application US/09602777A  
 ; Patent No. 6831165  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pompejus, Markus  
 ; APPLICANT: Kroger, Burkhard  
 ; APPLICANT: Schroder, Hartwig  
 ; APPLICANT: Zelder, Oskar  
 ; APPLICANT: Haberhauer, Gregor  
 ; TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS  
 ; TITLE OF INVENTION: INVOLVED IN HOMEOSTASIS AND ADAPTATION  
 ; FILE REFERENCE: BGI-128CP  
 ; CURRENT APPLICATION NUMBER: US/09/602,777A  
 ; CURRENT FILING DATE: 2000-06-23  
 ; PRIOR APPLICATION NUMBER: US 60/141031  
 ; PRIOR FILING DATE: 1999-06-25  
 ; PRIOR APPLICATION NUMBER: DE 19931636.8  
 ; PRIOR FILING DATE: 1999-07-08  
 ; PRIOR APPLICATION NUMBER: DE 19932125.6  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932126.4  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932127.2  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932128.0  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932129.9  
 ; PRIOR FILING DATE: 1999-07-19  
 ; PRIOR APPLICATION NUMBER: DE 19932226.0  
 ; PRIOR FILING DATE: 1999-07-09  
 ; PRIOR APPLICATION NUMBER: DE 19932920.6  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932922.2  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932924.9  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932928.1  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932930.3  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932933.8  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932935.4  
 ; PRIOR FILING DATE: 1999-07-14  
 ; PRIOR APPLICATION NUMBER: DE 19932973.7

```

/ FILING DATE:
/ CLASSIFICATION: 514
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Brook, David E.
/ REGISTRATION NUMBER: 22,592
/ REFERENCE/DOCKET NUMBER: CPI94-14
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617-861-6240
/ TELEFAX: 617-861-9540
/

```

; SEQ ID NO 4054

```
; LENGTH: 3344
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4054

Query Match          74.7%; Score 14.2; DB 3; Length 3344;
Best Local Similarity 84.2%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 2826 CCCAGAATGAGCCAAATC 2844

RESULT 74
US-09-566-921-63
; Sequence 63, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debora W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 63
; LENGTH: 3505
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 263336.12
US-09-566-921-63

Query Match          74.7%; Score 14.2; DB 3; Length 3505;
Best Local Similarity 84.2%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 2847 CCCAGAATGAGCCAAATC 2865

RESULT 75
US-09-949-016-16816
; Sequence 16816, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16816
; LENGTH: 8165
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16816

Query Match          74.7%; Score 14.2; DB 3; Length 8165;
Best Local Similarity 84.2%; Pred. No. 6e+02;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 13327 CCCCTGAATGCGGCTAAAC 13309

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 1339 CCCCTGAACGCGGCCAAGC 1357

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 76
US-09-949-016-13284/c
; Sequence 13284, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13284
; LENGTH: 9962
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13284

Query Match          74.7%; Score 14.2; DB 3; Length 9962;
Best Local Similarity 84.2%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 1051 CCCCTTAATGTGCTAATC 1033

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

RESULT 77
US-09-949-016-13659/c
; Sequence 13659, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13659
; LENGTH: 23105
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13659

Query Match          74.7%; Score 14.2; DB 3; Length 23105;
Best Local Similarity 84.2%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| ||||| |||||
Db 13327 CCCCTGAATGCGGCTAAAC 13309
```

```
RESULT 78
US-09-949-016-12582/c
; Sequence 12582, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12582
; LENGTH: 23108
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12582

Query Match          74.7%; Score 14.2; DB 3; Length 23108;
Best Local Similarity 84.2%; Pred. No. 6.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
DB 13330 CCCCTGAATGCGGTAAC 13312

RESULT 79
US-08-311-731A-124
; Sequence 124, Application US/08311731A
; Patent No. 6583266
; GENERAL INFORMATION:
; APPLICANT: SMITH, DOUGLAS
; APPLICANT: MAO, JEN-I
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES
; RELATING TO MYCOBACTERIUM TUBERCULOSIS AND LAPRAE FOR
; DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 411
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MASSACHUSETTS
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/311.731A
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 31,616
; REFERENCE/DOCKET NUMBER: C0044/7125
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/720-3500
; TELEFAX: 617/720-2441
; INFORMATION FOR SEQ ID NO: 124:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 36033 base pairs
```

```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: MYCOBACTERIUM LAPRAE
US-08-311-731A-124

Query Match          74.7%; Score 14.2; DB 3; Length 36033;
Best Local Similarity 84.2%; Pred. No. 7.1e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
DB 13061 CGCTTGAACGCGGCTAATC 13079

RESULT 80
US-09-949-016-12532/c
; Sequence 12532, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12532
; LENGTH: 49407
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(49407)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12532

Query Match          74.7%; Score 14.2; DB 3; Length 49407;
Best Local Similarity 84.2%; Pred. No. 7.4e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
   |||||
DB 26300 CTCCTGAATGCTGGTAATC 26282

RESULT 81
US-09-949-016-17045/c
; Sequence 17045, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```

RESULT 83
US-09-585-858-1
; Sequence 1, Application US/09585858
; Patent No. 6492161
; GENERAL INFORMATION:
; APPLICANT: Sigridur Hjorleifsdottir
; APPLICANT: Gudmundur O. Hreggvidsson
; APPLICANT: Olafur H. Fridjonsson
; APPLICANT: Arnthor Aevarsson
; APPLICANT: Jakob K. Kristjansson
; TITLE OF INVENTION: Bacteriophage RM378
; TITLE OF INVENTION: Host Organism
; FILE REFERENCE: 2739.1001-001
; CURRENT APPLICATION NUMBER: US/09/585,858
; CURRENT FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/137,120
; PRIOR FILING DATE: 1999-06-02

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RECORD 85
US-09-949-016-16476
; Sequence 16476, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTING
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 16476
; LENGTH: 141560
; TYPE: DNA

```

```
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(141560)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16476

Query Match          74.7%; Score 14.2; DB 3; Length 141560;
Best Local Similarity 84.2%; Pred. No. 8.2e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| ||||| |||||
DB 42787 CCCCTAATGCGGCTCAIC 42805

RESULT 86
US-09-949-016-15868
; Sequence 15868, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIORITY FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15868
; LENGTH: 374159
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15868

Query Match          74.7%; Score 14.2; DB 3; Length 374159;
Best Local Similarity 84.2%; Pred. No. 8.7e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
||||| ||||| ||||| |||||
DB 357750 CCCCTGAATGCGGCTAGTC 357768

RESULT 87
US-08-956-171E-136/c
; Sequence 136, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gil H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
US-08-956-171E-136

Query Match          73.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAATGCGGCTAAT 18
||||| ||||| ||||| |||||
DB 4156 TGAATGCGGCTAAT 4143

RESULT 88
US-08-781-986A-136/c
; Sequence 136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
```

```
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 136:
US-08-956-171E-136

Query Match          73.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 TGAATGCGGCTAAT 18
||||| ||||| ||||| |||||
DB 4156 TGAATGCGGCTAAT 4143

RESULT 88
US-08-781-986A-136/c
; Sequence 136, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11823 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-781-986A-136

Query Match      73.7%; Score 14; DB 3; Length 11823;
Best Local Similarity 100.0%; Pred. No. 8e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGGCGCTAAT 18
   |||||
Db 4156 TGAATGGCGCTAAT 4143

RESULT 89
US-09-270-767-8260
; Sequence 8260, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8260
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-8260

Query Match      72.6%; Score 13.8; DB 3; Length 300;
Best Local Similarity 88.2%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18
   |||||
Db 231 CCCAGATGGCGCTGAT 247

RESULT 90
US-09-270-767-23542
; Sequence 23542, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 23542
; LENGTH: 300
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-23542

Query Match      72.6%; Score 13.8; DB 3; Length 300;
Best Local Similarity 88.2%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18
   |||||
Db 231 CCCAGATGGCGCTGAT 247

RESULT 91
US-09-270-767-5089
; Sequence 5089, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
```

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; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5089
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-5089

Query Match      72.6%; Score 13.8; DB 3; Length 506;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCTGAATGGCGCTAATC 19
   |||||
Db 456 CCTGAATGGCGCTAGTC 472

RESULT 92
US-09-270-767-20371
; Sequence 20371, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20371
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-20371

Query Match      72.6%; Score 13.8; DB 3; Length 506;
Best Local Similarity 88.2%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 CCTGAATGGCGCTAATC 19
   |||||
Db 456 CCTGAATGGCGCTAGTC 472

RESULT 93
US-07-998-289B-9/c
; Sequence 9, Application US/07998289B
; Patent No. 6027876
; GENERAL INFORMATION:
; APPLICANT: Black, Bruce C
; APPLICANT: Taylor, Martin
; APPLICANT: Heckel, David G
; TITLE OF INVENTION: Method for Monitoring Pesticide
; TITLE OF INVENTION: Resistance
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Darby & Darby PC
; STREET: 805 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: US
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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APPLICATION NUMBER: US/07/998,289B  
FILING DATE: 30-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINSON, JOSEPH R  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/OA939  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 521 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-998-289B-9

Query Match 72.6%; Score 13.8; DB 3; Length 521;  
Best Local Similarity 88.2%; Pred. No. 7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATCGCGCTAAT 18  
Db 17 CCCTGCATCGCGCTCAT 1

RESULT 94  
US-07-998-289B-2/c  
Sequence 2, Application US/07998289B  
Patent No. 6027876  
GENERAL INFORMATION:  
APPLICANT: Black, Bruce C  
APPLICANT: Taylor, Martin  
APPLICANT: Heckel, David G  
TITLE OF INVENTION: Method for Monitoring Pesticide  
RESISTANCE  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Darby & Darby PC  
STREET: 805 Third Avenue  
CITY: New York  
STATE: New York  
COUNTRY: US  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/998,289B  
FILING DATE: 30-DEC-1992  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: ROBINSON, JOSEPH R  
REGISTRATION NUMBER: 33,448  
REFERENCE/DOCKET NUMBER: 0646/OA939  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-527-7700  
TELEFAX: 212-753-6237  
TELEX: 236687  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 567 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-07-998-289B-2

Query Match 72.6%; Score 13.8; DB 3; Length 567;  
Best Local Similarity 88.2%; Pred. No. 7e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CCCTGAATCGCGCTAAT 18  
Db 63 CCCTGCATCGCGCTCAT 47  
RESULT 95  
US-09-949-016-25349/c  
Sequence 25349, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 25349  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-25349

Query Match 72.6%; Score 13.8; DB 3; Length 601;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CCCTGAATCGCGCTAAT 18  
Db 283 CCCTGAATGTCCTAAT 267

RESULT 96  
US-09-949-016-69732/c  
Sequence 69732, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 69732  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-69732

Query Match 72.6%; Score 13.8; DB 3; Length 601;  
Best Local Similarity 88.2%; Pred. No. 7.1e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 2 CCCTGAATCGCGCTAAT 18

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Db      283  CCCTGAATGTGCTAAT 267
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RESULT 97
US-09-902-540-3264/c
; Sequence 3264, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3264
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-3264

Query Match      72.6%; Score 13.8; DB 3; Length 642;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      3  CCTGAATCGGCTAATC 19
|||||
Db      19  CCTGAACGGCCCAATC 3
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RESULT 98
US-09-533-559-6637/c
; Sequence 6637, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Jeffery R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849-200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6637
; LENGTH: 672
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(672)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-6637

Query Match      72.6%; Score 13.8; DB 3; Length 672;
Best Local Similarity 88.2%; Pred. No. 7.2e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      2  CCCTGAATCGGCTAAT 18
|||||
Db      163  CCCTCAATGTGCTAAT 147
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RESULT 99
US-09-134-000C-3216/c
; Sequence 3216, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3216
; LENGTH: 738
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-3216

Query Match      72.6%; Score 13.8; DB 3; Length 738;
Best Local Similarity 88.2%; Pred. No. 7.3e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1  CCCCTGAATCGGCTAA 17
|||||
Db      95  CCAATGAATCGGCTAA 79
|||||

RESULT 100
US-08-945-038-5
; Sequence 5, Application US/08945038
; Patent No. 6762295
; GENERAL INFORMATION:
; APPLICANT: Doidge, Christopher V.
; APPLICANT: Lee, Adrian
; APPLICANT: Radcliff, Fiona J.
; APPLICANT: Hocking, Dianna M.
; APPLICANT: Webb, Elizabeth A.
; TITLE OF INVENTION: PROTECTIVE HELICOBACTER ANTIGENS
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/945,038
; FILING DATE: 23-DEC-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU96/00225
; FILING DATE: 19-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN2575
; FILING DATE: 21-APR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN3931
; FILING DATE: 03-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: AU PN7565
; FILING DATE: 16-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768

```

REFERENCE/DOCKET NUMBER: 017227/0133  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1302 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
ORIGINAL SOURCE:  
ORGANISM: Helicobacter pylori  
IMMEDIATE SOURCE:  
CLONE: Clone G3.8  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1299  
US-08-945-038-5

Query Match 72.6%; Score 13.8; DB 3; Length 1302;  
Best Local Similarity 88.2%; Pred. No. 7.8e+02;  
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAA 17  
Db 421 CTCCTGAATGGCGCTAA 437

Search completed: March 8, 2006, 21:06:49  
Job time : 107.126 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 190.369 Seconds  
(without alignments)  
665.178 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 ccctggaatggcgtaatc 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

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N\_Geneseq\_21:\*

1: Geneseqn1980s:\*

2: Geneseqn1990s:\*

3: Geneseqn2000s:\*

4: Geneseqn2001as:\*

5: Geneseqn2001bs:\*

6: Geneseqn2002as:\*

7: Geneseqn2002bs:\*

8: Geneseqn2003as:\*

9: Geneseqn2003bs:\*

10: Geneseqn2003cs:\*

11: Geneseqn2003ds:\*

12: Geneseqn2004as:\*

13: Geneseqn2004bs:\*

14: Geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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1	19	100.0	19	10	ACF04788 Tissue ce
2	19	100.0	27	8	ACD26709 Enterovir
3	19	100.0	27	13	ADU47462 p1 probe
4	19	100.0	30	6	ABL53132 Micro-org
5	19	100.0	30	6	ABL53128 Micro-org
6	19	100.0	30	6	ABL53130 Micro-org
7	19	100.0	35	2	AAV23434 Polioviru
8	19	100.0	119	14	ABE56836 Human cox
9	19	100.0	173	14	ABE56856 Human ech
10	19	100.0	173	14	ABE56855 Human ech
11	19	100.0	176	3	AAZ58488 Recombina
12	19	100.0	180	14	ABE56834 Human cox
13	19	100.0	198	14	ABE56865 Human ech
14	19	100.0	198	14	ABE56853 Human ech
15	19	100.0	198	14	ABE56860 Human ech
16	19	100.0	198	14	ABE56854 Human ech
17	19	100.0	237	14	ABE56837 Human cox
18	19	100.0	237	14	ABE56848 Human cox
19	19	100.0	237	14	ABE56879 Human pol

20	19	100.0	237	14	ABE56875	Human pol
21	19	100.0	237	14	ABE56876	Human pol
22	19	100.0	237	14	ABE56877	Human pol
23	19	100.0	237	14	ABE56861	Human ech
24	19	100.0	237	14	ABE56857	Human ech
25	19	100.0	237	14	ABE56871	Human ent
26	19	100.0	237	14	ABE56872	Human pol
27	19	100.0	238	14	ABE56840	Human cox
28	19	100.0	238	14	ABE56850	Human cox
29	19	100.0	238	14	ABE56878	Human pol
30	19	100.0	238	14	ABE56849	Human cox
31	19	100.0	238	14	ABE56839	Human cox
32	19	100.0	238	14	ABE56846	Human cox
33	19	100.0	238	14	ABE56847	Human cox
34	19	100.0	238	14	ABE56838	Human cox
35	19	100.0	238	14	ABE56842	Human cox
36	19	100.0	238	14	ABE56832	Human cox
37	19	100.0	238	14	ABE56835	Human cox
38	19	100.0	238	14	ABE56851	Human cox
39	19	100.0	238	14	ABE56852	Human cox
40	19	100.0	238	14	ABE56874	Human pol
41	19	100.0	238	14	ABE56829	Consensus
42	19	100.0	238	14	ABE56843	Human cox
43	19	100.0	238	14	ABE56845	Human cox
44	19	100.0	238	14	ABE56870	Human ech
45	19	100.0	238	14	ABE56830	Human cox
46	19	100.0	238	14	ABE56833	Human cox
47	19	100.0	238	14	ABE56877	Human pol
48	19	100.0	238	14	ABE56859	Human ech
49	19	100.0	238	14	ABE56841	Human cox
50	19	100.0	238	14	ABE56831	Human cox
51	19	100.0	238	14	ABE56867	Human ech
52	19	100.0	238	14	ABE56844	Human cox
53	19	100.0	238	14	ABE56866	Human ech
54	19	100.0	238	14	ABE56882	Human pol
55	19	100.0	497	8	ABX12446	Coxsackie
56	19	100.0	502	8	ABX12451	Coxsackie
57	19	100.0	514	3	AAZ58487	Polioviru
58	19	100.0	520	6	ABL53112	Micro-org
59	19	100.0	521	6	ABL53111	Micro-org
60	19	100.0	525	6	ABL53113	Micro-org
61	19	100.0	548	8	ABX12448	Coxsackie
62	19	100.0	551	8	ABX12453	Coxsackie
63	19	100.0	552	8	ABX12452	Coxsackie
64	19	100.0	554	8	ABX12457	Coxsackie
65	19	100.0	556	8	ABX12449	Coxsackie
66	19	100.0	556	8	ABX12450	Coxsackie
67	19	100.0	559	8	ABX12456	Coxsackie
68	19	100.0	560	8	ABX12447	Coxsackie
69	19	100.0	562	8	ABX12454	Coxsackie
70	19	100.0	567	8	ABX12455	Coxsackie
71	19	100.0	628	2	AAQ58715	Polioviru
72	19	100.0	628	2	AAQ58726	Polioviru
73	19	100.0	639	12	ADP74707	Novel bic
74	19	100.0	646	4	AAZ58487	Echo viru
75	19	100.0	654	4	AAZ58153	Coxsackie
76	19	100.0	660	4	AAZ58174	Coxsackie
77	19	100.0	660	14	ABE56828	Coxsackie
78	19	100.0	682	13	ADU77356	Prima7 vi
79	19	100.0	709	14	AEA00424	Enterovir
80	19	100.0	743	14	ADW37919	Polioviru
81	19	100.0	745	4	AAZ58152	Coxsackie
82	19	100.0	745	8	ACC48197	Polioviru
83	19	100.0	810	12	ADP82873	Human cox
84	19	100.0	1560	13	ADU47469	Enterovir
85	19	100.0	2076	6	ABK14791	Plateler-
86	19	100.0	4148	5	AAH20890	Vector co
87	19	100.0	5252	12	ADOO7652	Tricistrio
88	19	100.0	7185	12	ADP74699	Novel bic
89	19	100.0	7185	12	ADP74701	Novel bic
90	19	100.0	7235	12	ADP74714	Novel bic
91	19	100.0	7235	12	ADP74715	Novel bic
92	19	100.0	7235	12	ADP74700	Novel bic

93	19	100.0	7235	12	ADP74713	Adp74713 Novel bic	c 166	15.4	81.1	32187	9	ADB60819	Adb60819 Connectiv
94	19	100.0	7392	8	ABX12440	Abx12440 Diabetoge	c 167	15.4	81.1	32193	4	ABK42662	Abk42662 Genomic s
95	19	100.0	7399	2	RAQ11816	Raq11816 RNA encod	c 168	15.4	81.1	32193	9	ADB60818	Adb60818 Connectiv
96	19	100.0	7399	10	ABV76134	Abv76134 Cxsackie	c 169	15.4	81.1	39353	4	AAK67232	Aak67232 Human imm
97	19	100.0	7400	3	AAZ98719	Aaz98719 Swine ves	c 170	15.4	81.1	39353	4	AAK65396	Aak65396 Human imm
98	19	100.0	7400	3	AAZ98717	Aaz98717 Swine ves	c 171	15.4	81.1	39358	4	AAK65397	Aak65397 Human imm
99	19	100.0	7400	3	AAZ98718	Aaz98718 Swine ves	c 172	15.4	81.1	39358	4	AAK67233	Aak67233 Human imm
100	19	100.0	7400	3	AAZ29863	Aaz29863 Swine ves	c 173	15	78.9	20	14	ADZ76560	Adz76560 Enterovir
101	19	100.0	7421	3	AAZ98720	Aaz98720 Swine ves	c 174	15	78.9	24	13	ADU61148	Adu61148 Polioviru
102	19	100.0	7431	2	AAQ30148	Aaq30148 Attenuate	c 175	15	78.9	35	2	AAV23435	Aav23435 Polioviru
103	19	100.0	7440	1	AAZ20042	Aaz20042 Sequence	c 176	15	78.9	35	2	AAV23437	Aav23437 Polioviru
104	19	100.0	7441	2	AAZ26152	Aaz26152 DNA sequ	c 177	15	78.9	534	8	ACA32459	Aca32459 Prokaryot
105	19	100.0	7873	8	ACC43138	Acc43138 Nucleotid	c 178	15	78.9	2780	5	AAZ93777	Aaz93777 DNA encod
106	19	100.0	7925	12	ADP74702	Adp74702 Novel bic	c 179	14.8	77.9	293	6	ABN77120	Abn77120 Human ORF
107	19	100.0	7943	8	ACC43139	Acc43139 Nucleotid	c 180	14.8	77.9	582	10	ACF70262	Acf70262 Phototrab
108	19	100.0	8298	2	AAV18096	Aav18096 pMCLDHAP	c 181	14.8	77.9	688	10	ADD17643	Add17643 DNA (Seqi
109	19	100.0	10448	6	ABK86535	Abk86535 EIAV base	c 182	14.8	77.9	688	10	ADD16044	Add16044 cDNA (Seq
110	19	100.0	10633	12	ADO07660	Ado07660 Viral vec	c 183	14.8	77.9	708	4	ABA89900	Aba89900 Escherich
111	19	100.0	11058	6	ABK86536	Abk86536 EIAV base	c 184	14.8	77.9	767	10	ADI22436	Adi22436 Rat liver
112	19	100.0	11326	2	AAV12373	Aav12373 ChimERIC	c 185	14.8	77.9	925	4	ABL10205	Ab10205 Drosophil
113	19	100.0	11746	12	ADO07659	Ado07659 Viral vec	c 186	14.8	77.9	1208	2	AAZ84058	Aaz84058 DNA encod
114	19	100.0	38246	12	ADO07662	Ado07662 Viral vec	c 187	14.8	77.9	1468	10	ADC35635	Acd35635 Wheat SSE
115	18	94.7	25	2	AAQ06254	Aaq06254 Primer fo	c 188	14.8	77.9	2000	10	ACC61482	Acc61482 Gene sequ
116	18	94.7	25	2	AAZ37545	Aaz37545 Enterovir	c 189	14.8	77.9	2000	10	ADK64645	Adk64645 Disease t
117	18	94.7	25	3	AAZ57426	Aaz57426 Blood typ	c 190	14.8	77.9	2534	4	ABL25378	Ab125378 Drosophil
118	18	94.7	25	4	AAZ09941	Aaz09941 PCR prime	c 191	14.8	77.9	2833	4	ABL22734	Ab122734 Drosophil
119	18	94.7	25	4	AAH03081	Aah03081 Microorga	c 192	14.8	77.9	3631	4	ABL10204	Ab10204 Drosophil
120	18	94.7	25	9	ADA27505	Ada27505 Microorga	c 193	14.8	77.9	6357	4	ABL11914	Ab111914 Drosophil
121	18	94.7	25	10	ADC55468	Adc55468 Primer sp	c 194	14.8	77.9	9057	9	ACD19181	Acd19181 E. coli 0
122	18	94.7	44	3	AAZ49429	Aaz49429 Enterohae	c 195	14.8	77.9	9057	10	ADC01294	Adc01294 Enterohae
123	18	94.7	195	10	ABZ69931	Abz69931 Polioviru	c 196	14.8	77.9	9972	6	ABS79000	Abz79000 E. coli C
124	18	94.7	237	14	ABZ56881	Abz56881 Human pol	c 197	14.8	77.9	9972	10	ADH80567	Adh80567 Escherich
125	18	94.7	237	14	ABZ56880	Abz56880 Human pol	c 198	14.8	77.9	9974	4	ABA88897	Aba88897 Escherich
126	18	94.7	7432	2	AAQ22965	Aaq22965 True type	c 199	14.8	77.9	12537	12	AAAT41705	Aat41705 Lymphocyt
127	17.4	91.6	198	14	ABZ56858	Abz56858 Human ech	c 200	14.8	77.9	15755	12	ADM66947	Adm66947 Murine ad
128	17.4	91.6	198	14	ABZ56863	Abz56863 Human ech	c 201	14.8	77.9	25233	4	AAH45310	Aah45310 Human SEE
129	17.4	91.6	237	14	ABZ56862	Abz56862 Human ech	c 202	14.8	77.9	37672	8	AAZ56120	Aaz56120 Mouse lrf
130	17.4	91.6	238	14	ABZ56864	Abz56864 Human ech	c 203	14.8	77.9	37672	9	ADA02483	Ada02483 Mouse lrf
131	17.4	91.6	248	2	AAQ10172	Aaq10172 5' non-co	c 204	14.8	77.9	37672	10	ADB72221	Adb72221 Mouse lrf
132	17.4	91.6	608	5	AAZ93057	Aaz93057 Human rhi	c 205	14.8	77.9	55050	6	ABQ75680	Abq75680 Human SEE
133	17.4	91.6	627	8	ABX11923	Abx11923 Human rhi	c 206	14.8	77.9	93483	9	ADA03083	Ada03083 Mouse mCG
134	17.4	91.6	627	8	ABX11971	Abx11971 Human rhi	c 207	14.8	77.9	93483	9	ADA06367	Ada06367 Mouse mCG
135	17.4	91.6	627	10	ADB84230	Adb84230 Rhinoviru	c 208	14.8	77.9	93483	10	ADB72821	Adb72821 Mouse mCG
136	17.4	91.6	627	10	ADA15642	Ada15642 Human rhi	c 209	14.8	77.9	93483	11	ADL27161	Adl27161 Mouse gen
137	17.4	91.6	627	14	ADV78854	Adv78854 Novel anc	c 210	14.8	77.9	110000	4	AAI99682_15	AAI99682_15 o
138	17.4	91.6	627	14	ADW71616	Adw71616 Human rhi	c 211	14.8	77.9	110000	4	AAI99683_15	AAI99683_15 o
139	17.4	91.6	7227	14	AAZ60194	Aaz60194 Sequence	c 212	14.8	77.9	110000	10	ACF65385_4	ACF65385_4 o
140	17	89.5	24	14	ADY39812	Ady39812 Enterovir	c 213	14.8	77.9	110000	10	ACF67367_33	ACF67367_33 o
141	16.4	86.3	19	14	AEA22931	Aea22931 Meningiti	c 214	14.8	77.9	110000	12	ADQ97328_2	ADQ97328_2 o
142	16.4	86.3	32	2	AAZ45153	Aaz45153 PCR prime	c 215	14.8	77.9	160921	11	ACN44962_2	ACN44962_2 o
143	16	84.2	103	2	AAQ06807	Aaq06807 Mutagenis	c 216	14.8	77.9	161334	11	ACN44334	Acn44334 Human gen
144	15.8	83.2	250	2	AAQ10171	Aaq10171 5' non-co	c 217	14.8	77.9	263852	13	ADN99460	Adn99460 Murine k1
145	15.8	83.2	610	1	AAZ81398	Aaz81398 Sequence	c 218	14.8	77.9	342748	14	ADZ13793	Adz13793 Human can
146	15.8	83.2	618	1	AAZ81397	Aaz81397 Sequence	c 219	14.4	75.8	145	6	ABK39676	Abk39676 cDNA enco
147	15.8	83.2	1024	14	ABZ65545	Abz65545 Rice geno	c 220	14.4	75.8	145	8	ACA12005	Aca12005 Human lun
148	15.8	83.2	1326	8	ACA31960	Acc31960 Prokaryot	c 221	14.4	75.8	145	8	ACA03191	Aca03191 Lung can
149	15.8	83.2	7100	8	AAQ03360	Aaq03360 Complete	c 222	14.4	75.8	145	10	ADH47243	Adh47243 Human lun
150	15.8	83.2	7100	2	AAQ03418	Aaq03418 Complete	c 223	14.4	75.8	145	13	ADJ21162	Adj21162 Human lun
151	15.8	83.2	7102	1	AAZ60044	Aaz60044 Sequence	c 224	14.4	75.8	482	11	ADW22162	Adw22162 Rat hepat
152	15.8	83.2	7102	1	AAZ81393	Aaz81393 Rhinoviru	c 225	14.4	75.8	663	4	AAF26362	Aaf26362 P. putida
153	15.8	83.2	7152	1	AAZ81390	Aaz81390 Sequence	c 226	14.4	75.8	810	8	ACA25005	Aca25005 Prokaryot
154	15.8	83.2	7152	1	AAZ80153	Aaz80153 Human Rhi	c 227	14.4	75.8	1389	5	AAZ87543	Aaz87543 DNA encod
155	15.4	81.1	21	2	AAQ26920	Aaq26920 PCR Prime	c 228	14.4	75.8	1494	14	ACL72006	Acl72006 M. xanthu
156	15.4	81.1	21	10	ADE37350	Ade37350 Enterovir	c 229	14.4	75.8	1957	13	ADX60014	Adx60014 Plant ful
157	15.4	81.1	743	1	AAZ70260	Aaz70260 Sequence	c 230	14.4	75.8	2307	4	ABL23687	Ab123687 Drosophil
158	15.4	81.1	750	6	ABK78684	Abk78684 Bacillus	c 231	14.4	75.8	2614	4	ABL01962	Ab101962 Drosophil
159	15.4	81.1	1269	11	ACH99447	Ach99447 Klebsiell	c 232	14.4	75.8	3889	10	ADB53544	Adb53544 Primary r
160	15.4	81.1	1633	2	AAZ14567	Aaz14567 H. pylori	c 233	14.4	75.8	5479	4	ABL23686	Ab123686 Drosophil
161	15.4	81.1	1707	1	AAZ50411	Aaz50411 Secretion	c 234	14.4	75.8	6380	14	ACL64428	Acl64428 M. xanthu
162	15.4	81.1	1720	11	ACL38298	Acl38298 Rice stre	c 235	14.4	75.8	7784	13	ADT04771	Adt04771 Escherich
163	15.4	81.1	1943	14	AEA49129	Aea49129 L. rhamno	c 236	14.4	75.8	7800	3	AAZ53860	Aaz53860 Neisseria
164	15.4	81.1	2000	11	ACL36559	Acl36559 Rice stre	c 237	14.4	75.8	8112	8	ACA42054	Aca42054 Prokaryot
165	15.4	81.1	32187	4	ABK42663	Abk42663 Genomic s	c 238	14.4	75.8	8397	8	ACA41510	Aca41510 Prokaryot

239	14.4	75.8	27425	3	AA533978	Aaa533978 DWP53 tum	312	14.2	74.7	3090	6	ABN79827	Abn79827 Fungal 2B
240	14.4	49914	3	AAA81471	Aaa81471 N. mening	313	14.2	74.7	3111	11	ACL26227	ACL26227 Rice abio	
c 241	14.4	75.8	70549	12	ADQ97436	Adq97436 Mouse can	c 314	14.2	74.7	3165	11	ADM02816	Adm02816 Human CDN
c 242	14.4	75.8	110000	3	AAA81490_05	Continuation (6 of	315	14.2	74.7	3344	2	AA71086	Aax71086 Human ala
c 243	14.4	75.8	110000	4	AA199682_20	Continuation (21 o	316	14.2	74.7	3344	2	AA339683	Aax339683 Renal can
c 244	14.4	75.8	110000	14	AD213747_0	Ad213747 Human can	317	14.2	74.7	3344	10	ADB31357	Adb31357 Bicalutam
c 245	14.4	75.8	347814	12	ADQ59440	Adq59440 Human can	318	14.2	74.7	3344	10	ABX74491	Abx74491 Human CDN
c 246	14.4	75.8	349980	3	AA221607	Aaf21607 Neisseria	319	14.2	74.7	3344	13	ADR24775	Adr24775 Breast ca
c 247	14.4	75.8	349980	6	ABN61848	Abn61848 Bifidobac	320	14.2	74.7	3344	13	ACN40037	Acn40037 Tumour-as
c 248	14.2	74.7	60	6	ABN44597	Abn44597 Human spl	321	14.2	74.7	3344	13	ADP23085	Adp23085 PRO polyP
c 249	14.2	74.7	387	13	ACN49849	Acn49849 Cotton pr	322	14.2	74.7	3344	14	ADY14359	Ady14359 DNA encod
c 250	14.2	74.7	403	3	AA226421	Aac26421 Human sec	323	14.2	74.7	3344	14	ADY75432	Ady75432 Human ala
c 251	14.2	74.7	467	6	ABX66436	Abx66436 Helicobac	324	14.2	74.7	3505	12	ADY16195	Ady16195 Human CDN
c 252	14.2	74.7	468	9	ACH28819	Acn28819 Human adu	325	14.2	74.7	3505	14	AEA43860	Aea43860 Drosophil
c 253	14.2	74.7	481	3	AA211840	Aac211840 Zea maye	c 326	14.2	74.7	3810	4	ABL05406	Abi05406 Drosophil
c 254	14.2	74.7	487	6	ABN63232	Abn63232 Human can	c 327	14.2	74.7	3814	4	ABL21026	Abi21026 Drosophil
c 255	14.2	74.7	512	6	ABN64886	Abn64886 Human can	c 328	14.2	74.7	4007	10	ADG42134	Adg42134 Human bra
c 256	14.2	74.7	524	13	ACN57786	Acn57786 Cotton gy	329	14.2	74.7	4281	4	ABL02573	Abi02573 Drosophil
c 257	14.2	74.7	530	13	ACN62066	Acn62066 Cotton gy	c 330	14.2	74.7	4381	9	AAU62526	Aal62526 Human tra
c 258	14.2	74.7	583	4	AAU36607	Aal36607 Human mus	c 331	14.2	74.7	4519	8	ADP47360	Aad47360 Human tra
c 259	14.2	74.7	583	8	ABX59595	Abx59595 cDNA enco	c 332	14.2	74.7	4603	12	ADP99221	Adp99221 Human tra
c 260	14.2	74.7	583	12	ADJ30345	Adj30345 Human mus	c 333	14.2	74.7	4603	12	ADP99221	Adp99221 Human tra
c 261	14.2	74.7	586	13	ACN61703	Acn61703 Cotton gy	c 334	14.2	74.7	4664	12	ADJ96595	Adj96595 Human tyr
c 262	14.2	74.7	593	4	AAU18216	Aal18216 Human bre	c 335	14.2	74.7	4771	4	ABL07514	Abi07514 Drosophil
c 263	14.2	74.7	597	13	ACN50736	Acn50736 Cotton an	c 336	14.2	74.7	5237	12	ADQ64500	Adq64500 Novel hum
c 264	14.2	74.7	608	3	AA709099	Aaf09099 Fusarium	337	14.2	74.7	5549	8	ACC57740	Acc57740 Human pro
c 265	14.2	74.7	608	13	ADU53140	Adu53140 Fusarium	338	14.2	74.7	5549	10	ADG38362	Adg38362 Human pro
c 266	14.2	74.7	608	14	ADZ91143	Adz91143 Fusarium	339	14.2	74.7	5677	10	ADG91195	Adg91195 Hepatic s
c 267	14.2	74.7	710	2	AAV32991	Aav32991 Human top	c 340	14.2	74.7	6587	4	ABL02572	Abi02572 Drosophil
c 268	14.2	74.7	774	10	ACF66321	Acf66321 Photorhab	c 341	14.2	74.7	7005	13	ADQ89655	Adq89655 Antagonis
c 269	14.2	74.7	781	10	ACF66296	Acf66296 Photorhab	c 342	14.2	74.7	8201	6	ABL34510	Abi34510 Human met
c 270	14.2	74.7	792	10	ACF67636	Acf67636 Photorhab	c 343	14.2	74.7	8201	6	ABL70539	Abi70539 Chemical
c 271	14.2	74.7	817	11	ADT94569	Adt94569 Colon can	c 344	14.2	74.7	8201	7	ADJ99771	Adj99771 Bisulphit
c 272	14.2	74.7	817	11	ADX41051	Adx41051 Human CDN	c 345	14.2	74.7	9407	4	AA559606	Aa559606 Propionib
c 273	14.2	74.7	866	4	ABL12071	Abi12071 Drosophil	346	14.2	74.7	9407	8	ACF64535	Acf64535 Propionib
c 274	14.2	74.7	895	6	ABX66710	Abx66710 Helicobac	347	14.2	74.7	10685	13	ADR84250	Adr84250 Aspergill
c 275	14.2	74.7	912	10	ACF68830	Acf68830 Photorhab	c 348	14.2	74.7	13075	4	ABL15354	Abi15354 Drosophil
c 276	14.2	74.7	926	5	AA593956	Aa593956 DNA encod	349	14.2	74.7	16929	12	ADJ12871	Adj12871 DNA fragm
c 277	14.2	74.7	939	8	ACA34971	Aca34971 Prokaryot	c 350	14.2	74.7	16929	12	ADJ12871	Adj12871 DNA fragm
c 278	14.2	74.7	981	6	ABT11491	Abt11491 Yeast sel	c 351	14.2	74.7	19802	4	ABL12950	Abi12950 Drosophil
c 279	14.2	74.7	985	6	ABS62890	Abs62890 Selected	c 352	14.2	74.7	22111	12	ADJ46536	Adj46536 Human req
c 280	14.2	74.7	985	6	ABT11464	Abt11464 Yeast sel	c 353	14.2	74.7	22111	12	ADJ46536	Adj46536 Human req
c 281	14.2	74.7	1020	11	ACH9265	Ach9265 Klebsiell	c 354	14.2	74.7	26933	13	ABD33416	Abd33416 Murine ca
c 282	14.2	74.7	1095	5	AAH66756	Aah66756 C glutami	c 355	14.2	74.7	26933	13	ABD33416	Abd33416 Murine ca
c 283	14.2	74.7	1095	8	ABQ94247	Abq94247 FLO11 gen	c 356	14.2	74.7	32572	6	AA517820	Aa517820 PadV-5 HN
c 284	14.2	74.7	1099	8	ACA22772	Ac22772 Prokaryot	c 357	14.2	74.7	33933	13	ABD33323	Abd33323 Human can
c 285	14.2	74.7	1101	3	AC53703	Ac53703 Arabidops	c 358	14.2	74.7	36033	10	ADB74375	Adb74375 Mycobacte
c 286	14.2	74.7	1104	6	ABQ88741	Abq88741 Breast sp	c 359	14.2	74.7	69770	10	ADC86870	Adc86870 Human GPC
c 287	14.2	74.7	1117	6	ABT11357	Abt11357 Yeast sel	c 360	14.2	74.7	75782	12	ADQ97795	Adq97795 Mouse can
c 288	14.2	74.7	1135	8	ACA22522	Ac22522 Prokaryot	c 361	14.2	74.7	96597	10	ADC85340	Adc85340 Human Lmo
c 289	14.2	74.7	1218	4	AAF71334	Aaf71334 Corynebac	c 362	14.2	74.7	96598	9	ADA02861	Ada02861 Mouse itp
c 290	14.2	74.7	1503	3	AA595495	Aa595495 Human sec	c 363	14.2	74.7	96598	12	ADM74456	Adm74456 Murine ca
c 291	14.2	74.7	1503	6	ABK74390	Abk74390 Bacillus	c 364	14.2	74.7	96598	12	ADM74456	Adm74456 Murine ca
c 292	14.2	74.7	1593	3	ACA49057	Ac49057 Arabidops	c 365	14.2	74.7	110000	10	ACF65383_1	Acf65383_1 Continuation (2 of
c 293	14.2	74.7	1612	4	ABL05407	Abi05407 Drosophil	c 366	14.2	74.7	110000	10	ACF67367_02	Acf67367_02 Continuation (3 of
c 294	14.2	74.7	1665	8	ADA26542	Ada26542 Arabidops	c 367	14.2	74.7	110000	14	ACF67367_16	Acf67367_16 Continuation (17 o
c 295	14.2	74.7	1755	4	ABL21027	Abi21027 Drosophi	c 368	14.2	74.7	110000	14	AEA61163_3	Aea61163_3 Continuation (4 of
c 296	14.2	74.7	1985	12	ADJ10845	Adj10845 Recombina	c 369	14.2	74.7	110000	14	AEA61163_4	Aea61163_4 Continuation (5 of
c 297	14.2	74.7	2063	3	ABQ88742	Abq88742 Breast sp	370	14.2	74.7	119057	13	ABD33460	Abd33460 Murine ca
c 298	14.2	74.7	2136	3	ACA44709	Ac44709 Arabidops	371	14.2	74.7	130480	4	AAF25833	Aaf25833 R. marinu
c 299	14.2	74.7	2136	6	ABE21298	Ab21298 Arabidops	372	14.2	74.7	132544	13	ADV99887	Adv99887 Nanchangm
c 300	14.2	74.7	2136	8	ADA68489	Ada68489 Arabidops	373	14.2	74.7	146733	12	ADQ97410	Adq97410 Mouse can
c 301	14.2	74.7	2423	2	AAQ51237	Aaq51237 Plant NAD	374	14.2	74.7	164772	10	ADL13904	Adl13904 Osteoarth
c 302	14.2	74.7	2445	13	ADO82137	Ado82137 Plant ful	375	14.2	74.7	166181	12	ADQ20461	Adq20461 Human sof
c 303	14.2	74.7	2592	6	ABK36053	Abk36053 cDNA sequ	376	14.2	74.7	166181	12	ADQ18633	Adq18633 Human sof
c 304	14.2	74.7	2668	4	ABL25154	Abi25154 Drosophil	377	14.2	74.7	203132	13	ABD33364	Abd33364 Murine ca
c 305	14.2	74.7	2907	13	ADQ89887	Adq89887 Antagonis	378	14.2	74.7	203132	14	ADZ13443	Adz13443 Murine ca
c 306	14.2	74.7	2910	10	ADAS2971	Ada2971 Human cod	c 379	14.2	74.7	249878	10	ACF65381	Acf65381 Photorhab
c 307	14.2	74.7	2927	3	AC76720	Ac76720 Human ORF	380	14.2	74.7	349980	5	AAH68529	Aah68529 C glutami
c 308	14.2	74.7	2944	4	ABL12070	Abi12070 Drosophil	381	14.2	73.7	14	2	AAQ50709	Aaq50709 ERM picor
c 309	14.2	74.7	3036	13	ADX62298	Adx62298 Plant ful	382	14.2	73.7	14	14	ABE56764	Abe56764 Enterovir
c 310	14.2	74.7	3080	4	ABL04732	Abi04732 Drosophil	383	14.2	73.7	19	8	ABZ68824	Abz68824 Primer us
c 311	14.2	74.7	3084	4	ABL05392	Abi05392 Drosophil	384	14.2	73.7	591	6	ABK62210	Abk62210 Rat seque

385	14	73.7	647	10	ACF66435	Acf66435 Phototrab	c 458	13.8	72.6	889	4	ABA07991	Abao7991 Human ova
386	14	73.7	966	8	ACA53923	Acas53923 Prokaryot	c 459	13.8	72.6	889	4	ABA07990	Abao7990 Human ova
387	14	73.7	966	8	ACF69113	Acf69113 Phototrab	c 460	13.8	72.6	935	3	AAC42055	Acac42055 Arabidops
388	14	73.7	1356	8	ACA43171	Acac43171 Prokaryot	c 461	13.8	72.6	935	3	ADs45749	Ades45749 Bacterial
389	14	73.7	1473	4	AAS52034	Aas52034 Staphyloc	c 462	13.8	72.6	993	13	ABL40772	Ab140772 Human pro
390	14	73.7	1512	8	ACF74373	Acf74373 Staphyloc	c 463	13.8	72.6	993	13	ADc26676	Adc26676 Human lip
391	14	73.7	1515	4	AAS54957	Aas54957 Staphyloc	c 464	13.8	72.6	1034	5	AAS70584	Aas70584 Human encod
392	14	73.7	1536	8	ACA20374	Acac20374 Prokaryot	c 465	13.8	72.6	1034	5	AAS92608	Aas92608 DNA encod
393	14	73.7	1641	10	ACF68994	Acf68994 Phototrab	c 466	13.8	72.6	1053	5	ADp29016	Adp29016 Human sec
394	14	73.7	1660	10	ADBS8863	Adbs8863 Toxicity-	c 467	13.8	72.6	1053	12	ADP29016	Adp29016 Human sec
395	14	73.7	1660	14	ADZ60815	Adz60815 Rat Hadhs	c 468	13.8	72.6	1099	8	ACA52166	Acas52166 Prokaryot
396	14	73.7	2254	12	ADP72855	Adp72855 Renal tox	c 469	13.8	72.6	1102	6	ABK75380	Abk75380 Bacillus
397	14	73.7	2465	4	ABL18148	Ab18148 Drosophil	c 470	13.8	72.6	1103	8	ACA49232	Acac49232 Prokaryot
398	14	73.7	4467	2	AXI19253	Axi19253 Corn dihy	c 471	13.8	72.6	1155	13	ADx31948	Adx31948 Plant ful
399	14	73.7	11823	2	AAV74447	Aav74447 Staphyloc	c 472	13.8	72.6	1218	8	ACA23053	Acac23053 Prokaryot
400	14	73.7	92076	13	ABD33368	Abd33368 Murine ca	c 473	13.8	72.6	1218	8	ACA23053	Acac23053 Prokaryot
401	14	73.7	110000	2	AZ01425_09	Continuation (10 o	c 474	13.8	72.6	1281	4	AAF56025	Aaf56025 Lactobaci
402	14	73.7	110000	10	ACF67367_18	Continuation (19 o	c 475	13.8	72.6	1302	2	AAT43045	Aat43045 Helicobac
403	14	73.7	110000	10	ACF67367_20	Continuation (21 o	c 476	13.8	72.6	1314	2	AAT68169	Aat68169 H. pylori
404	14	73.7	110000	10	ACF67367_23	Continuation (24 o	c 477	13.8	72.6	1326	8	ACA35579	Acac35579 Prokaryot
405	14	73.7	110000	10	ACF67367_24	Continuation (25 o	c 478	13.8	72.6	1335	8	ACA54257	Acac54257 Prokaryot
406	14	73.7	110000	10	ACF65386_4	Continuation (5 of	c 479	13.8	72.6	1356	4	ABL2679	Ab12679 Drosophil
407	14	73.7	210710	10	ACF65380	Acf65380 Phototrab	c 480	13.8	72.6	1356	13	ADQ89757	Adq89757 Antagonis
408	14	73.7	243072	10	ACF65382	Acf65382 Phototrab	c 481	13.8	72.6	1356	13	ADQ89757	Adq89757 Antagonis
409	13.8	72.6	29	5	ADV02873	Adv02873 Human BAC	c 482	13.8	72.6	1395	13	ADT45153	Adt45153 Bacterial
410	13.8	72.6	100	8	ACD75161	Ac75161 E. coli K	c 483	13.8	72.6	1404	5	AAH49409	Aah49409 D. melano
411	13.8	72.6	129	10	ADJ37814	Adj37814 Rat strok	c 484	13.8	72.6	1425	11	ACH98878	Ach98878 Klebsiell
412	13.8	72.6	129	12	ADI30602	Adi30602 Rat strok	c 485	13.8	72.6	1431	11	ACH95521	Ach95521 Klebsiell
413	13.8	72.6	254	7	ADS65209	Ads65209 Corn seed	c 486	13.8	72.6	1435	4	AAF56001	Aaf56001 Lactobaci
414	13.8	72.6	295	3	AAA42360	Aaa42360 Human sec	c 487	13.8	72.6	1451	5	AAS05853	Aas05853 Fruit fly
415	13.8	72.6	296	2	AAL12608	Aal12608 Human gen	c 488	13.8	72.6	1451	11	ADL14541	Adel14541 DNA encod
416	13.8	72.6	298	6	AAL75616	Ab175616 Corn tass	c 489	13.8	72.6	1451	11	ADL83389	Adl83389 Drosophil
417	13.8	72.6	387	10	ACF70133	Acf70133 Phototrab	c 490	13.8	72.6	1451	12	ADR03109	Adr03109 Drosophil
418	13.8	72.6	404	6	ABS98328	Abs98328 Human lac	c 491	13.8	72.6	1452	9	AAV91989	Adv91989 Dmnpck8 c
419	13.8	72.6	423	10	ADF81229	Adf81229 Leukaemia	c 492	13.8	72.6	1452	9	AAV91989	Adv91989 Dmnpck8 c
420	13.8	72.6	430	4	AAI62598	Aai62598 Human bre	c 493	13.8	72.6	1532	6	ABL40774	Ab140774 Human pro
421	13.8	72.6	430	4	AAI03781	Aai03781 Human rep	c 494	13.8	72.6	1532	6	ABL40774	Ab140774 Human pro
422	13.8	72.6	445	10	ADE59275	Ades9275 Rat gene	c 495	13.8	72.6	1532	6	ABL40773	Ab140773 Human pro
423	13.8	72.6	457	13	ACF82308	Acf82308 Human SIR	c 496	13.8	72.6	1532	6	ABL40773	Ab140773 Human pro
424	13.8	72.6	462	9	ACH13619	Ach13619 Human adu	c 497	13.8	72.6	1554	13	ADO82643	Ado82643 Plant ful
425	13.8	72.6	469	9	ACH19903	Ach19903 Human adu	c 498	13.8	72.6	1575	5	AAS71295	Aas71295 DNA encod
426	13.8	72.6	488	6	ABL40781	Ab140781 Human pro	c 499	13.8	72.6	1589	11	ACN45015	Acn45015 Human mRN
427	13.8	72.6	519	6	ABK74169	Abk74169 Bacillus	c 500	13.8	72.6	1630	12	ADO57322	Ado57322 DNA encod
428	13.8	72.6	549	10	ACD94383	Ac94383 Human col	c 500	13.8	72.6	1665	5	AAS92765	Aas92765 DNA encod
429	13.8	72.6	558	4	AAH34783	Aah34783 Human col							
430	13.8	72.6	558	10	ADK52783	Adk52783 Plant DNA							
431	13.8	72.6	567	2	AAQ71201	Aaq71201 scd72, a							
432	13.8	72.6	583	12	ADL83910	Adl83910 DNA up-re							
433	13.8	72.6	583	12	ADL83911	Adl83911 DNA up-re							
434	13.8	72.6	603	3	AAZ47454	Aaz47454 Glutathio							
435	13.8	72.6	642	14	ACL68801	Ac168801 M. xanthu							
436	13.8	72.6	645	10	ADK53443	Adk53443 Plant DNA							
437	13.8	72.6	654	4	AAH34361	Aah34361 Human col							
438	13.8	72.6	660	10	ADF82599	Adf82599 Leukaemia							
439	13.8	72.6	672	3	AAF14114	Aaf14114 Aspergill							
440	13.8	72.6	672	13	ADU58155	Adu58155 Aspergill							
441	13.8	72.6	672	14	ADZ36158	Adz36158 Aspergill							
442	13.8	72.6	673	4	AAO1669	Aao1669 Human rep							
443	13.8	72.6	673	4	ABA07589	Abao7589 Human ova							
444	13.8	72.6	693	2	AAT67402	Aat67402 H. pylori							
445	13.8	72.6	694	10	ACF66756	Acf66756 Phototrab							
446	13.8	72.6	697	10	ACF66728	Acf66728 Phototrab							
447	13.8	72.6	704	13	ADBS1386	Adbs1386 Bacterial							
448	13.8	72.6	705	10	ADK55596	Adk55596 Plant DNA							
449	13.8	72.6	719	6	ABQ68564	Abq68564 Listeria							
450	13.8	72.6	735	10	ADK59361	Adk59361 Plant DNA							
451	13.8	72.6	737	4	AAH70463	Aah70463 Human cer							
452	13.8	72.6	738	10	ADH85331	Adh85331 Enterococ							
453	13.8	72.6	759	6	ABL40776	Ab140776 Human pro							
454	13.8	72.6	846	8	ACA43170	Acac43170 Prokaryot							
455	13.8	72.6	872	13	ADX32098	Adx32098 Plant ful							
456	13.8	72.6	889	4	AAI05672	Aai05672 Human rep							
457	13.8	72.6	889	4	AAI05673	Aai05673 Human rep							

ALIGNMENTS

RESULT 1

ACF04788	ID	ACF04788	standard; DNA; 19 BP.
XX	XX	ACF04788;	
XX	XX	ACF04788;	
DT	18-DEC-2003	(first entry)	
XX	XX	Tissue cell culture procedure enterovirus control PCR primer #2.	
DE	XX	Tissue cell culture procedure enterovirus control PCR primer #2.	
XX	XX	RNA detection; crude cell lysate; human; tissue culture; PCR; primer;	
KW	XX	probe; ss.	
XX	XX	Enterovirus.	
XX	XX	WO2003064605-A2.	
XX	XX	07-AUG-2003.	
XX	XX	28-JAN-2003; 2003WO-US002439.	
XX	XX	28-JAN-2002; 2002US-0352402P.	
XX	XX	(AMBI-) AMBION INC.	



PI Paskloske BL;  
 XX WPI; 2003-748084/70.  
 XX

PT Producing cDNA from one or more biological units, useful for detecting a  
 PT specific sequence of RNA in a cell or tissue sample, comprises preparing  
 PT an admixture of the biological unit and the catabolic enzyme.  
 XX

PS Example 1; Page 41; 46pp; English.  
 XX

CC The present invention relates to a method of producing cDNA from one or  
 CC more biological units, comprising preparing an admixture of the  
 CC biological unit and the catabolic enzyme. This involves preparing cDNA  
 CC from one or more biological units by obtaining at least one biological  
 CC unit, obtaining at least one catabolic enzyme, preparing an admixture of  
 CC the biological unit and the catabolic enzyme and incubating the admixture  
 CC at a temperature where the catabolic enzyme is active and with reverse  
 CC transcriptase under conditions to allow reverse transcription. The method  
 CC is useful for detecting a specific sequence of RNA in a cell or tissue  
 CC sample, and for enzymatically manipulating the RNA in a crude cell  
 CC lysate. The kit is useful for producing cDNA in a biological unit. The  
 CC present sequence is a PCR primer/probe used in the exemplification of the  
 CC invention  
 XX

SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;  
 XX

Query Match 100.0%; Score 19; DB 10; Length 19;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

QY 1 CCCCTGAATGGGCTAATC 19  
 DB 1 CCCCTGAATGGGCTAATC 19  
 XX

RESULT 2  
 ACD26709  
 ID ACD26709 standard; DNA; 27 BP.  
 XX  
 AC ACD26709;  
 XX

DT 11-SEP-2003 (first entry)  
 XX

DE Enterovirus detection method associated primer #9.  
 XX

KW Enterovirus detection; primer; ss.  
 XX

OS Enterovirus.  
 XX

FN CN1366066-A.  
 XX

PD 28-AUG-2002.  
 XX

PF 15-JAN-2001; 2001CN-00100622.  
 XX

PR 15-JAN-2001; 2001CN-00100622.  
 XX

PA (JING-) JINGYU BIOLOGIC SCI TECHNOLOGY IND CO LT.  
 XX

PI Li G, Bai Q, Zeng Y;  
 XX

DR WPI; 2003-230558/23.  
 XX

PT Process, primer and probe for detecting and discriminating enterovirus.  
 XX

PS Claim 5; Page 1; 33pp; Chinese.  
 XX

CC The invention describes the application of nucleotide primer to detecting  
 CC enterovirus. The detection method and the reagent kit are disclosed. This  
 CC sequence represents an enterovirus detection method associated primer  
 XX

SQ Sequence 27 BP; 4 A; 11 C; 6 G; 6 T; 0 U; 0 Other;  
 XX

Query Match 100.0%; Score 19; DB 8; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

QY 1 CCCCTGAATGGGCTAATC 19  
 DB 9 CCCCTGAATGGGCTAATC 27  
 XX

RESULT 3  
 ADU47462  
 ID ADU47462 standard; DNA; 27 BP.  
 XX  
 AC ADU47462;  
 XX

DT 27-JAN-2005 (first entry)  
 XX

DE p1 probe used to detect enterovirus type 71 (EV71) in a sample.  
 XX

KW Detection; enterovirus type 71; probe; ss.  
 XX

OS Enterovirus.  
 XX

FN US6818397-B1.  
 XX

PD 16-NOV-2004.  
 XX

PF 28-NOV-2000; 2000US-00724678.  
 XX

PR 28-NOV-2000; 2000US-00724678.  
 XX

PA (CHIP-) CHIP BIOTECHNOLOGY INC.  
 XX

PI Lee X, Bair C, Tseng Y, Wang Y, Wang S;  
 XX

DR WPI; 2004-793563/78.  
 XX

PT New kit comprising a pair of oligonucleotide primers for nucleic acid  
 PT amplification, useful in detecting and differentiating an enterovirus in  
 PT a sample.  
 XX

PS Claim 1; SEQ ID NO 9; 14pp; English.  
 XX

CC The invention provides a method and a kit for detecting and  
 CC differentiating an enterovirus type 71 (EV71) in a sample. The method  
 CC involves contacting nucleic acids in the sample with a pair of primers to  
 CC form an amplification product; contacting the amplification product with  
 CC at least one synthetic nucleotide sequence fixed on a solid substrate and  
 CC detecting hybridisation. The present sequence is a probe used to detect  
 CC and differentiate enterovirus type 71 (EV71) in a sample.  
 XX

SQ Sequence 27 BP; 4 A; 11 C; 6 G; 6 T; 0 U; 0 Other;  
 XX

Query Match 100.0%; Score 19; DB 13; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 2;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX

QY 1 CCCCTGAATGGGCTAATC 19  
 DB 9 CCCCTGAATGGGCTAATC 27  
 XX

RESULT 4  
 ABL53132  
 ID ABL53132 standard; DNA; 30 BP.  
 XX  
 AC ABL53132;  
 XX

DT 29-AUG-2003 (revised)  
 XX

DT 25-JUN-2002 (first entry)  
 XX

DE Micro-organism detection probe #74.  
 XX



PT least three representative microbes.

PS Claim 24; Page 79; 85pp; French.

XX The present invention relates to a method for monitoring microbiological  
CC quality of an aqueous environmental medium that potentially contains many  
CC different microorganisms. A reference set of at least three  
CC microorganisms is chosen that, separately or collectively, represent  
CC microbiological quality. The test medium is treated, then any  
CC microorganisms, or their fragments, in the treated medium is contacted  
CC with a set of at least three probes for specific identification and  
CC multiple determination of selected microorganisms. This determination  
CC represents the level of microbiological quality. The method is useful for  
CC identifying and quantifying microorganisms in water and provides results  
CC that are used to control water purification/production processes. The  
CC present sequence is a probe which was used to illustrate the invention.  
CC (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 30 BP; 6 A; 12 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
|||  
Db 6 CCCCTGAATGCGGCTAATC 24

RESULT 7

AAV23434/C

ID AAV23434 standard; DNA; 35 BP.

XX

AC AAV23434;

XX 08-JUL-1998 (first entry)

XX Poliovirus DNA primer 438 used in method of the invention.

XX PCR primer; vaccine classification; poliovirus type 2 vaccine;  
KW attenuated poliovirus vaccine; neurovirulence; ss.

XX Synthetic.

OS Poliovirus.

XX US5728519-A.

XX 17-MAR-1998.

XX 21-DEC-1994; 94US-00361337.

XX 06-NOV-1990; 90US-00607742.

XX 18-MAY-1994; 94US-00246373.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Roninson I, Chumakov KM, Levenbook IS, Norwood LP;  
PI WPI; 1998-270433/24.

XX Determining acceptability of poliovirus vaccines - based on mutation  
PT reversion(s) and comparison to World Health Organisation standard.

XX Example; Col 23-24; 38pp; English.

XX This sequence represents a primer used in the method of the invention.  
CC The method is for classifying an unclassified live poliovirus type 2  
CC vaccine (attenuated by a G to A substitution at nucleotide position 481)  
CC as having an acceptable or unacceptable level of neurovirulence, and  
CC comprises, prior to vaccine administration: (a) selectively amplifying a  
CC region (I) of the poliovirus genome containing nucleotide position 481  
CC using selectively mismatched primers to introduce a site-specific  
CC mutation to create a restriction endonuclease (RE) site which includes

CC nucleotide position 481; (b) digesting an amount of (I) with a RE that  
CC specifically cleaves the amplified sequences in revertant viruses which  
CC contain an A to G reversion at nucleotide position 481; (c) digesting an  
CC amount of (I) with a RE that specifically cleaves the amplified sequences  
CC in non-revertant viruses which contain an A at nucleotide position 481;  
CC (d) quantifying the percentage of revertant viruses in the unclassified  
CC vaccine; and (e) comparing the percentage of revertant viruses in the  
CC unclassified vaccine to the percentage of revertant viruses in an  
CC accepted reference vaccine which can pass the monkey neurovirulence test  
CC utilised by the World Health Organisation, an unclassified vaccine with a  
CC higher percentage of A to G revertant viruses than in the reference  
CC vaccine being classified as unacceptable and an unclassified vaccine with  
CC an equal or lower percentage of A to G revertant viruses than in the  
CC reference vaccine classified as acceptable. The test can also be used to  
CC identify cells that are suitable for the culture of attenuated  
CC polioviruses

SQ Sequence 35 BP; 8 A; 8 C; 12 G; 7 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 2;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
|||  
Db 22 CCCCTGAATGCGGCTAATC 4

RESULT 8

ABE56836

ID ABE56836 standard; DNA; 119 BP.

XX

AC ABE56836;

XX 22-SEP-2005 (first entry)

XX Human coxsackievirus B2 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B2.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.  
XX (PRIC//) PRICE J A.

XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;  
XX WPI; 2005-512251/52.

XX GENBANK; Y09512.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 selected sequences of ABE56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more containers that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of ABE56764  
CC to ABE56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 119 BP; 26 A; 28 C; 36 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 9  
 AEB56856  
 ID AEB56856 standard; DNA; 173 BP.  
 XX AC AEB56856;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 5 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human echovirus 5.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF188359.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence,  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 2.5; 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATGCGGCTAATC 19  
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 10  
 AEB56855  
 ID AEB56855 standard; DNA; 173 BP.  
 XX AC AEB56855;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 5 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human echovirus 5.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF188358.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 173;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATGCGGCTAATC 19  
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 10  
 AEB56855  
 ID AEB56855 standard; DNA; 173 BP.  
 XX AC AEB56855;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 5 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human echovirus 5.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF188358.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence,  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

RESULT 11  
 AAZ58488  
 ID AAZ58488 standard; RNA; 176 BP.  
 XX AC AAZ58488;  
 XX DT 15-SEP-2003 (revised)  
 XX DT 23-MAY-2000 (first entry)  
 XX DE Recombinant poliovirus PVI(pr) IRES domain V-VI region.  
 XX Internal ribosomal entry site; IRES; picornavirus; PVI(pr); tumour;  
 KW cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma;  
 KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;  
 KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.  
 XX OS Human poliovirus 1.  
 OS Human rhinovirus sp; type 2.  
 OS Chimeric.  
 XX FH Key Location/Qualifiers  
 FT stem\_loop 1..109  
 FT /\*tag= a  
 FT /note= "domain V"  
 FT 138..176  
 FT /\*tag= b  
 FT /note= "domain VI"  
 FT WO200008166-A1.  
 XX PN 17-FEB-2000.  
 XX PD 09-APR-1999; 99WO-US007839.  
 XX PF 05-AUG-1998; 98US-00129686.  
 XX PR (UUNY ) UNIV NEW YORK STATE RES FOUND.  
 XX PA Gromeier M, Wimmer E;  
 XX PI WPI; 2000-205717/18.  
 XX DR Chimeric recombinant poliovirus useful for treating malignant tumors  
 XX PT comprises internal ribosomal entry site derived from picornaviruses.  
 XX PS Example 6; Fig 7; 99pp; English.  
 XX PS This sequence represents domains V-VI of the internal ribosomal entry  
 CC site (IRES) of PVI(pr), a recombinant, non-pathogenic oncolytic  
 CC poliovirus that carries the IRES of poliovirus type 1 Mahoney where the  
 CC terminal loop of regions of domain V and domain VI are substituted with  
 CC the corresponding fragments of human rhinovirus type 2 (HRV2). PVI(pr)  
 CC was characterized by a loss of neuropathogenicity, demonstrated by its  
 CC reduced ability to propagate within cells of neuronal origin and failure  
 CC to cause neurological disease in Cd155 tg mice. Oncolytic potential was  
 CC demonstrated against a panel of malignant cell lines. PVI(pr) is an  
 CC example of novel recombinant polioviruses (I) of the invention in which  
 CC the IRES of wild-type poliovirus is exchanged with the IRES of another  
 CC picornavirus, such as HRV2, and optionally the P1, P3 or 3' untranslated  
 CC region is exchanged with that of Sabin poliovirus. (I) are useful for  
 CC treating malignant tumors such as glioblastoma multiforme,  
 CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial  
 CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to  
 CC standardise OS field)  
 XX SQ Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 3; Length 176;  
 Best Local Similarity 78.9%; Pred. No. 2.5;  
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CCCCTGAATGGCGCTAATC 19

Db 4 CCCCGAAGCGCGUAUC 22  
 RESULT 12  
 AEB56834  
 ID AEB56834 standard; DNA; 180 BP.  
 XX AC AEB56834;  
 XX DT 22-SEP-2005 (first entry)  
 XX DE Human coxsackievirus B1 5' untranslated polynucleotide sequence.  
 KW DNA detection; enteroviral detection; ds.  
 XX OS Human coxsackievirus B1.  
 OS US2005158710-A1.  
 XX PN 21-JUL-2005.  
 XX PD 16-JAN-2004; 2004US-00760048.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX DR WPI; 2005-512251/52.  
 XX DR GENEANK; S76767.  
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PS detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; Fig 1A-D; 34pp; English.  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX SQ Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 CCCCTGAATGGCGCTAATC 19  
 Db 45 CCCCTGAATGGCGCTAATC 63  
 RESULT 13  
 AEB56865  
 ID AEB56865 standard; DNA; 198 BP.  
 XX AC AEB56865;  
 OY 1 CCCCTGAATGGCGCTAATC 19

```
XX 22-SEP-2005 (first entry)
XX DT
XX DE Human echovirus 12 5' untranslated polynucleotide sequence.
XX KW
XX OS DNA detection; enteroviral detection; ds.
XX PA
XX PA Human echovirus 12.
XX PA US2005158710-A1.
XX PD
XX PF 21-JUL-2005.
XX PR 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX TSANG S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11706.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I) and
XX (KI) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATCGGCTAATC 19
XX | | | | | | | | | |
XX Db 7 CCCCTGAATCGGCTAATC 25
XX
XX RESULT 14
XX AEB56853
XX ID AEB56853 standard; DNA; 198 BP.
XX AC AEB56853;
XX XX
XX 22-SEP-2005 (first entry)
XX DT
XX DE Human echovirus 2 5' untranslated polynucleotide sequence.
XX KW
XX OS DNA detection; enteroviral detection; ds.
XX PA
XX PA Human echovirus 2.
XX TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX TSANG S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11706.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I) and
XX (KI) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATCGGCTAATC 19
XX | | | | | | | | | |
XX Db 7 CCCCTGAATCGGCTAATC 25
XX
XX RESULT 15
XX AEB56860
XX ID AEB56860 standard; DNA; 198 BP.
XX AC AEB56860;
XX XX
XX 22-SEP-2005 (first entry)
XX DT
XX DE Human echovirus 9 5' untranslated polynucleotide sequence.
XX KW
XX OS DNA detection; enteroviral detection; ds.
XX PA
XX PA Human echovirus 9.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX TSANG S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11707.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequence. (I) and
XX (KI) are useful for detecting enterovirus target sequences. (I) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 14; Length 198;
XX Best Local Similarity 100.0%; Pred. No. 2.5;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 CCCCTGAATCGGCTAATC 19
XX | | | | | | | | | |
XX Db 7 CCCCTGAATCGGCTAATC 25
XX
XX RESULT 15
XX AEB56860
XX ID AEB56860 standard; DNA; 198 BP.
XX AC AEB56860;
XX XX
XX 22-SEP-2005 (first entry)
XX DT
XX DE Human echovirus 9 5' untranslated polynucleotide sequence.
XX KW
XX OS DNA detection; enteroviral detection; ds.
XX PA
XX PA Human echovirus 9.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
```

PA (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; U11710.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX Query Match 100.0%; Score 19; DB 14; Length 198;  
 XX Best Local Similarity 100.0%; Pred. No. 2.5;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGGGCTAATC 19  
 DB 7 CCCCTGAATGGGCTAATC 25

RESULT 16  
 AEB56854  
 ID AEB56854 standard; DNA; 198 BP.  
 XX AC AEB56854;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 4 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.  
 XX Human echovirus 4.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; U11708.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX Query Match 100.0%; Score 19; DB 14; Length 198;  
 XX Best Local Similarity 100.0%; Pred. No. 2.5;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGGGCTAATC 19  
 DB 7 CCCCTGAATGGGCTAATC 25

RESULT 17  
 AEB56837  
 ID AEB56837 standard; DNA; 237 BP.  
 XX AC AEB56837;  
 XX 22-SEP-2005 (first entry)  
 XX Human coxsackievirus B2 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.  
 XX Human coxsackievirus B2.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF081485.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (1), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (1) and  
CC specifically and selectively recognizes the enterovirus genome. (1)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 18  
AEB56848  
ID AEB56848 standard; DNA; 237 BP.  
XX  
AC AEB56848;  
XX  
XX  
XX 22-SEP-2005 (first entry)  
XX  
XX Human coxsackievirus B5 5' untranslated polynucleotide sequence.  
XX  
XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B5.  
XX US2005158710-A1.  
XX 21-JUL-2005.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX 16-JAN-2004; 2004US-00760048.  
XX (TSAN/) TSANG S.  
XX (PRIC/) PRICE J A.  
XX (HELL/) HELLYER T J.  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX GENBANK; AF114383.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (1), and one or more container that contains (1); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequence. (1), (M1) and  
XX (K1) are useful for detecting enterovirus target sequences. (1)  
XX specifically and selectively recognizes the enterovirus genome. (1)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 19  
AEB56879  
ID AEB56879 standard; DNA; 237 BP.  
XX  
XX  
AC AEB56879;  
XX  
XX 22-SEP-2005 (first entry)  
XX  
XX Human poliovirus 3 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.  
XX Human poliovirus 3.  
XX US2005158710-A1.  
XX 21-JUL-2005.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX 16-JAN-2004; 2004US-00760048.  
XX (TSAN/) TSANG S.  
XX (PRIC/) PRICE J A.  
XX (HELL/) HELLYER T J.  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX GENBANK; K01392.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; Fig 1A-D; 34pp; English.  
XX  
XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (1), and one or more container that contains (1); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequence. (1), (M1) and  
XX (K1) are useful for detecting enterovirus target sequences. (1)  
XX specifically and selectively recognizes the enterovirus genome. (1)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The  
XX present sequence represents a viral 5' untranslated polynucleotide  
XX sequence given in the exemplification of the present invention.

XX  
XX  
SQ Sequence 237 BP; 54 A; 57 C; 65 G; 61 T; 0 U; 0 Other;  
Query Match 100.0%; Score 19; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 CCCCTGAATCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATCGGCTAATC 65

## RESULT 20

AEBS6875  
 ID AEBS6875 standard; DNA; 237 BP.

XX AC AEBS6875;  
 XX XX

DT 22-SEP-2005 (first entry)

DE Human poliovirus 1 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; V01149.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 57 A; 54 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATCGGCTAATC 65

## RESULT 21

AEBS6876  
 ID AEBS6876 standard; DNA; 237 BP.

XX XX

AC AEBS6876;  
 XX 22-SEP-2005 (first entry)  
 XX Human poliovirus 1 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; V01150.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 56 A; 54 C; 63 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATCGGCTAATC 65

## RESULT 22

AEBS6873

ID AEBS6873 standard; DNA; 237 BP.

XX AC AEBS6873;

XX 22-SEP-2005 (first entry)

XX Human poliovirus 1 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AJ132961.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX target binding sequence of an oligonucleotide chosen from any one of the  
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 XX selected amplification or detection reaction. Also described: (1) a kit  
 XX (K1) comprising (I), and one or more container that contains (I); and (2)  
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 XX the target sequence using first amplification primer having a sequence  
 XX consisting essentially of target binding sequence of any one of AEB56764  
 XX to AEB56771 and optionally a sequence required for selected amplification  
 XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 XX specifically and selectively recognizes the enterovirus genome. (I)  
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
 XX genome and allows detection of broad range of enterovirus serotypes. The  
 XX present sequence represents a viral 5' untranslated polynucleotide  
 XX sequence given in the exemplification of the present invention.  
 XX Sequence 237 BP; 54 A; 57 C; 63 G; 63 T; 0 U; 0 Other;  
 XX Query Match 100.0%; Score 19; DB 14; Length 237;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 CCCCTGAATGCGGCTAATC 19  
 XX |||||  
 XX 47 CCCCTGAATGCGGCTAATC 65  
 XX  
 XX RESULT 23  
 XX AEB56861  
 XX ID AEB56861 standard; DNA; 237 BP.  
 XX AC AEB56861;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 9 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.  
 XX Human echovirus 9.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF083069.  
 XX

PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; X84981.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX target binding sequence of an oligonucleotide chosen from any one of the  
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 XX selected amplification or detection reaction. Also described: (1) a kit  
 XX (K1) comprising (I), and one or more container that contains (I); and (2)  
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 XX the target sequence using first amplification primer having a sequence  
 XX consisting essentially of target binding sequence of any one of AEB56764  
 XX to AEB56771 and optionally a sequence required for selected amplification  
 XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 XX specifically and selectively recognizes the enterovirus genome. (I)  
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
 XX genome and allows detection of broad range of enterovirus serotypes. The  
 XX present sequence represents a viral 5' untranslated polynucleotide  
 XX sequence given in the exemplification of the present invention.  
 XX Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;  
 XX Query Match 100.0%; Score 19; DB 14; Length 237;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6;  
 XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX 1 CCCCTGAATGCGGCTAATC 19  
 XX |||||  
 XX 46 CCCCTGAATGCGGCTAATC 64  
 XX  
 XX RESULT 24  
 XX AEB56857  
 XX ID AEB56857 standard; DNA; 237 BP.  
 XX AC AEB56857;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 5 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.  
 XX Human echovirus 5.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX GENBANK; AF083069.  
 XX

PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 49 A; 59 C; 63 G; 66 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 Db |||||  
 47 CCCCTGAATGCGGCTAATC 65

## RESULT 25

AEB56871  
 ID AEB56871 standard; DNA; 237 BP.

AC AEB56871;

DT 22-SEP-2005 (first entry)

DE Human enterovirus 70 5' untranslated polynucleotide sequence.

KW DNA detection; enteroviral detection; ds.

XX Human enterovirus 70.

XX US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.  
 DR GENBANK; D00820.

PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 Db |||||  
 47 CCCCTGAATGCGGCTAATC 65

## RESULT 26

AEB56872

ID AEB56872 standard; DNA; 237 BP.

AC AEB56872;

DT 22-SEP-2005 (first entry)

DE Human poliovirus 1 5' untranslated polynucleotide sequence.

KW DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

XX US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.  
 DR GENBANK; AJ132960.

PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 27  
 AEB56840  
 ID AEB56840 standard; DNA; 238 BP.  
 XX  
 AC AEB56840;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B3.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.

XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.  
 DR GENBANK; AH008164.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC (K2) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 28  
 AEB56850  
 ID AEB56850 standard; DNA; 238 BP.  
 XX  
 AC AEB56850;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B6 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B6.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.

XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.  
 DR GENBANK; AF039205.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 52 A; 59 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGGGCTAATC 65

RESULT 29  
 AEB56878  
 ID AEB56878 standard; DNA; 238 BP.

XX AC AEB56878;  
 XX XX 22-SEP-2005 (first entry)  
 XX XX Human poliovirus 2 5' untranslated polynucleotide sequence.  
 XX DE DNA detection; enteroviral detection; ds.  
 XX KW Human poliovirus 2.  
 XX OS US2005158710-A1.  
 XX PN 21-JUL-2005.  
 XX PD 16-JAN-2004; 2004US-00760048.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX PI WPI; 2005-512251/52.  
 XX DR GENBANK; X00595.  
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PT Disclosure; Fig 1A-D; 34pp; English.  
 XX PS The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX CC target binding sequence of an oligonucleotide chosen from any one of the  
 XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 XX CC selected amplification or detection reaction. Also described: (1) a kit  
 XX CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 XX CC the target sequence using first amplification primer having a sequence  
 XX CC consisting essentially of target binding sequence of any one of AEB56764  
 XX CC to AEB56771 and optionally a sequence required for selected amplification  
 XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 XX CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
 XX CC specifically and selectively recognizes the enterovirus genome. (I)  
 XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 XX CC genome and allows detection of broad range of enterovirus serotypes. The  
 XX CC present sequence represents a viral 5' untranslated polynucleotide  
 XX CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 56 A; 53 C; 66 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 30  
 AEB56849  
 ID AEB56849 standard; DNA; 238 BP.  
 XX AC AEB56849;  
 XX XX 22-SEP-2005 (first entry)  
 XX DE Human coxsackievirus B5 5' untranslated polynucleotide sequence.  
 XX KW DNA detection; enteroviral detection; ds.  
 XX XX

OS Human coxsackievirus B5.  
 XX PN US2005158710-A1.  
 XX XX 21-JUL-2005.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.  
 XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX PI WPI; 2005-512251/52.  
 XX DR GENBANK; X67706.  
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PT Disclosure; Fig 1A-D; 34pp; English.  
 XX PS The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX CC target binding sequence of an oligonucleotide chosen from any one of the  
 XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 XX CC selected amplification or detection reaction. Also described: (1) a kit  
 XX CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 XX CC the target sequence using first amplification primer having a sequence  
 XX CC consisting essentially of target binding sequence of any one of AEB56764  
 XX CC to AEB56771 and optionally a sequence required for selected amplification  
 XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 XX CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
 XX CC specifically and selectively recognizes the enterovirus genome. (I)  
 XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 XX CC genome and allows detection of broad range of enterovirus serotypes. The  
 XX CC present sequence represents a viral 5' untranslated polynucleotide  
 XX CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 31  
 AEB56839  
 ID AEB56839 standard; DNA; 238 BP.  
 XX AC AEB56839;  
 XX XX 22-SEP-2005 (first entry)  
 XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
 XX KW DNA detection; enteroviral detection; ds.  
 XX OS Human coxsackievirus B3.  
 XX PN US2005158710-A1.  
 XX PD 21-JUL-2005.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.

```
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; AF169670.
XX DR
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 52 A; 54 C; 63 G; 69 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 47 CCCCTGAATCGGCTAATC 65
RESULT 12
AEB56846
ID AEB56846 standard; DNA; 238 BP.
XX AC AEB56846;
XX DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus B4.
XX FN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; D00149.
XX CC
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 52 A; 54 C; 63 G; 69 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 47 CCCCTGAATCGGCTAATC 65
RESULT 33
AEB56847
ID AEB56847 standard; DNA; 238 BP.
XX AC AEB56847;
XX DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus B4.
XX FN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX WPI; 2005-512251/52.
XX DR GENBANK; X05690.
XX CC
XX CC Novel oligonucleotide comprising sequences for binding and amplifying or
XX CC detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 47 CCCCTGAATCGGCTAATC 65
```

CC selected amplification or detection reaction. Also described: (1) a kit  
 CC comprising (1), and one or more container that contains (1); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (1), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (1)  
 CC specifically and selectively recognizes the enterovirus genome. (1)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 XX SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGCGGCTAATC 19  
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 34  
 AEB56838  
 ID AEB56838 standard; DNA; 238 BP.  
 AC AEB56838;  
 DT 22-SEP-2005 (first entry)  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

OS Human coxsackievirus B3.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN//) TSANG S.

PA (PRIC//) PRICE J A.

PA (HELL//) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.

DR GENBANK; AF169665.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (1) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC comprising (1), and one or more container that contains (1); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (1), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (1)  
 CC specifically and selectively recognizes the enterovirus genome. (1)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 DB 47 CCCCTGAATGCGGCTAATC 65

RESULT 35  
 AEB56842  
 ID AEB56842 standard; DNA; 238 BP.  
 AC AEB56842;  
 DT 22-SEP-2005 (first entry).

DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

OS Human coxsackievirus B3.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN//) TSANG S.

PA (PRIC//) PRICE J A.

PA (HELL//) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

DR WPI; 2005-512251/52.

DR GENBANK; M16572.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (1) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC comprising (1), and one or more container that contains (1); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (1), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (1)  
 CC specifically and selectively recognizes the enterovirus genome. (1)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;







DR GENBANK; V01148.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a consensus viral 5' untranslated  
 CC polynucleotide sequence given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGCGCTAATC 19  
 Db 47 CCCCTGAATCGCGCTAATC 65  
 RESULT 41  
 AEB56829  
 ID AEB56829 standard; DNA; 238 BP.  
 AC AEB56829;  
 XX  
 XX 22-SEP-2005 (first entry)  
 DT  
 DE Consensus viral 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Synthetic.  
 XX  
 XX US2005158710-A1.  
 PN  
 XX 21-JUL-2005.  
 PD  
 XX 16-JAN-2004; 2004US-00760048.  
 PF  
 XX 16-JAN-2004; 2004US-00760048.  
 PR  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 XX Teang S, Price JA, Hellyer TJ;  
 PI  
 XX WPI; 2005-512251/52.  
 DR  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGCGCTAATC 19  
 Db 47 CCCCTGAATCGCGCTAATC 65  
 RESULT 42  
 AEB56843  
 ID AEB56843 standard; DNA; 238 BP.  
 XX  
 AC AEB56843;  
 XX  
 XX 22-SEP-2005 (first entry)  
 DT  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B3.  
 XX  
 XX US2005158710-A1.  
 PN  
 XX 21-JUL-2005.  
 PD  
 XX 16-JAN-2004; 2004US-00760048.  
 PF  
 XX 16-JAN-2004; 2004US-00760048.  
 PR  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 XX Teang S, Price JA, Hellyer TJ;  
 PI  
 XX WPI; 2005-512251/52.  
 DR  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 SX Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGCGGCTAATC 65

## RESULT 43

AEBS6845  
 ID AEBS6845 standard; DNA; 238 BP.

XX AC AEBS6845;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; U57056.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEBS6762 to AEBS6771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEBS6764  
 CC to AEBS6771; and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGCGGCTAATC 65

## RESULT 44

AEBS6870

ID AEBS6870 standard; DNA; 238 BP.

XX AC AEBS6870;

XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 30 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 30.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; AF162711.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEBS6762 to AEBS6771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEBS6764  
 CC to AEBS6771; and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 51 A; 56 C; 61 G; 70 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 2.6;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATGCGGCTAATC 65

## RESULT 45

AEB56830  
 ID AEB56830 standard; DNA; 238 BP.  
 XX  
 AC AEB56830;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus A9 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus A9.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; D00627.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 50 A; 58 C; 66 G; 64 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 47 CCCCTGAATCGGCTAATC 65  
 RESULT 46  
 AEB56833  
 ID AEB56833 standard; DNA; 238 BP.  
 XX  
 AC AEB56833;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus A24 5' untranslated polynucleotide sequence.  
 XX

KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus A24.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; D90457.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 53 A; 54 C; 64 G; 67 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 47 CCCCTGAATCGGCTAATC 65  
 RESULT 47  
 AEB56877  
 ID AEB56877 standard; DNA; 238 BP.  
 XX  
 AC AEB56877;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human poliovirus 2 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human poliovirus 2.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.

```
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX
DR WPI; 2005-512251/52.
DR GENBANK; M12197.
XX XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
DB 47 CCCCTGAATGCGGCTAATC 65
RESULT 48
AEB56859
ID AEB56859 standard; DNA; 238 BP.
XX AC AEB56859;
XX XX
DT 22-SEP-2005 (first entry)
XX DE Human echovirus 6 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 6.
XX XX
PN US2005158710-A1.
XX PD 21-JUL-2005.
XX XX
PF 16-JAN-2004; 2004US-00760048.
XX KW DNA detection; enteroviral detection; ds.
XX XX
OS Human echovirus 6.
XX XX
PN US2005158710-A1.
XX PD 21-JUL-2005.
XX XX
PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX
DR WPI; 2005-512251/52.
DR GENBANK; M74567.
XX XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CCCCTGAATGCGGCTAATC 19
DB 47 CCCCTGAATGCGGCTAATC 65
RESULT 49
AEB56841
ID AEB56841 standard; DNA; 238 BP.
XX AC AEB56841;
XX XX
DT 22-SEP-2005 (first entry)
XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus B3.
XX XX
PN US2005158710-A1.
XX PD 21-JUL-2005.
XX XX
PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX XX
DR WPI; 2005-512251/52.
DR GENBANK; M74567.
XX XX
PT Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
```

CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 52 A; 58 C; 65 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATCGGCTAATC 65

## RESULT 50

AEB56831  
 ID AEB56831 standard; DNA; 238 BP.

XX AC AEB56831;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus A16.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.  
 XX DR GENBANK; U05876.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 2.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 |||||  
 Db 47 CCCCTGAATCGGCTAATC 65

## RESULT 51

AEB56867  
 ID AEB56867 standard; DNA; 238 BP.

XX AC AEB56867;

XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 12 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 12.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.  
 XX DR GENBANK; X79047.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains: (1) a kit  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC sensitively and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 52  
AEB56844  
ID AEB56844 standard; DNA; 238 BP.  
XX  
AC AEB56844;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
OS Human coxsackievirus B3.  
XX  
PN US2005158710-A1.  
XX  
PD 21-JUL-2005.  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
DR GENBANK; M88483.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
PS Disclosure; Fig 1A-D; 34pp; English.

The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 47 CCCCTGAATGCGGCTAATC 65

Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 53  
AEB56866  
ID AEB56866 standard; DNA; 238 BP.  
XX  
AC AEB56866;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human echovirus 12 5' untranslated polynucleotide sequence.  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
OS Human echovirus 12.  
XX  
PN US2005158710-A1.  
XX  
PD 21-JUL-2005.  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
DR GENBANK; X77708.

Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

Disclosure; Fig 1A-D; 34pp; English.

The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (KI) comprising (I), and one or more container that contains (I); and (2) detecting (MI) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (I), (MI) and (KI) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 47 CCCCTGAATGCGGCTAATC 65

Query Match 100.0%; Score 19; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 2.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 47 CCCCTGAATGCGGCTAATC 65

RESULT 54  
AEB56882  
ID AEB56882 standard; DNA; 238 BP.  
XX  
AC AEB56882;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human poliovirus 3 5' untranslated polynucleotide sequence.

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XX DNA detection; enteroviral detection; ds.
KW Human poliovirus 3.
OS
XX
XX US2005158710-A1.
XX PN
XX
XX 21-JUL-2005.
XX PD
XX
XX 16-JAN-2004; 2004US-00760048.
XX PF
XX
XX 16-JAN-2004; 2004US-00760048.
XX PR
XX
XX (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX PI
XX WPI; 2005-512251/52.
XX DR
XX GENBANK; X04468.
XX DR
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX FT
XX Disclosure; Fig 1A-D; 34pp; English.
XX PS
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABB56764
XX CC to ABB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I) (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Dy 47 CCCCTGAATCGGCTAATC 65

RESULT 55
ABX12446
ID ABX12446 standard; DNA; 497 BP.
XX
XX AC ABX12446;
XX
XX 10-MAY-2003 (first entry)
XX DT
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #1.
XX DE
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX PD
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX PD
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX PN

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XX 27-DEC-2002.
PD
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX 20-JUN-2001; 2001SE-00002198.
XX PR
XX (INNO-) INNOVENTUS PROJECT AB.
XX PA
XX Tuvemo HT, Frisk GE, Yin H;
XX PI
XX WPI; 2003-278229/27.
XX DR
XX Polymerease chain reaction and primers for detecting nucleic acids from
XX PT the diabetogenic coxsackie B virus-4 strain VD2921.
XX FT
XX Disclosure; Page 72; 79pp; English.
XX PS
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX CC strain VD2921, particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX CC P3C and P3D nucleic acids). The methods and primers are used for the
XX CC detection of CBV-4 strain VD2921 which is associated with diabetes
XX CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX CC cells, can improve prognosis by allowing treatment e.g. with antiviral
XX CC drugs, to prevent further loss of beta cells and severe long term
XX CC consequences of diabetes including blindness, renal failure and leg
XX CC amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX CC (CBV-4) strain VD2921 associated polynucleotide
XX
XX SQ Sequence 497 BP; 119 A; 134 C; 129 G; 115 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 497;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Dy 365 CCCCTGAATCGGCTAATC 383

RESULT 56
ABX12451
ID ABX12451 standard; DNA; 502 BP.
XX
XX AC ABX12451;
XX
XX 10-MAY-2003 (first entry)
XX DT
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.
XX DE
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX PD
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX PD
XX 19-JUN-2002; 2002WO-IB003278.
XX PF
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX KW renal failure; leg amputation; ds.
XX
XX OS Cocksackievirus.
XX OS
XX WO2002103060-A2.
XX PN

```



PT Polymerase chain reaction and primers for detecting nucleic acids from  
 XX the diabetogenic coxsackie B virus-4 strain VD2921.  
 XX  
 XX  
 XX Disclosure; Page 73; 79pp; English.  
 XX  
 CC The invention describes a polymerase chain reaction (PCR) and primers for  
 CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 CC P3C and P3D nucleic acids). The methods and primers are used for the  
 CC detection of CBV-4 strain VD2921 which is associated with diabetes  
 CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
 CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
 CC drugs, to prevent further loss of beta cells and severe long term  
 CC consequences of diabetes including blindness, renal failure and leg  
 CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
 CC (CBV-4) strain VD2921 associated polynucleotide  
 XX  
 XX Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 19; DB 8; Length 502;  
 Best Local Similarity 100.0%; Pred. No. 2.8;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATCGCGCTAATC 19  
 DB 368 CCCCTGAATCGCGCTAATC 386  
 RESULT 57  
 AAZ58487  
 ID AAZ58487 standard; RNA; 514 BP.  
 XX  
 AC AAZ58487;  
 DT 15-SEP-2003 (revised)  
 DT 23-MAY-2000 (first entry)  
 XX  
 DE Poliovirus IRES domain II-VI region.  
 XX  
 XX Internal ribosomal entry site; IRES; picornavirus; tumour; cancer;  
 KW glioblastoma multiforme; medulloblastoma; mammary carcinoma;  
 KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;  
 KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.  
 XX  
 OS Human poliovirus 1.  
 XX  
 FH Key Location/Qualifiers  
 FT stem\_loop 25..63  
 FT /\*tag= a  
 FT /note= "domain II"  
 FT stem\_loop 70..83  
 FT /\*tag= b  
 FT stem\_loop 84..120  
 FT /\*tag= c  
 FT /note= "domain III"  
 FT stem\_loop 132..338  
 FT /\*tag= d  
 FT /note= "domain IV"  
 FT stem\_loop 183..209  
 FT /\*tag= e  
 FT /note= "domain V"  
 FT stem\_loop 273..292  
 FT /\*tag= f  
 FT stem\_loop 346..454  
 FT /\*tag= g  
 FT /note= "domain VI"  
 FT stem\_loop 481..513  
 FT /\*tag= h  
 FT /note= "domain VI"  
 XX  
 PN WO200008166-A1.  
 XX  
 PD 17-FEB-2000.

XX 09-APR-1999; 99WO-US007839.  
 XX  
 XX 05-AUG-1998; 98US-00129686.  
 XX  
 XX (UUNY ) UNIV NEW YORK STATE RES FOUND.  
 XX  
 XX Gromeier M, Wimmer E;  
 XX  
 XX WPI; 2000-205717/18.  
 XX  
 PT Chimeric recombinant poliovirus useful for treating malignant tumors  
 PT comprises internal ribosomal entry site derived from picornaviruses.  
 XX  
 XX Disclosure; Fig 2; 99pp; English.  
 XX  
 CC This sequence represents domains II-VI of the internal ribosomal entry  
 CC site (IRES) of wild-type poliovirus type 1 Mahoney. The invention  
 CC provides non-pathogenic, oncolytic, recombinant polioviruses (I) in which  
 CC the IRES of the wild-type poliovirus is exchanged with the IRES of  
 CC another picornavirus, such as human rhinovirus type 2, and optionally the  
 CC P1, P3 or 3' untranslated region is exchanged with that of Sabin  
 CC poliovirus. (I) may contain a composite IRES encompassing IRES domains  
 CC from both wild-type poliovirus and from another virus. (I) are useful for  
 CC treating malignant tumors such as glioblastoma multiforme,  
 CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial  
 CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to  
 CC standardise OS field)  
 XX  
 SQ Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 3; Length 514;  
 Best Local Similarity 78.9%; Pred. No. 2.8;  
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATCGCGCTAATC 19  
 DB 349 CCCCTGAATCGCGCTAATC 367  
 RESULT 58  
 ABL53112  
 ID ABL53112 standard; DNA; 520 BP.  
 XX  
 AC ABL53112;  
 DT 07-AUG-2003 (revised)  
 DT 25-JUN-2002 (first entry)  
 XX  
 XX Micro-organism detection probe #54.  
 XX  
 XX Probe; microorganism detection; microbiological quality;  
 XX water purification; ss.  
 XX  
 OS Coxsackievirus.  
 XX  
 XX WO200202811-A2.  
 XX  
 XX 10-JAN-2002.  
 XX  
 XX 06-JUL-2001; 2001WO-FR002191.  
 XX  
 XX 06-JUL-2000; 2000FR-00008839.  
 XX  
 XX (INNR ) BIO MERIEUX.  
 XX  
 XX Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;  
 XX Armand M, Laffaire P;  
 XX  
 XX WPI; 2002-148021/19.  
 XX  
 XX Monitoring microbiological quality of water, useful particularly for  
 XX controlling water purification, uses oligonucleotide probes to detect at

PT least three representative microbes.  
XX  
PS Claim 24; Page 75-76 ; 85pp; French.  
XX  
CC The present invention relates to a method for monitoring microbiological  
CC quality of an aqueous environmental medium that potentially contains many  
CC different microorganisms. A reference set of at least three  
CC microorganisms is chosen that, separately or collectively, represent  
CC microbiological quality. The test medium is treated, then any  
CC microorganisms, or their fragments, in the treated medium is contacted  
CC with a set of at least three probes for specific identification and  
CC multiple determination of selected microorganisms. This determination  
CC represents the level of microbiological quality. The method is useful for  
CC identifying and quantifying microorganisms in water and provides results  
CC that are used to control water purification/production processes. The  
CC present sequence is a probe which was used to illustrate the invention.  
CC (Updated on 07-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 520 BP; 113 A; 141 C; 131 G; 135 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 6; Length 520;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATCGCGCTAATC 19  
Db 386 CCCCTGAATCGCGCTAATC 404  
  
RESULT 59  
ABL53111  
ID ABL53111 standard; DNA; 521 BP.  
XX  
AC ABL53111;  
XX  
DT 07-AUG-2003 (revised)  
DT 25-JUN-2002 (first entry)  
XX  
DE Micro-organism detection probe #53.  
XX  
KW Probe; microorganism detection; microbiological quality;  
KW water purification; ss.  
XX  
OS Poliovirus.  
XX  
FN WO200202811-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-FR002191.  
XX  
PR 06-JUL-2000; 2000FR-00008839.  
XX  
PA (INNR ) BIO MERIEUX.  
XX  
PI Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;  
PI Armand M, Laffaire P;  
XX  
DR WPI; 2002-148021/19.  
XX  
PS Monitoring microbiological quality of water, useful particularly for  
PT controlling water purification, uses oligonucleotide probes to detect at  
PT least three representative microbes.  
XX  
XX Claim 24; Page 75; 85pp; French.  
XX  
CC The present invention relates to a method for monitoring microbiological  
CC quality of an aqueous environmental medium that potentially contains many  
CC different microorganisms. A reference set of at least three  
CC microorganisms is chosen that, separately or collectively, represent  
CC microbiological quality. The test medium is treated, then any  
CC microorganisms, or their fragments, in the treated medium is contacted  
CC with a set of at least three probes for specific identification and

CC multiple determination of selected microorganisms. This determination  
CC represents the level of microbiological quality. The method is useful for  
CC identifying and quantifying microorganisms in water and provides results  
CC that are used to control water purification/production processes. The  
CC present sequence is a probe which was used to illustrate the invention.  
CC (Updated on 07-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 521 BP; 113 A; 140 C; 138 G; 130 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 6; Length 521;  
Best Local Similarity 100.0%; Pred. No. 2.8;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATCGCGCTAATC 19  
Db 387 CCCCTGAATCGCGCTAATC 405  
  
RESULT 60  
ABL53113  
ID ABL53113 standard; DNA; 525 BP.  
XX  
AC ABL53113;  
XX  
DT 07-AUG-2003 (revised)  
DT 25-JUN-2002 (first entry)  
XX  
DE Micro-organism detection probe #55.  
XX  
KW Probe; microorganism detection; microbiological quality;  
KW water purification; ss.  
XX  
OS Echovirus sp.  
XX  
FN WO200202811-A2.  
XX  
PD 10-JAN-2002.  
XX  
PF 06-JUL-2001; 2001WO-FR002191.  
XX  
PR 06-JUL-2000; 2000FR-00008839.  
XX  
PA (INNR ) BIO MERIEUX.  
XX  
PI Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;  
PI Armand M, Laffaire P;  
XX  
DR WPI; 2002-148021/19.  
XX  
PS Monitoring microbiological quality of water, useful particularly for  
PT controlling water purification, uses oligonucleotide probes to detect at  
PT least three representative microbes.  
XX  
XX Claim 24; Page 76; 85pp; French.  
XX  
CC The present invention relates to a method for monitoring microbiological  
CC quality of an aqueous environmental medium that potentially contains many  
CC different microorganisms. A reference set of at least three  
CC microorganisms is chosen that, separately or collectively, represent  
CC microbiological quality. The test medium is treated, then any  
CC microorganisms, or their fragments, in the treated medium is contacted  
CC with a set of at least three probes for specific identification and  
CC multiple determination of selected microorganisms. This determination  
CC represents the level of microbiological quality. The method is useful for  
CC identifying and quantifying microorganisms in water and provides results  
CC that are used to control water purification/production processes. The  
CC present sequence is a probe which was used to illustrate the invention.  
CC (Updated on 07-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 525 BP; 117 A; 142 C; 135 G; 131 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 6; Length 525;  
Best Local Similarity 100.0%; Pred. No. 2.8;

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 391 CCCCTGAATGGGCTAATC 409

RESULT 61
ABX12448
ID ABX12448 standard; DNA; 548 BP.
AC ABX12448;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
XX
KW Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.
XX
KW Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 27-DEC-2002.
XX
PF 19-JUN-2002; 2002WO-IB003278.
XX
PR 20-JUN-2001; 2001SE-00002198.
XX
PA (INNO-) INNOVENTUS PROJECT AB.
XX
PI Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
XX
PT Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic cocksackie B virus-4 strain VD2921.
XX
PS Disclosure; Page 72; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic cocksackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic cocksackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 548 BP; 124 A; 145 C; 144 G; 135 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 8; Length 548;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 358 CCCCTGAATGGGCTAATC 376

RESULT 62
ABX12453
ID ABX12453 standard; DNA; 551 BP.
AC ABX12453;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #7.
XX
KW Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
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DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.
XX
KW Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
DT 27-DEC-2002.
XX
PF 19-JUN-2002; 2002WO-IB003278.
XX
PR 20-JUN-2001; 2001SE-00002198.
XX
PA (INNO-) INNOVENTUS PROJECT AB.
XX
PI Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
XX
PT Polymerase chain reaction and primers for detecting nucleic acids from
PT the diabetogenic cocksackie B virus-4 strain VD2921.
XX
PS Disclosure; Page 74; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic cocksackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents a diabetogenic cocksackie B virus 4
CC (CBV-4) strain VD2921 associated polynucleotide
XX
SQ Sequence 551 BP; 130 A; 147 C; 140 G; 134 T; 0 U; 0 Other;
Query Match 100.0%; Score 19; DB 8; Length 551;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
Db 364 CCCCTGAATGGGCTAATC 382

RESULT 63
ABX12452
ID ABX12452 standard; DNA; 552 BP.
XX
AC ABX12452;
XX
DT 10-MAY-2003 (first entry)
XX
DE Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #7.
XX
KW Cocksackie virus strain VD2921; diabetogenic cocksackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Cocksackievirus.
XX
PN WO2002103060-A2.
XX
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PD 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 552;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATCGGCTAATC 19
XX 365 CCCCTGAATCGGCTAATC 383
XX
XX RESULT 64
XX ABX12457
XX ID ABX12457 standard; DNA; 554 BP.
XX
XX AC ABX12457;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #12.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 552 BP; 131 A; 143 C; 140 G; 138 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 552;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATCGGCTAATC 19
XX 365 CCCCTGAATCGGCTAATC 383
XX
XX RESULT 64
XX ABX12457
XX ID ABX12457 standard; DNA; 554 BP.
XX
XX AC ABX12457;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #12.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term
XX consequences of diabetes including blindness, renal failure and leg
XX amputations. This sequence represents a diabetogenic coxsackie B virus 4
XX (CBV-4) strain VD2921 associated polynucleotide
XX
XX Sequence 554 BP; 130 A; 149 C; 142 G; 133 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 8; Length 554;
XX Best Local Similarity 100.0%; Pred. No. 2.9;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 CCCCTGAATCGGCTAATC 19
XX 362 CCCCTGAATCGGCTAATC 380
XX
XX Db
XX
XX RESULT 65
XX ABX12449
XX ID ABX12449 standard; DNA; 556 BP.
XX
XX AC ABX12449;
XX
XX 10-MAY-2003 (first entry)
XX
XX Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #4.
XX
XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;
XX renal failure; leg amputation; ds.
XX
XX Coxsackievirus.
XX
XX WO2002103060-A2.
XX
XX 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.
XX
XX 20-JUN-2001; 2001SE-00002198.
XX
XX (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
XX WPI; 2003-278229/27.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
XX Disclosure; Page 72-73; 79pp; English.
XX
XX The invention describes a polymerase chain reaction (PCR) and primers for
XX detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
XX strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
XX P3C and P3D nucleic acids). The methods and primers are used for the
XX detection of CBV-4 strain VD2921 which is associated with diabetes
XX (diabetogenic enterovirus). Early detection of the diabetes e.g.
XX detection of diabetogenic enteroviral RNA in peripheral mononuclear
XX cells, can improve prognosis by allowing treatment e.g. with antiviral
XX drugs, to prevent further loss of beta cells and severe long term

```

CC consequences of diabetes including blindness, renal failure and leg  
 CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
 CC (CBV-4) strain VD2921 associated polynucleotide

XX SQ Sequence 556 BP; 125 A; 153 C; 143 G; 135 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 8; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 366 CCCCTGAATGCGGCTAATC 384

## RESULT 66

ABX12450  
 ID ABX12450 standard; DNA; 556 BP.

XX AC ABX12450;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #5.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
 strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
 diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
 renal failure; leg amputation; ds.

XX OS Coxsackievirus.

XX PN WO2002103060-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-IB003278.

XX PR 20-JUN-2001; 2001SE-00002198.

XX PA (INNO-) INNOVENTUS PROJECT AB.

XX PI Tuvemo HT, Frisk GE, Yin H;

XX WPI; 2003-278229/27.

XX PT Polymerase chain reaction and primers for detecting nucleic acids from  
 the diabetogenic coxsackie B virus-4 strain VD2921.

XX PS Disclosure; Page 73; 79pp; English.

XX CC The invention describes a polymerase chain reaction (PCR) and primers for  
 detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 P3C and P3D nucleic acids). The methods and primers are used for the  
 detection of CBV-4 strain VD2921 which is associated with diabetes  
 (diabetogenic enterovirus). Early detection of the diabetes e.g.

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 cells, can improve prognosis by allowing treatment e.g. with antiviral  
 drugs, to prevent further loss of beta cells and severe long term  
 consequences of diabetes including blindness, renal failure and leg  
 amputations. This sequence represents a diabetogenic coxsackie B virus 4  
 (CBV-4) strain VD2921 associated polynucleotide

XX SQ Sequence 556 BP; 127 A; 147 C; 145 G; 137 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 8; Length 556;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 365 CCCCTGAATGCGGCTAATC 383

## RESULT 67

ABX12456

XX ID ABX12456 standard; DNA; 559 BP.

XX AC ABX12456;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #11.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
 strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
 diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
 renal failure; leg amputation; ds.

XX OS Coxsackievirus.

XX PN WO2002103060-A2.

XX PD 27-DEC-2002.

XX PF 19-JUN-2002; 2002WO-IB003278.

XX PR 20-JUN-2001; 2001SE-00002198.

XX PA (INNO-) INNOVENTUS PROJECT AB.

XX PI Tuvemo HT, Frisk GE, Yin H;

XX WPI; 2003-278229/27.

XX PT Polymerase chain reaction and primers for detecting nucleic acids from  
 the diabetogenic coxsackie B virus-4 strain VD2921.

XX PS Disclosure; Page 74-75; 79pp; English.

XX CC The invention describes a polymerase chain reaction (PCR) and primers for  
 detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 P3C and P3D nucleic acids). The methods and primers are used for the  
 detection of CBV-4 strain VD2921 which is associated with diabetes  
 (diabetogenic enterovirus). Early detection of the diabetes e.g.  
 detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 cells, can improve prognosis by allowing treatment e.g. with antiviral  
 drugs, to prevent further loss of beta cells and severe long term  
 consequences of diabetes including blindness, renal failure and leg  
 amputations. This sequence represents a diabetogenic coxsackie B virus 4  
 (CBV-4) strain VD2921 associated polynucleotide.

XX SQ Sequence 559 BP; 134 A; 150 C; 140 G; 135 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 19; DB 8; Length 559;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 362 CCCCTGAATGCGGCTAATC 380

## RESULT 68

ABX12447

XX ID ABX12447 standard; DNA; 560 BP.

XX AC ABX12447;

XX DT 10-MAY-2003 (first entry)

XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #2.

XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;

KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
KW renal failure; leg amputation; ds.  
XX Cocksackievirus.  
OS  
XX WO2002103060-A2.  
FN  
XX  
XX 27-DEC-2002.  
PD  
XX  
XX 19-JUN-2002; 2002WO-IB003278.  
PF  
XX  
XX 20-JUN-2001; 2001SE-00002198.  
PR  
XX  
XX (INNO-) INNOVENTUS PROJECT AB.  
PA  
XX  
XX Tuvemo HT, Frisk GE, Yin H;  
PI  
XX  
XX WPI; 2003-278229/27.  
DR  
XX  
XX Polymerase chain reaction and primers for detecting nucleic acids from  
PT the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX Disclosure; Page 72; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for  
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
CC P3C and P3D nucleic acids). The methods and primers are used for the  
CC detection of CBV-4 strain VD2921 which is associated with diabetes  
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
CC drugs, to prevent further loss of beta cells and severe long term  
CC consequences of diabetes including blindness, renal failure and leg  
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
CC (CBV-4) strain VD2921 associated polynucleotide  
XX  
SQ Sequence 560 BP; 135 A; 143 C; 144 G; 138 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 8; Length 560;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATGGCGCTAATC 19  
Db 361 CCCCTGAATGGCGCTAATC 379  
  
RESULT 69  
ABX12454  
ID ABX12454 standard; DNA; 562 BP.  
AC  
XX ABX12454;  
XX  
XX 10-MAY-2003 (first entry)  
DT  
XX  
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #9.  
DE  
XX  
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
KW renal failure; leg amputation; ds.  
XX  
XX Cocksackievirus.  
OS  
XX WO2002103060-A2.  
FN  
XX  
XX 27-DEC-2002.  
PD  
XX  
XX 19-JUN-2002; 2002WO-IB003278.  
PF  
XX  
XX 20-JUN-2001; 2001SE-00002198.  
PR

XX (INNO-) INNOVENTUS PROJECT AB.  
PA  
XX  
XX Tuvemo HT, Frisk GE, Yin H;  
PI  
XX  
XX WPI; 2003-278229/27.  
DR  
XX  
XX Polymerase chain reaction and primers for detecting nucleic acids from  
PT the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX Disclosure; Page 74; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for  
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
CC P3C and P3D nucleic acids). The methods and primers are used for the  
CC detection of CBV-4 strain VD2921 which is associated with diabetes  
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
CC drugs, to prevent further loss of beta cells and severe long term  
CC consequences of diabetes including blindness, renal failure and leg  
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
CC (CBV-4) strain VD2921 associated polynucleotide  
XX  
SQ Sequence 562 BP; 134 A; 148 C; 140 G; 140 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 19; DB 8; Length 562;  
Best Local Similarity 100.0%; Pred. No. 2.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 CCCCTGAATGGCGCTAATC 19  
Db 365 CCCCTGAATGGCGCTAATC 383  
  
RESULT 70  
ABX12455  
ID ABX12455 standard; DNA; 567 BP.  
AC  
XX ABX12455;  
XX  
XX 10-MAY-2003 (first entry)  
DT  
XX  
XX Cocksackie B virus 4 (CBV-4) strain VD2921 associated DNA #10.  
DE  
XX  
XX Cocksackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
KW renal failure; leg amputation; ds.  
XX  
XX Cocksackievirus.  
OS  
XX WO2002103060-A2.  
FN  
XX  
XX 27-DEC-2002.  
PD  
XX  
XX 19-JUN-2002; 2002WO-IB003278.  
PF  
XX  
XX 20-JUN-2001; 2001SE-00002198.  
PR  
XX  
XX (INNO-) INNOVENTUS PROJECT AB.  
PA  
XX  
XX Tuvemo HT, Frisk GE, Yin H;  
PI  
XX  
XX WPI; 2003-278229/27.  
DR  
XX  
XX Polymerase chain reaction and primers for detecting nucleic acids from  
PT the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX Disclosure; Page 74; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for

CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 CC P3C and P3D nucleic acids). The methods and primers are used for the  
 CC detection of CBV-4 strain VD2921 which is associated with diabetes  
 CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
 CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
 CC drugs, to prevent further loss of beta cells and severe long term  
 CC consequences of diabetes including blindness, renal failure and leg  
 CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
 CC (CBV-4) strain VD2921 associated polynucleotide  
 XX  
 SQ Sequence 567 BP; 140 A; 147 C; 141 G; 139 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 567;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 DB 366 CCCCTGAATGCGGCTAATC 384  
 |||||

RESULT 71  
 AAQ58715  
 ID AAQ58715 standard; DNA; 628 BP.

XX AC AAQ58715;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 29-SEP-1994 (first entry)  
 XX  
 DE Poliovirus type 1 5'-UTR with C to G subatn. at position 610.  
 XX  
 KW Platelet-Derived Growth Factor; heterodimer; PDGF-AB;  
 KW recombinant protein production; PDGF-A chain; PDGF-B chain;  
 KW bicistronic vector system; ss.  
 XX  
 OS Human poliovirus 1 Mahoney.

PH Key Location/Qualifiers  
 FT 5'UTR 1..628  
 FT /tag= a  
 FT mutation 610  
 FT /tag= b  
 FT /note= "wild-type C has been substituted by G"  
 XX

PN WO9405786-A1.  
 XX  
 PD 17-MAR-1994.  
 XX  
 XX 26-AUG-1993; 93WO-EP002295.  
 XX  
 XX 27-AUG-1992; 92DE-04228457.  
 XX  
 PA (BEIE ) BEIERSDORF AG.  
 PA (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.  
 XX  
 PI Eichner W, Achterberg V, Doerschner A, Meyer-Ingold W, Mielke H;  
 PI Dirks W, Wirth M, Hauser H;  
 XX  
 DR WPI; 1994-101191/12.

XX Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a  
 PT polycistronic vector system in mammalian host cells for equimolar prodn  
 PT of A- and B-chains.  
 XX

PS Claim 5; Page 41; 64pp; German.

XX A PDGF-AB heterodimer is recombinantly produced using a bicistronic  
 CC expression unit in which a sequence responsible for internal translation  
 CC start (designated "IRES") is located between cistrons coding for the PDGF

CC -B and PDGF-A chains. The preferred IRES sequence for inclusion in the  
 CC bicistronic construct is the 5'-UTR from Poliovirus type 1 Mahoney strain  
 CC of sequence AAQ58715. (Updated on 25-MAR-2003 to correct PN field.)  
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 628;  
 Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
 DB 451 CCCCTGAATGCGGCTAATC 469  
 |||||

RESULT 72  
 AAQ58726  
 ID AAQ58726 standard; DNA; 628 BP.

XX AC AAQ58726;  
 XX  
 DT 27-AUG-2003 (revised)  
 DT 25-MAR-2003 (revised)  
 DT 29-SEP-1994 (first entry)  
 XX  
 DE Poliovirus type 1 5'-UTR with C to G subatn. at position 610.  
 XX  
 KW Multicistronic expression unit; recombinant protein production;  
 KW internal translation start; initiation; 5'-untranslated region; ss.  
 XX  
 OS Human poliovirus 1 Mahoney.

PH Key Location/Qualifiers  
 FT 5'UTR 1..628  
 FT /tag= a  
 FT mutation 610  
 FT /tag= b  
 FT /note= "wild-type C has been substituted by G"  
 XX

PN WO9405785-A1.  
 XX  
 PD 17-MAR-1994.  
 XX  
 XX 26-AUG-1993; 93WO-EP002294.  
 XX  
 XX 27-AUG-1992; 92DE-04228458.  
 XX  
 PA (BEIE ) BEIERSDORF AG.  
 PA (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.  
 XX  
 PI Dirks W, Wirth M, Hauser H, Eichner W, Achterberg V;  
 PI Doerschner A, Meyer-Ingold W, Mielke H;  
 XX  
 DR WPI; 1994-101190/12.

XX New multicistronic expression units - for producing equimolar amts. of  
 PT polypeptide(s) in mammalian cells as hosts.

PS Claim 6; Page 50; 109pp; German.

XX Heterodimeric proteins can be recombinantly produced using a  
 CC multicistronic (esp. bicistronic) expression unit in which a sequence  
 CC responsible for internal translation start (designated "IRES") is located  
 CC between cistrons coding for the different subunits. The preferred IRES  
 CC sequence is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence  
 CC AAQ58726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-  
 CC AUG-2003 to correct OS field.)

XX SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 2; Length 628;  
 Best Local Similarity 100.0%; Pred. No. 2.9;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 Db 451 CCCCTGAATGGGCTAATC 469

RESULT 73

ID ADP74707 standard; DNA; 639 BP.

XX AC ADP74707;

DT 26-AUG-2004 (first entry)

DE Novel bicistronic retroviral vector related poliovirus IRES sequence.

XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
 KW severe combined immune deficiency syndrome; protein expression;  
 KW antisense; ds; gene.

XX OS Unidentified.

XX EP1428886-A1.

XX PD 16-JUN-2004.

XX PF 09-DEC-2002; 2002EP-00027555.

XX PR 09-DEC-2002; 2002EP-00027555.

XX PA (CELL-) CELTECH GMBH BIOTECHNOLOGIE.

XX FI Heberlein C, Gindullis F, Hannemann J, Strathmann G;

XX DR WPI; 2004-452367/43.

XX Bicistronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 FT stem cell and myeloproliferative sarcoma viruses.

XX PS Disclosure; Page 70; 91pp; German.

XX The present invention relates to a new bicistronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence fragment shown in the exemplification of the invention.

XX SQ Sequence 639 BP; 146 A; 171 C; 164 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 639;

Best Local Similarity 100.0%; Pred. No. 2.9;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 Db 455 CCCCTGAATGGGCTAATC 473

RESULT 74

ID AAC85153 standard; RNA; 646 BP.

XX AC AAC85153;

XX DT 08-MAY-2001 (first entry)

XX

DE Echo virus (ECV12) 5' non-translated region (NTR) sequence.

XX Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;  
 KW Cocksackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.  
 XX OS Echo virus.

XX Key Location/Qualifiers

XX stem\_loop 2..87

FT /\*tag= a

FT /note= "Domain I"

FT 103..180

FT /\*tag= b

FT /note= "Domain II"

FT 183..232

FT /\*tag= c

FT /note= "Domain III"

FT 240..443

FT /\*tag= d

FT /note= "Domain IV"

FT 451..559

FT /\*tag= e

FT /note= "Domain V"

FT 586..622

FT /\*tag= f

FT /note= "Domain VI"

FT 623..643

FT /\*tag= g

FT /note= "Domain VII"

XX WO200104136-A1.

XX PD 18-JAN-2001.

XX PF 08-JUL-2000; 2000WO-US018681.

XX PR 09-JUL-1999; 99US-0143104P.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Romero JR, Bradrick SS, Dunn JJ;

XX WPI; 2001-138310/14.

XX Recombinant enterovirus genome for use as vector or vaccine, modified by  
 PT replacing a part or all of its 5'non-translated region by 5'NTR of  
 FT enterovirus genome that encodes virus modified in tropism or virulence.

XX Disclosure; Fig 2; 49pp; English.

XX The invention provides an enterovirus genome (I) for use as a vector or  
 CC vaccine, modified to produce a virus (VI) having a restricted or altered  
 CC species or tissue tropism, compared to an equivalent unmodified virus, or  
 CC modified to produce an attenuated virus (V2), by replacing a part or all  
 CC of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an  
 CC enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or  
 CC vector in targeting genes of interest to specific cells or tissues. (I)  
 CC is also useful for diagnostic purposes, e.g. to identify virulent, versus  
 CC nonvirulent strains of an enterovirus. The present sequence represents  
 CC the 5' NTR (non-translated region) sequence of echo virus (ECV12)

XX SQ Sequence 646 BP; 145 A; 176 C; 163 G; 0 T; 162 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 646;

Best Local Similarity 78.9%; Pred. No. 2.9;

Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19

Db 454 CCCCTGAATGGGCTAATC 472

RESULT 75



```

AAC85173
ID AAC85173 standard; DNA; 654 BP.
XX
AC AAC85173;
XX
DT 08-MAY-2001 (first entry)
XX
DE Cxsackievirus B3 (CVB3)/AS 5' non-translated region (NTR) sequence.
XX
KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX
OS Cxsackievirus.
XX
FN WO200104136-A1.
XX
PD 18-JAN-2001.
XX
PF 08-JUL-2000; 2000WO-US018681.
XX
PR 09-JUL-1999; 99US-0143104P.
XX
PA (UYNE-) UNIV NEBRASKA.
XX
PI Romero JR, Bradrick SS, Dunn JJ;
XX
WPI; 2001-138310/14.
XX
Recombinant enterovirus genome for use as vector or vaccine, modified by
replacing a part or all of its 5' non-translated region by 5'NTR of
enterovirus genome that encodes virus modified in tropism or virulence.
XX
PS Example 2; Page 24; 49pp; English.
XX
The invention provides an enterovirus genome (I) for use as a vector or
vaccine, modified to produce a virus (VI) having a restricted or altered
species or tissue tropism, compared to an equivalent unmodified virus, or
modified to produce an attenuated virus (V2), by replacing a part or all
of the 5' non-translated region (5'NTR) of (I) with a 5'NTR of an
enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
vector in targeting genes of interest to specific cells or tissues. (I)
is also useful for diagnostic purposes, e.g. to identify virulent, versus
nonvirulent strains of an enterovirus. The present sequence represents
the 5' NTR (non-translated region) of the cardiovirulent enterovirus
Cxsackievirus B3 (CVB3)/AS strain
XX
SQ Sequence 654 BP; 166 A; 161 C; 159 G; 168 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 654;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
Db 367 CCCCTGAATGGGCTAATC 385

RESULT 76
AAC85174
ID AAC85174 standard; DNA; 660 BP.
XX
AC AAC85174;
XX
DT 08-MAY-2001 (first entry)
XX
DE Cxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
XX
KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX
OS Cxsackievirus.
XX
FN WO200104136-A1.

```

```

XX 18-JAN-2001.
XX
PD 08-JUL-2000; 2000WO-US018681.
XX
PF 09-JUL-1999; 99US-0143104P.
XX
PR (UYNE-) UNIV NEBRASKA.
XX
PI Romero JR, Bradrick SS, Dunn JJ;
XX
WPI; 2001-138310/14.
XX
Recombinant enterovirus genome for use as vector or vaccine, modified by
replacing a part or all of its 5' non-translated region by 5'NTR of
enterovirus genome that encodes virus modified in tropism or virulence.
XX
PS Example 2; Page 25; 49pp; English.
XX
The invention provides an enterovirus genome (I) for use as a vector or
vaccine, modified to produce a virus (VI) having a restricted or altered
species or tissue tropism, compared to an equivalent unmodified virus, or
modified to produce an attenuated virus (V2), by replacing a part or all
of the 5' non-translated region (5'NTR) of (I) with a 5'NTR of an
enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
vector in targeting genes of interest to specific cells or tissues. (I)
is also useful for diagnostic purposes, e.g. to identify virulent, versus
nonvirulent strains of an enterovirus. The present sequence represents
the 5' NTR (non-translated region) of a non-cardiovirulent enterovirus
Cxsackievirus B3 (CVB3)/CO strain
XX
SQ Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 4; Length 660;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGGCTAATC 19
Db 373 CCCCTGAATGGGCTAATC 391

RESULT 77
AEB56828
ID AEB56828 standard; DNA; 660 BP.
XX
AC AEB56828;
XX
DT 22-SEP-2005 (first entry)
XX
DE Cxsackie virus B5 polynucleotide sequence SEQ ID NO:67.
XX
KW DNA detection; enteroviral detection; ds.
XX
OS Human cxsackievirus B5.
XX
PN US2005158710-A1.
XX
PD 21-JUL-2005.
XX
PP 16-JAN-2004; 2004US-00760048.
XX
PR 16-JAN-2004; 2004US-00760048.
XX
PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
DR WPI; 2005-512251/52.
DR GENBANK; AF169665.
XX

```

PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; SEQ ID NO 67; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a coxsackie virus B5 polynucleotide sequence,  
CC which is given in the exemplification of the present invention. Note: the  
CC present sequence is designated as SEQ ID NO:67 in the Sequence Listing.  
CC but corresponds with the sequence given in figure 2 designated SEQ ID  
CC NO:14 in the description of the drawings.

XX Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 14; Length 660;  
Best Local Similarity 100.0%; Pred. NO. 2.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 373 CCCCTGAATCGGCTAATC 391

## RESULT 78

ADU77356  
ID ADU77356 standard; DNA; 682 BP.  
XX  
XX AC ADU77356;  
XX  
DT 10-FEB-2005 (first entry)  
XX  
DE Prima7 virus 5' UTR region DNA.  
XX  
XX Enteroviral genus related disease; Prima7-related disease; gene therapy;  
XX ds.  
XX Prima7 virus.  
XX OS  
XX EP1479761-A1.  
XX PN  
XX 24-NOV-2004.  
XX PD  
XX 21-MAY-2003; 2003EP-00076529.  
XX PF  
XX 21-MAY-2003; 2003EP-00076529.  
XX PR  
XX (PRIM-) PRIMAGEN HOLDING BV.  
XX PA  
XX Maas HCGI, Van Den Broek PJM, Mang R;  
XX PI  
XX WPI; 2004-823915/82.  
XX DR  
XX New isolated or recombinant virus, useful for detecting a molecule  
XX capable of specifically binding the virus in a sample, and as a vaccine  
XX or medicament for treating or preventing Prima7-related disease.  
XX PT  
XX Example; SEQ ID NO 39; 51pp; English.  
XX PS  
XX The present invention provides a new isolated or recombinant virus called  
XX Prima7 (which belong to enteroviral species) comprising a nucleic acid  
CC

CC sequence or its functional part, derivative or analogue of the said  
CC virus. The invention is useful for detecting and/or identifying a Prima7  
CC enterovirus in a sample and for diagnosing an enteroviral genus related  
CC disease. The vaccine or medicament prepared from the Prima7 virus is  
CC useful for preventing and/or treating a Prima7-related disease. The  
CC invention is also useful in gene therapy. The present sequence is Prima7  
CC virus 5' UTR region DNA.

XX Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 13; Length 682;  
Best Local Similarity 100.0%; Pred. NO. 2.9;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 390 CCCCTGAATCGGCTAATC 408

## RESULT 79

AEA00424  
ID AEA00424 standard; DNA; 709 BP.  
XX  
XX AC AEA00424;  
XX  
DT 28-JUL-2005 (first entry)  
XX  
DE Enterovirus 71 5' untranslated region internal ribosome entry site DNA.  
XX  
XX vector; neurological disease; ds; gene therapy;  
XX internal ribosome entry site; cystic fibrosis; cns-gen.;  
XX respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;  
XX factor IX deficiency; Duchenne dystrophy; muscular-gen.;  
XX Becker's disease; cancer; cytostatic; neoplasm;  
XX acquired immune deficiency syndrome; anti-hiv; infectious disease;  
XX antimicrobial.  
XX  
XX Human enterovirus 71; strain TW/2086/98.  
XX OS  
XX US2005112095-A1.  
XX PN  
XX 26-MAY-2005.  
XX PD  
XX 08-JUL-2003; 2003US-00614283.  
XX PF  
XX 09-JUL-2002; 2002US-0394269P.  
XX PR  
XX (HSUT/) HSU T.  
XX PA (WUT/) WU T.  
XX PA (LEEJ/) LEE J.  
XX  
XX Hsu T, Wu T, Lee J;  
XX PI  
XX WPI; 2005-371616/38.  
XX DR  
XX New nucleic acid vector for the expression of at least two cistrons  
XX comprising a nucleotide sequence comprising an internal ribosome entry  
XX site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient  
XX having e.g. AIDS.  
XX PT  
XX Example 2; SEQ ID NO 1; 23pp; English.  
XX PS  
XX The present invention relates to a nucleic acid vector for the expression  
XX of at least two cistrons. The vector comprises a promoter operably linked  
XX to a nucleotide sequence comprising at least two cistrons and at least  
XX one nucleotide sequence comprising an internal ribosome entry site (IRES)  
XX selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or  
XX Encephalomyocarditis virus (EMCV). The invention also provides a method  
XX for screening of anti-viral compounds using the IRES. The invention is  
XX useful for the genetic treatment of patients with cystic fibrosis,  
XX hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and  
XX other bacterial or infectious diseases due to a pathogenic organism and  
XX in gene therapy. The present sequence is the enterovirus 71 5'

```

CC untranslated region (UTR) IRES DNA.
SQ Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;

Query Match      100.0%; Score 19; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 420 CCCCTGAATGCGGCTAATC 438

RESULT 80
ADW37919
ID ADW37919 standard; cDNA; 743 BP.
XX
AC ADW37919;
XX
XX
XX
XX 24-MAR-2005 (first entry)
XX
DE Poliovirus type 1 strain mahoney internal ribosomal entry site cDNA.
XX
KW SARS-coronavirus virus-like particle; SARS-Cov-VLP;
KW cellular immune response; humoral immune response; vaccine;
KW immunogenicity; cytotoxic T-lymphocyte; internal ribosomal entry site;
KW IRES; ss.
XX
OS Human poliovirus 1.
XX
XX
XX
XX US2005002953-A1.
XX
XX 06-JAN-2005.
XX
XX 04-MAY-2004; 2004US-00839729.
XX
XX 06-MAY-2003; 2003US-0468703P.
XX
XX (HERO/) HEROLD J.
XX
XX Herold J;
XX
XX WPI; 2005-065191/07.
XX
XX New system comprising one or more recombinant vectors that expresses the
XX SARS-Cov E-protein, SARS-Cov M-protein, and SARS-Cov S-protein, useful
XX for making SARS-coronavirus virus-like particles.
XX
XX Example 2; SEQ ID NO 21; 111pp; English.
XX
XX The present invention provides a system for making SARS-coronavirus virus
XX -like particles (SARS-Cov-VLPs) comprising one or more recombinant
XX vectors that express the SARS-Cov E (small membrane)-protein, SARS-Cov
XX M (membrane)-protein and SARS-Cov S (spike)-protein. The invention is
XX useful for inducing cellular and/or humoral immune response. The
XX invention is also useful to reduce the symptoms of SARS-Cov infections
XX and in vaccine preparations. The present sequence is Poliovirus type 1
XX strain mahoney internal ribosomal entry site (IRES) cDNA. This cDNA
XX sequence is used in the preparation of plasmid for the expression of SARS
XX -Cov M, E and S proteins.
XX
SQ Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;

Query Match      100.0%; Score 19; DB 14; Length 743;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 448 CCCCTGAATGCGGCTAATC 466

RESULT 81
AAC85152
ID AAC85152 standard; RNA; 745 BP.
XX
AC AAC85152;
XX
XX 08-MAY-2001 (first entry)
XX
XX Cxsackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
XX
XX Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
XX Cxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX
XX Cxsackievirus.
XX
XX Key Location/Qualifiers
XX stem_loop 2..87
XX /*tag= d
XX /note= "Domain I"
XX stem_loop 10..34
XX /*tag= a
XX /note= "stemloop B"
XX stem_loop 35..45
XX /*tag= b
XX /note= "stemloop C"
XX stem_loop 57..70
XX /*tag= c
XX /note= "stemloop D"
XX stem_loop 105..181
XX /*tag= e
XX /note= "Domain II"
XX stem_loop 184..233
XX /*tag= f
XX /note= "Domain III"
XX stem_loop 241..444
XX /*tag= g
XX /note= "Domain IV"
XX stem_loop 452..560
XX /*tag= h
XX /note= "Domain V"
XX stem_loop 587..623
XX /*tag= i
XX /note= "Domain VI"
XX stem_loop 624..644
XX /*tag= j
XX /note= "Domain VII"
XX
XX WO200104136-A1.
XX
XX 18-JAN-2001.
XX
XX 08-JUL-2000; 2000WO-US018681.
XX
XX 09-JUL-1999; 99US-0143104P.
XX
XX (UYNE-) UNIV NEBRASKA.
XX
XX Romero JR, Bradrick SS, Dunn JJ;
XX WPI; 2001-138310/14.
XX
XX Recombinant enterovirus genome for use as vector or vaccine, modified by
XX replacing a part or all of its 5'non-translated region by 5'NTR of
XX enterovirus genome that encodes virus modified in tropism or virulence.
XX
XX Disclosure; Fig 1; 49pp; English.
XX
XX The invention provides an enterovirus genome (I) for use as a vector or
XX vaccine, modified to produce a virus (V1) having a restricted or altered
XX species or tissue tropism, compared to an equivalent unmodified virus, or
XX modified to produce an attenuated virus (V2), by replacing a part or all
XX of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
XX enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
XX vector in targeting genes of interest to specific cells or tissues. (I)

```

CC is also useful for diagnostic purposes, e.g. to identify virulent, versus  
 CC nonvirulent strains of an enterovirus. The present sequence represents  
 CC the enterovirus Cxsackievirus B3 (CVB3) 5' NTR (non-translated region)  
 CC sequence

XX  
 XX Sequence 745 BP; 184 A; 192 C; 181 G; 1 T; 187 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 4; Length 745;  
 Best Local Similarity 78.9%; Pred. No. 3;  
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 |||||:|||||:|||||:  
 Db 455 CCCUGAUGCGGCUAUC 473

RESULT 82  
 ACC48197  
 ID ACC48197 standard; cDNA; 745 BP.  
 XX  
 AC ACC48197;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Poliovirus internal ribosome entry site-containing mRNA 5' UTR.  
 XX  
 KW Internal ribosome entry site; IRES; translation; ss.  
 XX  
 OS Poliovirus.

XX Key Location/Qualifiers  
 XX 5'UTR 1..742  
 XX /\*tag= a

XX WO2003020927-A2.  
 XX 13-MAR-2003.  
 XX 03-SEP-2002; 2002WO-EP009843.  
 XX 04-SEP-2001; 2001DE-01043237.  
 XX (ICON-) ICON GENETICS INC.  
 XX Atabekov J, Dorokhov Y, Skulachev M, Ivanov P, Ivanov P, Gleba Y;  
 XX WPI; 2003-313089/30.  
 XX Creating nucleic acid sequence for carrying out translation by internal  
 XX ribosome entry site element and expressing nucleotide sequence of  
 XX interest in eukaryotic cell, by creating a nucleic acid having adenine-  
 XX rich block.  
 XX Disclosure; Fig 3; 48pp; English.

XX The present sequence is that of a known internal ribosome entry site  
 XX (IRES) element contained in the 5' untranslated region of poliovirus  
 XX mRNA. The invention provides a method of creating an artificial IRES  
 XX element having an adenine-rich (40-100 mol%) nucleic acid block of at  
 XX least 25 nucleotides and capable of causing cap-independent translation  
 XX of a downstream nucleotide sequence of interest in eukaryotic cells, such  
 XX as plant, animal or yeast cells (claimed). A method of identifying  
 XX nucleic acid elements having IRES activity involving genome database  
 XX searches is also provided. The methods allow the creation or  
 XX identification of IRES elements that are universal with cross-kingdom and  
 XX tailor-made activity

XX Sequence 745 BP; 163 A; 202 C; 193 G; 187 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 8; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 |||||:|||||:|||||:  
 Db 454 CCCCTGAATCGGCTAATC 472

RESULT 83  
 ADP82873  
 ID ADP82873 standard; DNA; 810 BP.  
 XX  
 AC ADP82873;  
 XX  
 DT 23-SEP-2004 (first entry)  
 XX  
 DE Human coxsackievirus B1 complete genomic DNA.  
 XX  
 KW hMPV detection; ds.  
 XX  
 OS Human coxsackievirus B1.  
 XX  
 PN WO2004057021-A2.  
 XX  
 PD 08-JUL-2004.  
 XX  
 PF 19-DEC-2003; 2003WO-CA001994.  
 XX  
 PR 19-DEC-2002; 2002CA-02411264.  
 XX  
 PR 24-JAN-2003; 2003CA-02418004.  
 XX  
 PA (UYLA-) UNIV LAVAL.

XX Boivin G;  
 XX WPI; 2004-500307/47.  
 XX  
 XX Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample  
 XX comprises contacting the at least one probe and/or primer with the sample  
 XX to allow annealing of the probe and/or primer with the nucleic acid  
 XX sequence.  
 XX Claim 32; SEQ ID NO 137; 158pp; English.

XX The invention relates to a novel method for detecting and/or quantifying  
 XX Human metapneumovirus (hMPV) in a sample comprising providing at least  
 XX one probe or primer specific for a nucleic acid sequence of hMPV,  
 XX contacting the one probe and/or primer with the sample to allow annealing  
 XX of the probe and/or primer with the nucleic acid sequence and detecting  
 XX and/or quantifying the nucleic acid sequence using the annealed probe  
 XX and/or primer. The method of the invention may be useful for detecting  
 XX and/or quantifying Human metapneumovirus (hMPV) in a sample. The current  
 XX sequence is that of the Human coxsackievirus B1 complete genomic DNA of  
 XX the invention.

XX Sequence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 12; Length 810;  
 Best Local Similarity 100.0%; Pred. No. 3;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 |||||:|||||:|||||:  
 Db 4 CCCCTGAATCGGCTAATC 22

RESULT 84  
 ADU47469  
 ID ADU47469 standard; cDNA; 1560 BP.

XX  
 AC ADU47469;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Enterovirus type 71 (EV71) cDNA.  
 XX

KW Detection; enterovirus type 71; EV71; ss.  
 XX Enterovirus.  
 XX Key Location/Qualifiers  
 FH primer\_bind 72..87  
 FT /\*tag= a  
 FT /note= "f1 primer"  
 FT primer\_bind 167..187  
 FT /\*tag= b  
 FT /note= "f2 primer"  
 FT primer\_bind 248..266  
 FT /\*tag= c  
 FT /note= "f3 primer"  
 FT primer\_bind 423..439  
 FT /\*tag= d  
 FT /note= "f5 primer"  
 FT misc\_binding 448..474  
 FT /\*tag= e  
 FT /bound\_moiety= "p1 probe"  
 FT misc\_binding 514..546  
 FT /\*tag= f  
 FT /bound\_moiety= "p2 probe"  
 FT misc\_binding 547..574  
 FT /\*tag= g  
 FT /bound\_moiety= "p3 probe"  
 FT primer\_bind 583..602  
 FT /\*tag= h  
 FT /note= "r2 primer"  
 FT primer\_bind 627..645  
 FT /\*tag= i  
 FT /note= "r1 primer"  
 FT primer\_bind 1179..1198  
 FT /\*tag= j  
 FT /note= "f7 primer"  
 FT misc\_binding 1344..1373  
 FT /\*tag= k  
 FT /bound\_moiety= "16-1 probe"  
 FT misc\_binding 1390..1419  
 FT /\*tag= l  
 FT /bound\_moiety= "71-2/16-2 probe"  
 FT misc\_binding 1454..1481  
 FT /\*tag= m  
 FT /bound\_moiety= "71-3 probe"  
 FT primer\_bind 1485..1504  
 FT /\*tag= n  
 FT /note= "r3 primer"  
 FT  
 XX US6818397-B1.  
 XX  
 XX 16-NOV-2004.  
 XX  
 XX 28-NOV-2000; 2000US-00724678.  
 XX  
 XX 28-NOV-2000; 2000US-00724678.  
 XX  
 XX (CHIP-) CHIP BIOTECHNOLOGY INC.  
 XX  
 XX Lee K, Bair C, Tseng Y, Wang Y, Wang S;  
 XX  
 XX WPI; 2004-793563/78.  
 DR GENBANK; U22521.  
 DR  
 XX New kit comprising a pair of oligonucleotide primers for nucleic acid  
 PT amplification, useful in detecting and differentiating an enterovirus in  
 PT a sample.  
 PT  
 XX Disclosure; SEQ ID NO 16; 14pp; English.  
 XX  
 XX The invention provides a method and a kit for detecting and  
 CC differentiating an enterovirus type 71 (EV71) in a sample. The method  
 CC involves contacting nucleic acids in the sample with a pair of primers to  
 CC form an amplification product; contacting the amplification product with

CC at least one synthetic nucleotide sequence fixed on a solid substrate and  
 CC detecting hybridisation. The present sequence is the enterovirus type 71  
 CC (EV71) cDNA.  
 XX  
 SQ Sequence 1560 BP; 421 A; 401 C; 346 G; 392 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 13; Length 1560;  
 Best Local Similarity 100.0%; Pred. No. 3.3;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGCGGCTAATC 19  
 DB 456 CCCCTGAATGCGGCTAATC 474  
 RESULT 85  
 ABK14791  
 ID ABK14791 standard; DNA; 2076 BP.  
 XX  
 AC ABK14791;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Platelet-derived growth factor expression cassette insert used in pBC701.  
 XX  
 KW Platelet-derived growth factor; PDGF; transgenic; milk; gene;  
 KW wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease;  
 KW venous stasis ulcer; periodontal regeneration; bone formation;  
 KW prosthetic vascular graft; pBC701; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO200198520-A1.  
 XX  
 XX 27-DEC-2001.  
 XX  
 XX 19-JUN-2001; 2001WO-US041044.  
 XX  
 XX 19-JUN-2000; 2000US-0212406P.  
 XX  
 XX (GENZ ) GENZYME TRANSGENICS CORP.  
 XX  
 XX Echelard Y, Meade H, Eichner W, Sommermeier K;  
 XX  
 XX WPI; 2002-083329/11.  
 XX  
 XX Production of platelet derived growth factor (PDGF) comprises expression  
 XX in the milk of a non-human transgenic animal.  
 XX  
 XX Example 1; Fig 1; 59pp; English.  
 XX  
 XX The invention relates to the production of platelet-derived growth factor  
 XX (PDGF) comprising a transgenic mammal whose somatic and germ cells  
 XX comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a  
 XX promoter directing expression into mammalian gland epithelial cells, and  
 XX obtaining the milk from the transgenic mammal where at least 30% of the  
 XX PDGF in the milk is as a dimer. Also described is a method of producing a  
 XX transgenic mammal capable of expressing an active PDGF molecule in milk.  
 XX Pharmaceutical compositions can be obtained from this milk and can be  
 XX used to stimulate or enhance the wound healing process, in particular  
 XX diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.  
 XX Transgenic PDGF (II) can also be used in the treatment of periodontal  
 XX regeneration, stimulation of bone formation, ophthalmic diseases or  
 XX healing of prosthetic vascular grafts. (III) can also be used for non-  
 XX medical applications, e.g., as a supplement for cell culture media or as  
 XX a component of diagnostic kits. The present sequence represents the  
 XX platelet-derived growth factor expression cassette insert used in pBC701  
 XX vector of the invention  
 XX  
 XX Sequence 2076 BP; 441 A; 612 C; 607 G; 416 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 6; Length 2076;  
 Best Local Similarity 100.0%; Pred. No. 3.4;

```
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 1203 CCCCTGAATCGGCTAATC 1221

RESULT 86
AAH20890
ID AAH20890 standard; DNA; 4148 BP.
XX
AC AAH20890;
XX
DT 11-SEP-2003 (revised)
DT 24-AUG-2001 (first entry)
XX
DE Vector containing HIV gp41 DNA SEQ ID 1.
XX
DE Transmembrane anchor; gene therapy; endoplasmic reticulum; gp41;
KW antiviral; HIV replication inhibitor; T lymphocyte; viral infection;
KW hematopoietic stem cell; ds.
XX
OS Human immunodeficiency virus 1.
XX
FH Key Location/Qualifiers
FT CDS 1438..1773
FT /*tag= a
XX
PN WO200137881-A2.
XX
XX 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-EP011733.
XX
PR 25-NOV-1999; 99DE-01057838.
XX
PA (PETT-) PETTE INST HEINRICH.
XX
PI Von Laer M;
XX
DR WPI; 2001-367622/38.
DR P-PSDB; AAB86198.
XX
PT New nucleic acid encoding membrane-anchored gp41 fusion protein, useful
PT for gene therapy of human immunodeficiency virus (HIV) infection,
PT prevents entry of virus into cells.
XX
XX Claim 11; Page 28-30; 39pp; German.
XX
PS This invention describes a novel nucleic acid (I) comprising elements
CC that encode a signal peptide (SP) that provides transfer of expressed
CC polypeptide into the endoplasmic reticulum, a fragment (FI) of HIV gp41
CC protein, containing a segment from a heptad repeat region, a
CC transmembrane anchor (MSD) of a type I membrane protein and a flexible
CC linker (hinge) linking FI and MSD, therefore the formula of (I) is SP-FI-
CC hinge-MSD. The products of the invention have antiviral activity and act
CC as HIV replication inhibitors. Vectors containing (I), also T lymphocytes
CC or hematopoietic stem cells transfected in vitro with (I), are used in
CC gene therapy of HIV infection. (Updated on 11-SEP-2003 to standardise OS
CC field)
XX
SQ Sequence 4148 BP; 880 A; 1177 C; 1103 G; 988 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 5; Length 4148;
Best Local Similarity 100.0%; Pred. No. 3.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 2245 CCCCTGAATCGGCTAATC 2263

RESULT 87
```

```
AD007652
ID AD007652 standard; DNA; 5252 BP.
XX
AC AD007652;
XX
DT 15-JUL-2004 (first entry)
XX
DE Tricistronic expression cassette containing murine coding sequences.
XX
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;
KW immunostimulant; expression cassette; viral vector; interleukin-12;
KW co-stimulatory protein; cancer; infection; ds; gene.
XX
OS Mus sp.
OS Synthetic.
OS Unidentified.
XX
PN WO2004035799-A2.
XX
PD 29-APR-2004.
XX
PF 10-OCT-2003; 2003WO-EP011252.
XX
PR 11-OCT-2002; 2002DE-01048141.
XX
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
XX
PI Waehler R, Schnieders F;
XX
DR WPI; 2004-357221/33.
XX
PT Viral vector that expresses single-chain interleukin-12 and costimulator,
PT useful for treatment of tumors, viral infections, e.g. human
PT immunodeficiency virus, and prion diseases.
XX
PS Disclosure; Fig 18; 129pp; German.
XX
CC The present invention relates to a viral vector that includes a nucleic
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory
CC protein. Viral vectors and virus particles derived from them are useful
CC for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The
CC present sequence is a tricistronic expression cassette used in the
CC exemplification of the invention.
XX
SQ Sequence 5252 BP; 1347 A; 1386 C; 1300 G; 1219 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 5252;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 2739 CCCCTGAATCGGCTAATC 2757

RESULT 88
ADP74699
ID ADP74699 standard; DNA; 7185 BP.
XX
AC ADP74699;
XX
XX 26-AUG-2004 (first entry)
XX
DE Novel bicistronic retroviral vector related vector #1.
XX
KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
KW severe combined immune deficiency syndrome; protein expression;
KW antisense; ds; gene.
XX
OS Synthetic.
OS Unidentified.
XX
```

FH Key Location/Qualifiers  
 FT LTR 424..994  
 FT /tag= a  
 FT /standard\_name= "5'-LTR"  
 FT 5'UTR 995..1487  
 FT /tag= b  
 FT CDS 1488..2615  
 FT /tag= c  
 FT /product= "HSV-TK"  
 FT misc\_RNA 2626..3250  
 FT /tag= d  
 FT /standard\_name= "IRES"  
 FT CDS 3298..4098  
 FT /tag= e  
 FT /product= "neo"  
 FT LTR 4345..4931  
 FT /tag= f  
 FT /standard\_name= "3'-LTR"  
 XX  
 PN EP1428886-A1.  
 XX  
 XX 16-JUN-2004.  
 PD  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 PF  
 XX 09-DEC-2002; 2002EP-00027555.  
 PR  
 XX (CELL-) CELLSCH GMBH BIOTECHNOLOGIE.  
 PA  
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
 PI  
 XX WPI; 2004-452367/43.  
 DR  
 XX  
 XX Bisticronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 PT stem cell and myeloproliferative sarcoma viruses.  
 PT  
 XX Disclosure; Page 58-59; 91pp; German.  
 PS  
 XX The present invention relates to a new bisticronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX  
 XX Sequence 7185 BP; 1579 A; 2013 C; 1943 G; 1650 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 19; DB 12; Length 7185;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGCGGCTAATC 19  
 Db 3074 CCCCTGAATGCGGCTAATC 3092  
 RESULT 89  
 ADP74701  
 ID ADP74701 standard; DNA; 7185 BP.  
 XX  
 AC ADP74701;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX Novel bisticronic retroviral vector related vector #3.  
 DE  
 XX immunosuppressive; gene therapy; vector; bisticronic retroviral vector;  
 KW severe combined immune deficiency syndrome; protein expression;

KW antisense; ds; gene.  
 XX  
 XX Synthetic.  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT LTR 424..994  
 FT /tag= a  
 FT /standard\_name= "5'-LTR"  
 FT 5'UTR 995..1487  
 FT /tag= b  
 FT CDS 1488..2615  
 FT /tag= c  
 FT /product= "HSV-TK splice variant"  
 FT misc\_RNA 2626..3250  
 FT /tag= d  
 FT /standard\_name= "IRES"  
 FT CDS 3298..4098  
 FT /tag= e  
 FT /product= "neo"  
 FT LTR 4345..4931  
 FT /tag= f  
 FT /standard\_name= "3'-LTR"  
 XX  
 PN EP1428886-A1.  
 XX  
 XX 16-JUN-2004.  
 PD  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 PF  
 XX 09-DEC-2002; 2002EP-00027555.  
 PR  
 XX (CELL-) CELLSCH GMBH BIOTECHNOLOGIE.  
 PA  
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
 PI  
 XX WPI; 2004-452367/43.  
 DR  
 XX  
 XX Bisticronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 PT stem cell and myeloproliferative sarcoma viruses.  
 PT  
 XX Disclosure; Page 63-65; 91pp; German.  
 PS  
 XX The present invention relates to a new bisticronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX  
 XX Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 19; DB 12; Length 7185;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CCCCTGAATGCGGCTAATC 19  
 Db 3074 CCCCTGAATGCGGCTAATC 3092  
 RESULT 90  
 ADP74714  
 ID ADP74714 standard; DNA; 7235 BP.  
 XX  
 AC ADP74714;  
 XX  
 XX 26-AUG-2004 (first entry)  
 DT

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XX DE Novel bicistronic retroviral vector related vector #6.
XX AC
XX ADP74715;
XX DT 26-AUG-2004 (first entry)
XX DE Novel bicistronic retroviral vector related vector #7.
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX KW severe combined immune deficiency syndrome; protein expression;
XX KW antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /*tag= a
XX FT /standard_name= "5'-LTR"
XX FT 5'UTR 995..1537
XX FT /*tag= b
XX FT CDS 1538..2665
XX FT /*tag= c
XX FT /product= "HSV-TK splice variant"
XX FT misc_RNA 2676..3300
XX FT /*tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3348..4148
XX FT /*tag= e
XX FT /product= "neo"
XX FT LTR 4395..4981
XX FT /*tag= f
XX FT /standard_name= "3'-LTR"
XX EPI428886-A1.
XX PN
XX PD 16-JUN-2004.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR 09-DEC-2002; 2002EP-00027555.
XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX PS
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7235 BP; 1594 A; 2025 C; 1950 G; 1666 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 3124 CCCCTGAATCGGCTAATC 3142
|||||

RESULT 91
ADP74715

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ID ADP74715 standard; DNA; 7235 BP.
XX AC
XX ADP74715;
XX DT 26-AUG-2004 (first entry)
XX DE Novel bicistronic retroviral vector related vector #7.
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX KW severe combined immune deficiency syndrome; protein expression;
XX KW antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX FH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /*tag= a
XX FT /standard_name= "5'-LTR"
XX FT 5'UTR 995..1537
XX FT /*tag= b
XX FT CDS 1538..2665
XX FT /*tag= c
XX FT /product= "HSV-TK splice variant"
XX FT misc_RNA 2676..3300
XX FT /*tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3348..4148
XX FT /*tag= e
XX FT /product= "neo"
XX FT LTR 4395..4981
XX FT /*tag= f
XX FT /standard_name= "3'-LTR"
XX EPI428886-A1.
XX PN
XX PD 16-JUN-2004.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR 09-DEC-2002; 2002EP-00027555.
XX PA (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX PS
XX CC Bicistronic retroviral vector, useful in gene therapy, particularly of
XX CC graft versus host disease, contains components of both murine embryonic
XX CC stem cell and myeloproliferative sarcoma viruses.
XX CC Disclosure; Page 78-79; 91pp; German.
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7235 BP; 1595 A; 2025 C; 1949 G; 1666 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CCCCTGAATCGGCTAATC 19
|||||

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CC vector sequence shown in the exemplification of the invention.
XX
SQ Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 12; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGCTAATC 19
Db 3124 CCCCTGAATCGCGCTAATC 3142

RESULT 94
ABX12440
ID ABX12440 standard; DNA; 7392 BP.
XX
AC ABX12440;
DT 10-MAY-2003 (first entry)
XX
DE Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.
XX
KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;
KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;
KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;
KW renal failure; leg amputation; ds.
XX
OS Coxsackievirus.
XX
XX Key Location/Qualifiers
FH misc_feature 1..87
FT /tag= a
FT /note= "Specifically claimed in claim 16"
FT misc_feature 88..512
FT /tag= b
FT /note= "Specifically claimed in claim 19"
FT misc_feature 513..742
FT /tag= c
FT /note= "Specifically claimed in claim 22"
FT misc_feature 743..952
FT /tag= d
FT /note= "Specifically claimed in claim 25"
FT CDS 743..7303
FT /tag= f
FT /product= "Polyprotein"
FT misc_feature 743..952
FT /tag= e
FT /note= "Specifically claimed in claim 26"
FT misc_feature 953..1726
FT /tag= g
FT /note= "Specifically claimed in claim 29"
FT misc_feature 1727..2441
FT /tag= h
FT /note= "Specifically claimed in claim 32"
FT misc_feature 2442..3296
FT /tag= i
FT /note= "Specifically claimed in claim 35"
FT misc_feature 3297..3737
FT /tag= j
FT /note= "Specifically claimed in claim 38"
FT misc_feature 3738..4033
FT /tag= k
FT /note= "Specifically claimed in claim 41"
FT misc_feature 4034..5029
FT /tag= l
FT /note= "Specifically claimed in claim 44"
XX
FN WO2002103060-A2.
XX
PD 27-DEC-2002.
XX
XX 19-JUN-2002; 2002WO-IB003278.

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XX 20-JUN-2001; 2001SE-00002198.
XX
FA (INNO-) INNOVENTUS PROJECT AB.
XX
XX Tuvemo HT, Frisk GE, Yin H;
XX
DR WPI; 2003-278229/27.
DR P-PSDB; ABG75961.
XX
XX Polymerase chain reaction and primers for detecting nucleic acids from
XX the diabetogenic coxsackie B virus-4 strain VD2921.
XX
PS Example 5; Page 64-66; 79pp; English.
XX
CC The invention describes a polymerase chain reaction (PCR) and primers for
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,
CC P3C and P3D nucleic acids). The methods and primers are used for the
CC detection of CBV-4 strain VD2921 which is associated with diabetes
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear
CC cells, can improve prognosis by allowing treatment e.g. with antiviral
CC drugs, to prevent further loss of beta cells and severe long term
CC consequences of diabetes including blindness, renal failure and leg
CC amputations. This sequence represents the genome of diabetogenic
CC coxsackie B virus 4 (CBV-4) strain VD2921
XX
SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 8; Length 7392;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGCTAATC 19
Db 455 CCCCTGAATCGCGCTAATC 473

RESULT 95
AAQ11816
ID AAQ11816 standard; RNA; 7399 BP.
XX
AC AAQ11816;
XX
XX 25-MAR-2003 (revised)
DT 05-AUG-1991 (first entry)
XX
XX RNA encoding enteroviral polypeptide.
XX
XX Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis;
XX encephalitis; pancreatitis; post viral fatigue syndrome; ss.
XX
XX Enterovirus sp.
XX
XX Key Location/Qualifiers
FH CDS 742..7299
FT /tag= a
FT /product= "enteroviral polypeptide"
XX
XX DE3939200-A.
XX
XX 29-MAY-1991.
XX
XX 27-NOV-1989; 89DE-03939200.
XX
XX 27-NOV-1989; 89DE-03939200.
XX
XX (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.
XX
XX Kandolf R;
XX
XX WPI; 1991-165150/23.

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DR P-PSDB; AAR12141.  
 XX New enteroviral polypeptide for raising group specific antibodies - for  
 PT detecting any type of enterovirus in blood or serum, also new DNA  
 PT encoding it.  
 XX  
 XX Claim 7; Page 17-21; 26pp; German.  
 XX  
 CC This RNA encodes an enteroviral polypeptide which is used to raise poly-  
 CC or monoclonal antibodies (Abs). These are useful in assays for detecting  
 CC enterovirus specific antigens, as an indication of enteroviral disease.  
 CC All 70 serotypes of the enteroviral family can be detected. Diseases such  
 CC as myocarditis, myositis, meningitis, encephalitis and pancreatitis can  
 CC be diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 XX Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 0 T; 1740 U; 0 Other;  
 SQ

Query Match 100.0%; Score 19; DB 2; Length 7399;  
 Best Local Similarity 78.9%; Pred. No. 4;  
 Matches 15; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 1 CCCCTGAATGCGGCTAATC 19  
 ||||:||||:||||:||||:  
 454 CCCUGAAGCGGCUAUC 472

RESULT 96  
 ABV76134  
 ID ABV76134 standard; DNA; 7399 BP.  
 XX  
 XX ABV76134;  
 AC  
 XX  
 DT 07-MAR-2003 (first entry)  
 DE  
 DE Coxsackievirus capsid protein VP1 nucleic acid.  
 KW Gene therapy; vector; hepatitis B virus; cardiovascular disease; heart;  
 KW cardiant; vasotropic; antiarrhythmic; antiarteriosclerotic;  
 KW capsid protein; gene; ss.  
 XX  
 XX Coxsackievirus.  
 XX  
 XX WO200287594-A1.  
 XX  
 PD 07-NOV-2002.  
 XX  
 XX 30-APR-2002; 2002WO-US013644.  
 XX  
 XX 30-APR-2001; 2001US-0287423P.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Chien KR, Hoshijima M;  
 XX  
 XX WPI; 2003-111844/10.  
 DR  
 XX Novel non-viral vector comprises vesicular membrane with hepatitis B  
 PT envelope protein with cardiac targeting sequence, and nucleotide sequence  
 PT for gene therapy useful for treating, e.g., heart failure, arrhythmia and  
 PT atherosclerosis.  
 XX  
 XX Disclosure; Page 27-31; 53pp; English.  
 PS  
 CC The present sequence is that of a coxsackie virus B3 capsid protein VP1  
 CC nucleic acid. The invention provides a non-viral vesicle vector for the  
 CC delivery of nucleic acid to various cardiac cell types. The vesicle  
 CC vector contains the hepatitis B virus envelope protein in which at least  
 CC part of the liver targeting sequence is deleted and replaced with a  
 CC specific cardiac cell targeting sequence. For example, the coxsackie  
 CC virus B3, VP1 sequence can be used to target the vector to  
 CC cardiomyocytes. The vesicle vector can be delivered intravenously or  
 CC intra-arterially rather than by more invasive methods such as direct  
 CC cardiac injection. It can be used to deliver gene products to replace or

CC enhance expression of proteins for treatment of heart failure,  
 CC arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis,  
 CC etc. The vesicles are highly stable and can be produced in large  
 CC quantities, making them ideal for gene therapy  
 XX  
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 1740 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 19; DB 10; Length 7399;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 1 CCCCTGAATGCGGCTAATC 19  
 ||||:||||:||||:||||:  
 454 CCCCTGAATGCGGCTAATC 472

RESULT 97  
 AAZ98719  
 ID AAZ98719 standard; cDNA; 7400 BP.  
 XX  
 XX AAZ98719;  
 AC  
 DT 20-JUN-2000 (first entry)  
 DE  
 DE Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.  
 KW Swine vesicular disease virus; SVDV; swine vesicular disease;  
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 KW differentiation; vaccine; prevent; ss.  
 XX  
 XX Swine vesicular disease virus.  
 OS  
 FH Key Location/Qualifiers  
 FT misc\_feature 2693..2710  
 FT /\*tag= a  
 FT /note= "Nucleotides in this position replace the wild-  
 FT type nucleotide sequence of strain Taiwan Yu-Li (see  
 XX AAZ98717)"  
 XX  
 PN EP982403-A1.  
 PD  
 PD 01-MAR-2000.  
 XX  
 XX 14-AUG-1998; 98EP-00306486.  
 XX  
 XX 14-AUG-1998; 98EP-00306486.  
 PR  
 XX (BIOT-) DEV CENT BIOTECHNOLOGY.  
 XX  
 XX Hwang CL, Lo C, Yang Y, Jeng K, Chang EL;  
 XX  
 XX WPI; 2000-258616/23.  
 XX  
 XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines  
 XX to prevent swine vesicular disease.  
 XX  
 XX Claim 4; Page; 66pp; English.  
 PS  
 CC This sequence represents the full length Swine vesicular disease virus  
 CC (SVDV) gene sequence from the SVDV strain N3. SVDV is the causative agent  
 CC of swine vesicular disease, which is very similar to foot and mouth  
 CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA  
 CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and  
 CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the  
 CC prophylaxis of swine vesicular disease. The invention also includes a  
 CC method for differentiating the mutant SVDV nucleotide sequences from the  
 CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease  
 CC virus through the use of polymerase chain reaction. Note: This sequence  
 CC is not present in the specification, but has been derived from the wild-  
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages  
 CC 34-38 of the specification  
 XX  
 XX Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 19; DB 3; Length 7400;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 454 CCCCTGAATGGGCTAATC 472

## RESULT 98

AAZ98717  
 ID AAZ98717 standard; cDNA; 7400 BP.

AC AAZ98717;

DT 20-JUN-2000 (first entry)

XX Swine vesicular disease virus (SVDV) gene sequence.

XX Swine vesicular disease virus; SVDV; swine vesicular disease;  
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 KW differentiation; vaccine; prevent; ss.

XX Swine vesicular disease virus.

XX EP982403-A1.

XX 01-MAR-2000.

XX 14-AUG-1998; 98EP-00306486.

XX 14-AUG-1998; 98EP-00306486.

XX (BIOT-) DEV CENT BIOTECHNOLOGY.

XX Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines  
 PT to prevent swine vesicular disease.

XX Claim 1; Page 34-38; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus  
 CC (SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the  
 CC causative agent of swine vesicular disease, which is very similar to foot  
 CC and mouth disease. The invention relates to the wild-type Taiwan Yu-Li  
 CC strain cDNA sequence, and the gene sequences of the mutant SVDV strains  
 CC N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a  
 CC vaccine for the prophylaxis of swine vesicular disease. The invention  
 CC also includes a method for differentiating the mutant SVDV nucleotide  
 CC sequences from the wild type strain of SVDV, coxsackievirus and foot-and-  
 CC mouth disease virus through the use of polymerase chain reaction

XX Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 7400;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 454 CCCCTGAATGGGCTAATC 472

## RESULT 99

AAZ98718

ID AAZ98718 standard; cDNA; 7400 BP.

XX AAZ98718;

XX

DT 20-JUN-2000 (first entry)  
 XX Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.  
 DE Swine vesicular disease virus; SVDV; swine vesicular disease;  
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 KW differentiation; vaccine; prevent; ss.  
 XX Swine vesicular disease virus.

XX Key Location/Qualifiers  
 FH misc\_feature /tag= a  
 FT 2705..2710  
 FT /note= "Nucleotides in this position replace the wild-  
 FT type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"

XX EP982403-A1.

XX 01-MAR-2000.

XX 14-AUG-1998; 98EP-00306486.

XX 14-AUG-1998; 98EP-00306486.

XX (BIOT-) DEV CENT BIOTECHNOLOGY.

XX Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines  
 DR to prevent swine vesicular disease.

XX Claim 3; Page; 66pp; English.

XX This sequence represents the full length Swine vesicular disease virus  
 CC (SVDV) gene sequence from the SVDV strain H21. SVDV is the causative  
 CC agent of swine vesicular disease, which is very similar to foot and mouth  
 CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA  
 CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and  
 CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the  
 CC prophylaxis of swine vesicular disease. The invention also includes a  
 CC method for differentiating the mutant SVDV nucleotide sequences from the  
 CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease  
 CC virus through the use of polymerase chain reaction. Note: This sequence  
 CC is not present in the specification, but has been derived from the wild-  
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages  
 CC 34-38 of the specification

XX Sequence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;

Query Match 100.0%; Score 19; DB 3; Length 7400;  
 Best Local Similarity 100.0%; Pred. No. 4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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 Db 454 CCCCTGAATGGGCTAATC 472

## RESULT 100

AAZ29863

ID AAZ29863 standard; cDNA; 7400 BP.

XX AAZ29863;

XX AC

XX 30-AUG-2000 (first entry)

XX Swine vesicular disease virus (SVDV) nucleotide sequence.

XX Swine vesicular disease virus; SVDV; vesicular disease; vaccine; ss.

XX Swine vesicular disease virus.

```

XX
PN CN1244583-A.
XX
XX 16-FEB-2000.
XX
XX 12-AUG-1998; 98CN-00117165.
XX
XX 12-AUG-1998; 98CN-00117165.
XX
XX (BIOL-) BIOLOGICAL TECHNOLOGY DEV CENT.
XX
XX Huang Q, Luo Z, Yang Y;
XX
XX WPI; 2000-388169/34.
XX
XX Native swine vesicular disease virus gene and its variant - useful as
XX PT vaccines.
XX
XX Claim 1; Page 1-5; 54pp; Chinese.
XX
XX The present invention describes a native swine vesicular disease virus
XX (SVDV) gene and its variant. Also described are: (1) an expression
XX plasmid containing the gene; (2) preparation of the gene and its variant;
XX and (3) a vaccine comprising the gene or its variant. The new gene is
XX useful for the treatment of vesicular disease. The present sequence
XX represents a specifically claimed SVDV nucleotide sequence from the
XX present invention
XX
XX Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 19; DB 3; Length 7400;
XX Best Local Similarity 100.0%; Pred. No. 4;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CCCCTGAATCGGCTAATC 19
   |||||
DB 454 CCCCTGAATCGGCTAATC 472

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GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:09:45 ; Search time 802.058 Seconds  
(without alignments)  
1346.567 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 cccctgaatgcggctaacc 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sy.\*

12: gb\_un.\*

13: gb\_vl.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	100.0	30	6 AX348200 ✓	Sequence
3	19	100.0	30	6 AX348202 ✓	Sequence
4	19	100.0	30	6 AX348204 ✓	Sequence
5	19	100.0	39	6 AX711149	Sequence
6	19	100.0	100	13 POLIBRA	D00260 Human polio
7	19	100.0	100	13 POLIHK	D00257 Human polio
8	19	100.0	100	13 POLISAL	D00254 Human polio
9	19	100.0	100	13 POLIUSA	D00261 Human polio
10	19	100.0	100	13 POLISAR2	D00255 Human polio
11	19	100.0	100	13 POLIBRA	D00263 Human polio
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14	19	100.0	100	13 POL3YUN	D00262 Human polio
15	19	100.0	109	13 DQ029090	DQ029090 Human ech
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27	19	100.0	145	13	HEN312091	AJ312091 Human cox
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384	19	100.0	197	13	E30295210	AJ295210 Echovirus	457	19	100.0	316	13	ECV7337	AJ007337 Echovirus
385	19	100.0	198	13	S79276	S79276 (5' region)	458	19	100.0	316	13	ECV7338	AJ007338 Echovirus
386	19	100.0	236	13	AJ783784	AJ783784 Human pol	459	19	100.0	316	13	ECV7339	AJ007339 Echovirus
387	19	100.0	264	13	AJ783779	AJ783779 Human pol	460	19	100.0	316	13	ECV7341	AJ007341 Echovirus
388	19	100.0	266	13	AY271448	AY271448 Human ent	461	19	100.0	316	13	ECV7342	AJ007342 Echovirus
389	19	100.0	266	13	AY271449	AY271449 Human ent	462	19	100.0	316	13	ECV7343	AJ007343 Echovirus
390	19	100.0	266	13	AY271450	AY271450 Human ent	463	19	100.0	316	13	ECV7344	AJ007344 Echovirus
391	19	100.0	266	13	AY271451	AY271451 Human ent	464	19	100.0	317	13	ECV7340	AJ007340 Echovirus
392	19	100.0	266	13	AY271452	AY271452 Human ent	465	19	100.0	317	13	ECV7346	AJ007346 Echovirus
393	19	100.0	266	13	AY271453	AY271453 Human ent	466	19	100.0	319	13	HEC579630	AJ579630 Human ech
394	19	100.0	266	13	AY271454	AY271454 Human ent	467	19	100.0	319	13	HEC579631	AJ579631 Human ech
395	19	100.0	266	13	AY271455	AY271455 Human ent	468	19	100.0	319	13	HEC579632	AJ579632 Human ech
396	19	100.0	266	13	AY271456	AY271456 Human ent	469	19	100.0	319	13	HEC579633	AJ579633 Human ech
397	19	100.0	266	13	AY271457	AY271457 Human ent	470	19	100.0	319	13	HEC579634	AJ579634 Human ech
398	19	100.0	266	13	AY271458	AY271458 Human ent	471	19	100.0	319	13	HEC579635	AJ579635 Human ech
399	19	100.0	266	13	AY271459	AY271459 Human ent	472	19	100.0	319	13	HEC579636	AJ579636 Human ech
400	19	100.0	266	13	AY271460	AY271460 Human ent	473	19	100.0	319	13	HEC579637	AJ579637 Human ech
401	19	100.0	266	13	AY271461	AY271461 Human ent	474	19	100.0	319	13	HEC579638	AJ579638 Human ech
402	19	100.0	266	13	AY271462	AY271462 Human ent	475	19	100.0	319	13	HEC579639	AJ579639 Human ech
403	19	100.0	266	13	AY271463	AY271463 Human ent	476	19	100.0	319	13	HEC579640	AJ579640 Human ech
404	19	100.0	266	13	AY271464	AY271464 Human ent	477	19	100.0	330	13	AF542452	AF542452 Human rhi
405	19	100.0	266	13	AY271465	AY271465 Human ent	478	19	100.0	338	6	CQ964036	CQ964036 Sequence
406	19	100.0	266	13	AY271466	AY271466 Human ent	479	19	100.0	339	6	CQ964030	CQ964030 Sequence
407	19	100.0	266	13	AY271467	AY271467 Human ent	480	19	100.0	340	6	CQ964029	CQ964029 Sequence
408	19	100.0	266	13	AY271469	AY271469 Human ent	481	19	100.0	340	6	CQ964031	CQ964031 Sequence
409	19	100.0	266	13	AY271470	AY271470 Human ent	482	19	100.0	340	6	CQ964032	CQ964032 Sequence
410	19	100.0	266	13	AY271471	AY271471 Human ent	483	19	100.0	340	6	CQ964033	CQ964033 Sequence
411	19	100.0	266	13	AY271473	AY271473 Human ent	484	19	100.0	340	6	CQ964034	CQ964034 Sequence
412	19	100.0	266	13	AY271475	AY271475 Human ent	485	19	100.0	340	6	CQ964035	CQ964035 Sequence
413	19	100.0	266	13	AY271476	AY271476 Human ent	486	19	100.0	345	13	E9U37767	U37767 Echovirus 9
414	19	100.0	266	13	AY271477	AY271477 Human ent	487	19	100.0	346	13	AF412341	AF412341 Human cox
415	19	100.0	266	13	AY271478	AY271478 Human ent	488	19	100.0	346	13	AF412342	AF412342 Human cox
416	19	100.0	266	13	AY271479	AY271479 Human ent	489	19	100.0	346	13	AF412343	AF412343 Human cox
417	19	100.0	267	13	AY271472	AY271472 Human ent	490	19	100.0	346	13	AF412344	AF412344 Human cox
418	19	100.0	267	13	AY271474	AY271474 Human ent	491	19	100.0	346	13	AF412345	AF412345 Human cox
419	19	100.0	269	13	AY935539	AY935539 Human cox	492	19	100.0	346	13	AF412346	AF412346 Human cox
420	19	100.0	269	13	AY935540	AY935540 Human cox	493	19	100.0	346	13	AF412348	AF412348 Human cox
421	19	100.0	269	13	AY935542	AY935542 Human cox	494	19	100.0	346	13	AF412349	AF412349 Human cox
422	19	100.0	269	13	AY935543	AY935543 Human cox	495	19	100.0	346	13	AF412357	AF412357 Human cox
423	19	100.0	275	13	HCO417545	HCO417545 Human cox	496	19	100.0	346	13	AF412358	AF412358 Human cox
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425	19	100.0	275	13	HCO417549	HCO417549 Human cox	498	19	100.0	346	13	AF412360	AF412360 Human ech
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428	19	100.0	296	13	AJ783735	AJ783735 Human pol							
429	19	100.0	296	13	CVU30919	CVU30919 Coxsackievi							
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431	19	100.0	296	13	CVU30924	CVU30924 Coxsackievi							
432	19	100.0	296	13	CVU30929	CVU30929 Coxsackievi							
433	19	100.0	297	13	CVU30915	CVU30915 Coxsackievi							
434	19	100.0	297	13	CVU30916	CVU30916 Coxsackievi							
435	19	100.0	297	13	CVU30917	CVU30917 Coxsackievi							
436	19	100.0	297	13	CVU30918	CVU30918 Coxsackievi							
437	19	100.0	297	13	CVU30920	CVU30920 Coxsackievi							
438	19	100.0	297	13	CVU30921	CVU30921 Coxsackievi							
439	19	100.0	297	13	CVU30925	CVU30925 Coxsackievi							
440	19	100.0	297	13	CVU30927	CVU30927 Coxsackievi							
441	19	100.0	297	13	CVU30928	CVU30928 Coxsackievi							
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443	19	100.0	297	13	E2U11707	E2U11707 Echovirus 2							
444	19	100.0	297	13	E4U11708	E4U11708 Echovirus 4							
445	19	100.0	297	13	E9U11710	E9U11710 Echovirus 9							
446	19	100.0	298	13	CBU31213	CBU31213 Coxsackievi							
447	19	100.0	298	13	CVU30922	CVU30922 Coxsackievi							
448	19	100.0	298	13	CVU30926	CVU30926 Coxsackievi							
449	19	100.0	299	13	CBU31212	CBU31212 Coxsackievi							
450	19	100.0	300	13	AJ783781	AJ783781 Human pol							
451	19	100.0	302	13	AJ783775	AJ783775 Human pol							
452	19	100.0	309	13	AJ783770	AJ783770 Human pol							
453	19	100.0	314	13	ECV7345	AJ007345 Echovirus							
454	19	100.0	315	13	AJ783774	AJ783774 Human pol							
455	19	100.0	316	13	ECV7335	AJ007335 Echovirus							
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ALIGNMENTS

RESULT 1	AR595531	AR595531	Sequence 9 from patent US 6818397.	27 bp	DNA	linear	PAT 15-DEC-2004
LOCUS	AR595531	Sequence 9 from patent US 6818397.					
DEFINITION	AR595531	Sequence 9 from patent US 6818397.					
ACCESSION	AR595531	Sequence 9 from patent US 6818397.					
VERSION	AR595531.1	GI:56646343					
KEYWORDS	Unknown.						
SOURCE	Unknown.						
ORGANISM	Unknown.						
REFERENCE	1 (bases 1 to 27)						
AUTHORS	Lee, K.-H., Bair, C.-H., Teeng, Y.-Y., Wang, Y.-W. and Wang, S.-H.						
TITLE	Methods for detecting and differentiating enteroviruses and the primers and probes therefor						
JOURNAL	Patent: US 6818397-A 9 16-NOV-2004;						
FEATURES	Dr. Chip Biotechnology Incorporation; Taichung; TWX;						
source	Location/Qualifiers						
ORIGIN	1..27						
Query Match	100.0%;	Score 19;	DB 6;	Length 27;			

Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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Db 9 CCCCTGAATGGGCTAATC 27

RESULT 2  
AX348200  
LOCUS AX348200 30 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 70 from Patent WO0202811.  
ACCESSION AX348200  
VERSION AX348200.1 GI:18614300  
KEYWORDS  
SOURCE Human poliovirus 2  
ORGANISM Human poliovirus 2

REFERENCE 1  
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B., Vernet, G., Armand, M.A. and Laffaire, P.  
TITLE Method for controlling the microbiological quality of an aqueous medium and kit therefor  
JOURNAL Patent: WO 0202811-A 70 10-JAN-2002;  
BIO MERIEUX (FR)

FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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Db 7 CCCCTGAATGGGCTAATC 25

RESULT 3  
AX348202  
LOCUS AX348202 30 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 72 from Patent WO0202811.  
ACCESSION AX348202  
VERSION AX348202.1 GI:18614302  
KEYWORDS  
SOURCE Human coxsackievirus A21

REFERENCE 1  
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B., Vernet, G., Armand, M.A. and Laffaire, P.  
TITLE Method for controlling the microbiological quality of an aqueous medium and kit therefor  
JOURNAL Patent: WO 0202811-A 72 10-JAN-2002;  
BIO MERIEUX (FR)

FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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Db 6 CCCCTGAATGGGCTAATC 24

## RESULT 4

AX348204  
LOCUS AX348204 30 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 74 from Patent WO0202811.  
ACCESSION AX348204  
VERSION AX348204.1 GI:18614304  
KEYWORDS  
SOURCE Human echovirus 12  
ORGANISM Human echovirus 12

REFERENCE 1  
AUTHORS Renaud, P., Guillot, E., Mabilat, C., Vachon, C., Lacroix, B., Vernet, G., Armand, M.A. and Laffaire, P.  
TITLE Method for controlling the microbiological quality of an aqueous medium and kit therefor  
JOURNAL Patent: WO 0202811-A 74 10-JAN-2002;  
BIO MERIEUX (FR)

FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 9.4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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Db 11 CCCCTGAATGGGCTAATC 29

## RESULT 5

AX711149  
LOCUS AX711149 39 bp RNA linear PAT 11-APR-2003  
DEFINITION Sequence 449 from Patent EP1288296.  
ACCESSION AX711149  
VERSION AX711149.1 GI:29787530  
KEYWORDS  
SOURCE unidentified  
ORGANISM unclassified sequences.

REFERENCE 1  
AUTHORS Draper, K.G., McSwiggen, J.A., Holecsek, J.J., Dudycz, L.W., Macejak, D.G. and Mamone, J.A.  
TITLE Method and reagent for inhibiting HBV viral replication  
JOURNAL Patent: EP 1288296-A 449 05-MAR-2003;  
RIBOZYME PHARMACEUTICALS, INC. (US)

FEATURES  
source Location/Qualifiers  
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## ORIGIN

Query Match 100.0%; Score 19; DB 6; Length 39;  
Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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Db 13 CCCCTGAATGGGCTAATC 31

## RESULT 6

POL1BRA  
LOCUS POL1BRA 100 bp RNA linear VRL 21-MAY-2003

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DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/8-3827/Brazil/81.
ACCESSION D00260
VERSION D00260.1 GI:222344
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
source
Location/Qualifiers
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/mol_type="genomic RNA"
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/db_xref="taxon:12080"
/notes="451 bp downstream of the 5' end of virion RNA."
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 7
POLIHK
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/15/HK/81.
ACCESSION D00257
VERSION D00257.1 GI:222345
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 7
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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Location/Qualifiers
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/db_xref="taxon:12080"
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5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
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Db 7 CCCCTGAATCGGCTAATC 25

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Db 7 CCCCTGAATCGGCTAATC 25
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POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, vaccine strains
Sabin 1, Cox, CHAT.
ACCESSION D00254
VERSION D00254.1 GI:222346
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
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Location/Qualifiers
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5'UTR
variation
36
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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Location/Qualifiers
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Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 9
POLIUSA
LOCUS
DEFINITION Human poliovirus 1 RNA, 5'UTR, partial sequence, wild-type isolate
PI/2171/USA/77.
ACCESSION D00261
VERSION D00261.1 GI:222347
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
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Location/Qualifiers
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
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Db 7 CCCCTGAATCGGCTAATC 25

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/note="451 bp downstream of the 5' end of virion RNA."
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Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 7 CCCCTGAATGGCGCTAATC 25

RESULT 10
POL2SA2 100 bp RNA linear VRL 21-MAY-2003
LOCUS Human poliovirus 2 RNA, 5'UTR, partial sequence, vaccine strain
DEFINITION Sabin 2.
ACCESSION D00255
VERSION D00255.1 GI:222350
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 2
ORGANISM Human poliovirus 2
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].

FEATURES
source
1. .100
/organism="Human poliovirus 2"
/mol_type="genomic RNA"
/strain="vaccine strain Sabin 2"
/db_xref="taxon:12083"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 7 CCCCTGAATGGCGCTAATC 25

RESULT 11
POL3BRA 100 bp RNA linear VRL 21-MAY-2003
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
DEFINITION P3/3054/Brazil/81.
ACCESSION D00263
VERSION D00263.1 GI:222351
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].

FEATURES
source
1. .100
/organism="Human poliovirus 3"
/mol_type="genomic RNA"
/strain="wild-type isolate P3/3054/Brazil/81"
/db_xref="taxon:12086"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 7 CCCCTGAATGGCGCTAATC 25

RESULT 12
POL3FIN 100 bp RNA linear VRL 21-MAY-2003
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolates
DEFINITION P3/Fin/60212/85, P3/Fin/25725/85.
ACCESSION D00258
VERSION D00258.1 GI:222352
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
polioviruses which include vaccine strains of serotype 1, 2, 3 and
wild-type isolates of serotype 1, 3 were determined in [1].

FEATURES
source
1. .100
/organism="Human poliovirus 3"
/mol_type="genomic RNA"
/strain="wild-type isolates P3/Fin/60212/85,
P3/Fin/25725/85"
/db_xref="taxon:12086"
/note="451 bp downstream of the 5' end of virion RNA."
<1. >100

5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 7 CCCCTGAATGGCGCTAATC 25

RESULT 13
POL3VDB 100 bp RNA linear VRL 21-MAY-2003
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, vaccine strain
DEFINITION USOL-D-BAC.
ACCESSION D00259
VERSION D00259.1 GI:222354
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
VIRUSES: ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
        replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
        polioviruses which include vaccine strains of serotype 1, 2, 3 and
        wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
    source
        Location/Qualifiers
            1..100
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            /mol_type="genomic RNA"
            /strain="vaccine strain USOL-D-BAC"
            /db_xref="taxon:12086"
            /note="451 bp downstream of the 5' end of virion RNA."
            <1..>100
    5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 14
POL3YUN
LOCUS Human poliovirus 3 RNA, 5'UTR, partial sequence, wild-type isolate
        P3/Yunan/2/84.
DEFINITION
ACCESSION D00262
VERSION D00262.1 GI:222355
KEYWORDS 5' non-coding region; poliovirus.
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 100)
AUTHORS Minor,P.D. and Dunn,G.
TITLE The effect of sequences in the 5' non-coding region on the
        replication of polioviruses in the human gut
JOURNAL J. Gen. Virol. 69 (Pt 5), 1091-1096 (1988)
PUBMED 2836553
COMMENT The genomic sequences of a portion of the 5' non-coding region of
        polioviruses which include vaccine strains of serotype 1, 2, 3 and
        wild-type isolates of serotype 1, 3 were determined in [1].
FEATURES
    source
        Location/Qualifiers
            1..100
            /organism="Human poliovirus 3"
            /mol_type="genomic RNA"
            /isolate="wild-type isolate P3/Yunan/2/84"
            /db_xref="taxon:12086"
            /note="451 bp downstream of the 5' end of virion RNA."
            <1..>100
    5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 100;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 7 CCCCTGAATCGGCTAATC 25

RESULT 15
DQ029090
LOCUS Human echovirus 11 strain MON-ES9 5' UTR.
DEFINITION
ACCESSION DQ029090

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VERSION DQ029090.1 GI:66473298
KEYWORDS Human echovirus 11
SOURCE Human echovirus 11
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
        isolates ECHO virus type 11 with different replicative capacities
        phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
        Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
    source
        Location/Qualifiers
            1..109
            /organism="Human echovirus 11"
            /viroion
            /mol_type="genomic RNA"
            /strain="MON-ES9"
            /db_xref="taxon:12078"
            /country="Tunisia"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"
    5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
    |||||
Db 4 CCCCTGAATCGGCTAATC 22

RESULT 16
DQ029091
LOCUS Human echovirus 11 strain MON-ES36 5' UTR.
DEFINITION
ACCESSION DQ029091
VERSION DQ029091.1 GI:66473299
KEYWORDS Human echovirus 11
SOURCE Human echovirus 11
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Nucleotide sequences of the IRES domains IV and V of natural
        isolates ECHO virus type 11 with different replicative capacities
        phenotypes
JOURNAL Unpublished (2005)
REFERENCE 2 (bases 1 to 109)
AUTHORS Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
        N'Saibia,S. and Aouni,M.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
        Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
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        Location/Qualifiers
            1..109
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            /viroion
            /mol_type="genomic RNA"
            /strain="MON-ES36"
            /db_xref="taxon:12078"
            /country="Tunisia"
            <1..>109
    5'UTR

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ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 17
LOCUS      DQ029092      109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 11 strain STE-5793 5' UTR.
ACCESSION  DQ029092
VERSION    DQ029092.1 GI:66473300
KEYWORDS
SOURCE     Human echovirus 11
ORGANISM   Human echovirus 11
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL    Unpublished (2005)
REFERENCE  2 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES   source
            1..109
            /organism="Human echovirus 11"
            /viral
            /mol_type="genomic RNA"
            /strain="STE-5793"
            /db_xref="taxon:12078"
            /country="France"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 18
LOCUS      DQ029094      109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 11 strain STE-11730 5' UTR.
ACCESSION  DQ029094
VERSION    DQ029094.1 GI:66473302
KEYWORDS
SOURCE     Human echovirus 11
ORGANISM   Human echovirus 11
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL    Unpublished (2005)
REFERENCE  2 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES   source
            1..109
            /organism="Human echovirus 11"
            /viral
            /mol_type="genomic RNA"
            /strain="STE-5793"
            /db_xref="taxon:12078"
            /country="France"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 19
LOCUS      DQ029095      109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 2 strain MON-ECV2 5' UTR.
ACCESSION  DQ029095
VERSION    DQ029095.1 GI:66473303
KEYWORDS
SOURCE     Human echovirus 2
ORGANISM   Human echovirus 2
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL    Unpublished (2005)
REFERENCE  2 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES   source
            1..109
            /organism="Human echovirus 2"
            /viral
            /mol_type="genomic RNA"
            /strain="MON-ECV2"
            /db_xref="taxon:35294"
            /country="Tunisia"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22
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phenotypes
Unpublished (2005)
2 (bases 1 to 109)
Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
Direct Submission
Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
Location/Qualifiers
1..109
/organism="Human echovirus 11"
/viral
/mol_type="genomic RNA"
/strain="STE-11730"
/db_xref="taxon:12078"
/country="France"
<1..>109
/note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22

RESULT 19
LOCUS      DQ029095      109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 2 strain MON-ECV2 5' UTR.
ACCESSION  DQ029095
VERSION    DQ029095.1 GI:66473303
KEYWORDS
SOURCE     Human echovirus 2
ORGANISM   Human echovirus 2
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL    Unpublished (2005)
REFERENCE  2 (bases 1 to 109)
AUTHORS    Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE      Direct Submission
JOURNAL    Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES   source
            1..109
            /organism="Human echovirus 2"
            /viral
            /mol_type="genomic RNA"
            /strain="MON-ECV2"
            /db_xref="taxon:35294"
            /country="Tunisia"
            <1..>109
            /note="domain V of IRES (internal ribosome entry site)"

5'UTR

ORIGIN
/Note="domain V of IRES (internal ribosome entry site)"

Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 4 CCCCTGAATGCGGCTAATC 22
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RESULT 20
DQ029096
LOCUS      DQ029096                109 bp      RNA      linear      VRL 29-MAY-2005
DEFINITION Human echovirus 12 strain Travis prototype 5' UTR.
ACCESSION  DQ029096
VERSION     DQ029096.1 GI:66473304
KEYWORDS
SOURCE      Human echovirus 12
ORGANISM    Human echovirus 12
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 109)
AUTHORS     Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE       Nucleotide sequences of the IRES domains IV and V of natural
            isolates ECHO virus type 11 with different replicative capacities
            phenotypes
JOURNAL      Unpublished (2005)
REFERENCE   2 (bases 1 to 109)
AUTHORS     Charbi,J., Elhjar,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
            N'Saibia,S. and Aouni,M.
TITLE       Direct Submission
JOURNAL      Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
            Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES    Location/Qualifiers
             source
               1..109
               /organism="Human echovirus 12"
               /viroion
               /mol_type="genomic RNA"
               /strain="Travis prototype"
               /db_xref="taxon:35293"
             <1..>109
             /note="domain V of IRES (internal ribosome entry site)"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGCGCTAATC 19
        |||||||
Db      4 CCCCTGAATCGCGCTAATC 22

RESULT 21
AF380621
LOCUS      AF380621                120 bp ss-RNA      linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380621
VERSION     AF380621.1 GI:14290213
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Direct Submission
JOURNAL      Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES    Location/Qualifiers
             source
               1..120
               /organism="Human poliovirus 1"
               /viroion
               /mol_type="genomic RNA"
               /specific_host="Homo sapiens"
               /db_xref="taxon:12080"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGCGCTAATC 19
        |||||||
Db      9 CCCCTGAATCGCGCTAATC 27

RESULT 22
AF380622
LOCUS      AF380622                120 bp ss-RNA      linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380622
VERSION     AF380622.1 GI:14290214
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Direct Submission
JOURNAL      Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES    Location/Qualifiers
             source
               1..120
               /organism="Human poliovirus 1"
               /viroion
               /mol_type="genomic RNA"
               /specific_host="Homo sapiens"
               /db_xref="taxon:12080"
               /note="wild type isolate from 1999"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGCGCTAATC 19
        |||||||
Db      9 CCCCTGAATCGCGCTAATC 27

RESULT 23
AF380624
LOCUS      AF380624                120 bp ss-RNA      linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 3 5' untranslated region, partial sequence.
ACCESSION  AF380624
VERSION     AF380624.1 GI:14290216
KEYWORDS
SOURCE      Human poliovirus 3
ORGANISM    Human poliovirus 3
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Direct Submission

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5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGCGCTAATC 19
        |||||||
Db      9 CCCCTGAATCGCGCTAATC 27

RESULT 22
AF380622
LOCUS      AF380622                120 bp ss-RNA      linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 1 5' untranslated region, partial sequence.
ACCESSION  AF380622
VERSION     AF380622.1 GI:14290214
KEYWORDS
SOURCE      Human poliovirus 1
ORGANISM    Human poliovirus 1
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Direct Submission
JOURNAL      Submitted (14-MAY-2001) Medical Microbiology, University of Wales,
            College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK
FEATURES    Location/Qualifiers
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               1..120
               /organism="Human poliovirus 1"
               /viroion
               /mol_type="genomic RNA"
               /specific_host="Homo sapiens"
               /db_xref="taxon:12080"
               /note="wild type isolate from 1999"

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 120;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGCGCTAATC 19
        |||||||
Db      9 CCCCTGAATCGCGCTAATC 27

RESULT 23
AF380624
LOCUS      AF380624                120 bp ss-RNA      linear      VRL 05-JUN-2001
DEFINITION Human poliovirus 3 5' untranslated region, partial sequence.
ACCESSION  AF380624
VERSION     AF380624.1 GI:14290216
KEYWORDS
SOURCE      Human poliovirus 3
ORGANISM    Human poliovirus 3
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Detection and Typing of Enteroviruses by Analysis of the 2C Gene
            Sequence
JOURNAL      Unpublished
REFERENCE   2 (bases 1 to 120)
AUTHORS     Mengistu,A., Neale,M.L. and Fox,J.D.
TITLE       Direct Submission

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JOURNAL Submitted (14-MAY-2001) Medical Microbiology, University of Wales,  
College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK

FEATURES  
source Location/Qualifiers  
1. .120  
/organism="Human poliovirus 3"  
/viral  
/mol\_type="genomic RNA"  
/specific\_host="Homo sapiens"  
/db\_xref="taxon:12086"  
/note="wild type isolate from 1999"  
<1. .>120

5'UTR  
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 120;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CCCCTGAATCGGCTAATC 19  
|||||  
DB 9 CCCCTGAATCGGCTAATC 27  
|||||

RESULT 24

AF380623 122 bp ss-RNA linear VRL 05-JUN-2000

LOCUS Human poliovirus 2 5' untranslated region, partial sequence.  
DEFINITION Human poliovirus 2  
ACCESSION AF380623  
VERSION AF380623.1 GI:14290215  
KEYWORDS  
SOURCE Human poliovirus 2  
ORGANISM Human poliovirus 2  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 122)  
AUTHORS Mengistu, A., Neale, M.L. and Fox, J.D.  
TITLE Detection and Typing of Enteroviruses by Analysis of the 2C Gene  
Sequence  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 122)  
AUTHORS Mengistu, A., Neale, M.L. and Fox, J.D.  
TITLE Direct Submission  
JOURNAL Submitted (14-MAY-2001) Medical Microbiology, University of Wales,  
College of Medicine, Heath Park, Cardiff, Wales CF14 4XN, UK

FEATURES  
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/organism="Human poliovirus 2"  
/viral  
/mol\_type="genomic RNA"  
/specific\_host="Homo sapiens"  
/db\_xref="taxon:12083"  
/note="wild type isolate from 1999"  
<1. .>122

5'UTR  
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 122;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 CCCCTGAATCGGCTAATC 19  
|||||  
DB 10 CCCCTGAATCGGCTAATC 28  
|||||

RESULT 25

AJ783777 128 bp RNA linear VRL 12-AUG-2000

LOCUS Human poliovirus 1, partial 5'UTR, genomic RNA, isolate P20.  
DEFINITION Human poliovirus 1  
ACCESSION AJ783777  
VERSION AJ783777.1 GI:72534022  
KEYWORDS  
SOURCE Human poliovirus 1  
ORGANISM Human poliovirus 1  
Viruses; ssRNA positive-strand viruses, no DNA stage;

KEYWORDS	Enterovirus 5506/SIN/001309
SOURCE	Enterovirus 5506/SIN/001309
ORGANISM	Viruses: ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 147)
AUTHORS	Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
TITLE	Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers
JOURNAL	J. Clin. Microbiol. 40 (8): 2823-2827 (2002)

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Query Match      100.0%; Score 19; DB 13; Length 147;
Best Local Similarity 100.0%; Pred. NO. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAATC 19
    |||||
Db 8 CCCTGAATCGGCTAATC 26
    |||||

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RESULT 30  
AF314004

LOCUS AF314004 153 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5589/SIN/001809 5' UTR, partial sequence.  
ACCESSION AF314004  
VERSION AF314004.2 GI:131111667  
KEYWORDS  
SOURCE  
ORGANISM Enterovirus 5589/SIN/001809  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 153)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
12149336  
2 (bases 1 to 153)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
3 (bases 1 to 153)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667227.  
FEATURES  
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/mol\_type="mRNA"  
/strain="5589/SIN/001809"  
/db\_xref="taxon:150718"  
<1..>153  
5'UTR  
ORIGIN  
Query Match 100.0%; Score 19; DB 13; Length 153;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 8 CCCCTGAATGCGGCTAATC 26  
RESULT 31  
AF314003  
LOCUS AF314003 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5627/SIN/002009 5' UTR, partial sequence.  
ACCESSION AF314003  
VERSION AF314003.2 GI:131111666  
KEYWORDS  
SOURCE Enterovirus 5627/SIN/002009  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
12149336  
2 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REFERENCE 3 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.  
FEATURES  
source 1..154  
/organism="Enterovirus 5627/SIN/002009"  
/mol\_type="mRNA"  
/strain="5627/SIN/002009"  
/db\_xref="taxon:150720"  
<1..>154  
5'UTR  
ORIGIN  
Query Match 100.0%; Score 19; DB 13; Length 154;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 8 CCCCTGAATGCGGCTAATC 26  
RESULT 33  
AF314005  
LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.  
ACCESSION AF314005  
VERSION AF314005.2 GI:13111668  
KEYWORDS  
SOURCE Enterovirus 5656/SIN/002209  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
12149336  
2 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REFERENCE 3 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.  
FEATURES  
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/strain="5656/SIN/002209"  
/db\_xref="taxon:150720"  
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Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CCCCTGAATGCGGCTAATC 19  
|||||  
Db 8 CCCCTGAATGCGGCTAATC 26  
RESULT 33

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AF314007
LOCUS AF314007 154 bp mRNA linear VRL 31-JUL-2002
DEFINITION Enterovirus 5536/SIN/001409 5' UTR, partial sequence.
ACCESSION AF314007
VERSION AF314007.2 GI:13111669
KEYWORDS
SOURCE
ORGANISM Enterovirus 5536/SIN/001409
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
3 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Sequence update by submitter
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667230.
FEATURES
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/mol_type="mRNA"
/strain="5536/SIN/001409"
/db_xref="taxon:150716"
<1..>154
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
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Db 8 CCCCTGAATGCGCTAATC 26

RESULT 34
AF314008 154 bp mRNA linear VRL 31-JUL-2002
LOCUS AF314008
DEFINITION Enterovirus 5546/SIN/000009 5' UTR, partial sequence.
ACCESSION AF314008
VERSION AF314008.1 GI:12667231
KEYWORDS
SOURCE
ORGANISM Enterovirus 5546/SIN/000009
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES
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/db_xref="taxon:150717"
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5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | |
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 35
AF314008 154 bp mRNA linear VRL 31-JUL-2002
LOCUS AF314008
DEFINITION Enterovirus 5546/SIN/000009 5' UTR, partial sequence.
ACCESSION AF314008
VERSION AF314008.1 GI:13591397
KEYWORDS
SOURCE
ORGANISM Enterovirus TS/SIN/001002
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (22-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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/organism="Enterovirus TS/SIN/001002"
/mol_type="genomic RNA"
/strain="TS/SIN/001002"
/db_xref="taxon:155431"
/note="isolated from throat swab"
<1..>154
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5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | |
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 36
AF314008 154 bp mRNA linear VRL 10-APR-2001
LOCUS AF314008
DEFINITION Enterovirus TF/SIN/000704 5' UTR, partial sequence.
ACCESSION AF314008
VERSION AF314008.1 GI:13591398
KEYWORDS
SOURCE
ORGANISM Enterovirus TF/SIN/000704
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
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/organism="Enterovirus 5546/SIN/000009"
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/db_xref="taxon:150717"
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source
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | |
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 35
AF314008 154 bp RNA linear VRL 31-JUL-2002
LOCUS AF314008
DEFINITION Enterovirus TS/SIN/001002 5'UTR, partial sequence.
ACCESSION AY027864
VERSION AY027864.1 GI:13591397
KEYWORDS
SOURCE
ORGANISM Enterovirus TS/SIN/001002
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
REFERENCE
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (22-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
1..154
/organism="Enterovirus TS/SIN/001002"
/mol_type="genomic RNA"
/strain="TS/SIN/001002"
/db_xref="taxon:155431"
/note="isolated from throat swab"
<1..>154
source
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGCTAATC 19
| | | | | | | | | | | | | | | | | | | |
Db 8 CCCCTGAATGCGCTAATC 26

RESULT 36
AF314008 154 bp RNA linear VRL 10-APR-2001
LOCUS AF314008
DEFINITION Enterovirus TF/SIN/000704 5'UTR, partial sequence.
ACCESSION AY027865
VERSION AY027865.1 GI:13591398
KEYWORDS
SOURCE
ORGANISM Enterovirus TF/SIN/000704
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
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TITLE      Enterovirus strains from an outbreak of Hand, Foot and Mouth
            disease in Singapore (2000)
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 154)
AUTHORS    Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Direct Submission
JOURNAL    Submitted (22-FEB-2001) Microbiology, National University of
            Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES   Location/Qualifiers
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            1..154
            /organism="Enterovirus TF/SIN/000704"
            /mol_type="genomic RNA"
            /strain="TF/SIN/000704"
            /db_xref="taxon:155429"
            /note="Isolated from tissue fluid"
            <1..>154

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CCCCTGAATGCGGCTAATC 19
    |||||
Db   8 CCCCTGAATGCGGCTAATC 26

RESULT 37
AY027866
LOCUS      154 bp RNA linear VRL 10-APR-2001
DEFINITION Enterovirus 5571/SIN/001809 5'UTR, partial sequence.
ACCESSION  AY027866
VERSION    AY027866.1 GI:13591399
KEYWORDS
SOURCE
ORGANISM   Enterovirus 5571/SIN/001809
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 154)
AUTHORS    Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Enterovirus strains from an outbreak of Hand, Foot and Mouth
            disease in Singapore (2000)
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 154)
AUTHORS    Singh, S., Chow, V.T.K. and Poh, C.L.
TITLE      Direct Submission
JOURNAL    Submitted (22-FEB-2001) Microbiology, National University of
            Singapore, 5 Science Drive 2, Singapore 117597, Singapore
FEATURES   Location/Qualifiers
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            1..154
            /organism="Enterovirus 5571/SIN/001809"
            /mol_type="genomic RNA"
            /strain="5571/SIN/001809"
            /db_xref="taxon:155430"
            /note="Isolated from stool sample"
            <1..>154

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 154;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CCCCTGAATGCGGCTAATC 19
    |||||
Db   8 CCCCTGAATGCGGCTAATC 26

RESULT 38
HCO295181/c
LOCUS      171 bp RNA linear VRL 15-MAY-2001
DEFINITION Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate
            IT999-21.
ACCESSION  AJ295181

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VERSION    AJ295181.1 GI:14139958
KEYWORDS   Human coxsackievirus B5
SOURCE     Human coxsackievirus B5
ORGANISM   Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1
AUTHORS    Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,
            Zaniratti, S., Cattani, P., Manzara, S., Fadda, G., Comparcola, D. and
            Ticca, P.
TITLE      A phylogenetic analysis of the two echovirus 30 isolated in Rome
            (Italy) in 1997 from an outbreak of aseptic meningitis associated
            with swimming pools
JOURNAL    Unpublished
REFERENCE  2 (bases 1 to 171)
AUTHORS    Muscillo, M.
TITLE      Direct Submission
JOURNAL    Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
            Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
            00161, Italy
FEATURES   Location/Qualifiers
            source
            1..171
            /organism="Human coxsackievirus B5"
            /mol_type="genomic RNA"
            /strain="F/Roma99"
            /isolate="ITA99-21"
            /specific_host="Homo sapiens"
            /db_xref="taxon:12074"
            /note="sporadic case of aseptic meningitis; BGM cell
            culture of stools from a four years old child"
            <1..>171

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 171;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1 CCCCTGAATGCGGCTAATC 19
    |||||
Db   155 CCCCTGAATGCGGCTAATC 137

RESULT 39
HEN312088
LOCUS      172 bp RNA linear VRL 02-JUL-2003
DEFINITION Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
ACCESSION  AJ312088
VERSION    AJ312088.1 GI:16555706
KEYWORDS   Human enterovirus 71
SOURCE     Human enterovirus 71
ORGANISM   Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE  1
AUTHORS    Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
            Fadda, G.
TITLE      Molecular identification and typing of enteroviruses isolated from
            clinical specimens
JOURNAL    J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
PUBMED     12454151
REFERENCE  2 (bases 1 to 172)
AUTHORS    Muscillo, M.
TITLE      Direct Submission
JOURNAL    Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
            Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
            00161, Italy
FEATURES   Location/Qualifiers
            source
            1..172
            /organism="Human enterovirus 71"
            /viral
            /mol_type="genomic RNA"
            /strain="/di/Roma98"
            /isolate="IT98-5114"

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**SOURCE**  
**ORGAN**

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Query Match 100.0%; Score 19; DB 13; Length 185;  
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
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 Db 14 CCCCTGAATGCGGCTAATC 32  
 |||||

RESULT 43  
 AF521434 185 bp RNA linear VRL 17-JUN-2003  
 LOCUS Human coxsackievirus B5 isolate BE00-15 5' UTR, partial sequence.  
 DEFINITION AF521434  
 ACCESSION AF521434.1 GI:31790776  
 VERSION  
 KEYWORDS  
 SOURCE Human coxsackievirus B5  
 ORGANISM Human coxsackievirus B5  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, A.M. and Van Ranst, M.  
 TITLE Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
 PUBMED 12767006  
 REFERENCE 2 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
 10, Leuven BE-3000, Belgium

FEATURES  
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 /viralion  
 /mol\_type="genomic RNA"  
 /isolate="BE00-15"  
 /isolation\_source="patient 15 - zipcode Belgium 9820"  
 /db\_xref="taxon:12074"  
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5'UTR  
 ORIGIN

## FEATURES

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 /viralion  
 /mol\_type="genomic RNA"  
 /isolate="BE00-15"  
 /isolation\_source="patient 15 - zipcode Belgium 9820"  
 /db\_xref="taxon:12074"  
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## ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
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 Db 14 CCCCTGAATGCGGCTAATC 32  
 |||||

RESULT 44  
 AF521435 185 bp RNA linear VRL 17-JUN-2003  
 LOCUS Human coxsackievirus B5 isolate BE00-1 5' UTR, partial sequence.  
 DEFINITION AF521435  
 ACCESSION AF521435.1 GI:31790777  
 VERSION  
 KEYWORDS  
 SOURCE Human coxsackievirus B5  
 ORGANISM Human coxsackievirus B5  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, A.M. and Van Ranst, M.  
 TITLE Molecular typing and epidemiology of enteroviruses identified from

## FEATURES

source  
 1..185  
 /organism="Human coxsackievirus B5"  
 /viralion  
 /mol\_type="genomic RNA"  
 /isolate="BE00-1"  
 /isolation\_source="patient 1 - zipcode Belgium 3001"  
 /db\_xref="taxon:41846"  
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## ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 9.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## FEATURES

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 /viralion  
 /mol\_type="genomic RNA"  
 /isolate="BE00-1"  
 /isolation\_source="patient 1 - zipcode Belgium 3001"  
 /db\_xref="taxon:41846"  
 <1..>185

## 5'UTR

## ORIGIN

an outbreak of aseptic meningitis in Belgium during the summer of  
 2000

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

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## 1..185

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## /viralion

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## Query Match

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## Matches

## Conservative

## Mismatches

## Indels

## Gaps

## Qy

## Db

## RESULT 45

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

## 1..185

## /organism="Human coxsackievirus 30"

## /viralion

## /mol\_type="genomic RNA"

## /isolate="BE00-2"

## /isolation\_source="patient 2 - zipcode Belgium 3001"

## /db\_xref="taxon:41846"

## &lt;1..&gt;185

## 5'UTR

## ORIGIN

## Query Match

## Best Local Similarity

## Matches

## Conservative

## Mismatches

## Indels

## Gaps

Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 14 CCCCTGAATCGGCTAATC 32

RESULT 46  
 AF521437

LOCUS AF521437 185 bp RNA linear VRL 17-JUN-2003  
 DEFINITION Human echovirus 6 isolate BE00-3 5' UTR, partial sequence.  
 ACCESSION AF521437  
 VERSION AF521437.1 GI:31790779  
 KEYWORDS  
 SOURCE Human echovirus 6  
 ORGANISM Human echovirus 6  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, A.M. and Van Ranst, M.  
 TITLE Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
 PUBMED 12767006  
 REFERENCE 2 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
 10, Leuven BE-3000, Belgium

FEATURES  
 source Location/Qualifiers  
 1..185  
 /organism="Human echovirus 6"  
 /viral  
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 /isolation\_source="patient 3 - zipcode Belgium 3545"  
 /db\_xref="taxon:12062"

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 Query Match 100.0%; Score 19; DB 13; Length 185;  
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Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 14 CCCCTGAATCGGCTAATC 32

RESULT 47  
 AF521438

LOCUS AF521438 185 bp RNA linear VRL 17-JUN-2003  
 DEFINITION Human echovirus 6 isolate BE00-4 5' UTR, partial sequence.  
 ACCESSION AF521438  
 VERSION AF521438.1 GI:31790780  
 KEYWORDS  
 SOURCE Human echovirus 6  
 ORGANISM Human echovirus 6  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, A.M. and Van Ranst, M.  
 TITLE Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
 PUBMED 12767006  
 REFERENCE 2 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
 10, Leuven BE-3000, Belgium

FEATURES  
 source Location/Qualifiers  
 1..185  
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 /viral  
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 /isolation\_source="patient 4 - zipcode Belgium 3290"  
 /db\_xref="taxon:12062"

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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 14 CCCCTGAATCGGCTAATC 32

RESULT 48  
 AF521439

LOCUS AF521439 185 bp RNA linear VRL 17-JUN-2003  
 DEFINITION Human echovirus 6 isolate BE00-5 5' UTR, partial sequence.  
 ACCESSION AF521439  
 VERSION AF521439.1 GI:31790781  
 KEYWORDS  
 SOURCE Human echovirus 6  
 ORGANISM Human echovirus 6  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, A.M. and Van Ranst, M.  
 TITLE Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
 PUBMED 12767006  
 REFERENCE 2 (bases 1 to 185)  
 AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission  
 JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
 10, Leuven BE-3000, Belgium

FEATURES  
 source Location/Qualifiers  
 1..185  
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 /viral  
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 /isolation\_source="patient 5 - zipcode Belgium 3290"  
 /db\_xref="taxon:12062"

5'UTR  
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 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
 Db 14 CCCCTGAATCGGCTAATC 32



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RESULT 49
AF521440
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 185)
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

AUTHORS
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

JOURNAL
J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED
12767006

REFERENCE
2 (bases 1 to 185)
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/virion
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/isolate="BE00-6"
/isolation_source="patient 6 - zipcode Belgium 9400"
/db_xref="taxon:41846"
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5'UTR
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 50
AF521441
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 185)
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

AUTHORS
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

JOURNAL
J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED
12767006

REFERENCE
2 (bases 1 to 185)
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
1..185
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/virion
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/isolate="BE00-7"
/isolation_source="patient 7 - zipcode Belgium 3290"
/db_xref="taxon:12062"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 51
AF521442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

JOURNAL
J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED
12767006

REFERENCE
2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 52
AF521443
LOCUS
DEFINITION

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for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/virion
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QY 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 51
AF521442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000

JOURNAL
J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED
12767006

REFERENCE
2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
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/virion
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/isolate="BE00-8"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 52
AF521443
LOCUS
DEFINITION

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ACCESSION AF521443
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KEYWORDS
SOURCE Human echovirus 6
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REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
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location/Qualifiers
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<1..>185
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32
RESULT 53
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DEFINITION Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.
ACCESSION AF521444
VERSION AF521444.1 GI:31790786
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
location/Qualifiers
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/db_xref="taxon:12062"
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32
RESULT 55
AF521446
LOCUS Human echovirus 16 isolate BE00-13 5' UTR, partial sequence. VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
ACCESSION AF521446
VERSION AF521446.1 GI:31790788
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
location/Qualifiers
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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32
RESULT 55
AF521446
LOCUS Human echovirus 16 isolate BE00-13 5' UTR, partial sequence. VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
ACCESSION AF521446
VERSION AF521446.1 GI:31790788
KEYWORDS
SOURCE Human echovirus 16
ORGANISM Human echovirus 16
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGCGGCTAATC 19
Db 14 CCCCTGAATGCGGCTAATC 32
```

Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

REFERENCE  
AUTHORS Thoenen, I., Lemey, P., Van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission

JOURNAL  
PUBMED Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers

1. .185  
/organism="Human echovirus 30"  
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/db\_xref="taxon:47504"  
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5'UTR  
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 56  
AF521447  
LOCUS Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AF521447.1 GI:31790789

VERSION AF521447.1 GI:31790789

KEYWORDS Human echovirus 30  
SOURCE Human echovirus 30  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

REFERENCE  
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission

JOURNAL  
PUBMED Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers

1. .185  
/organism="Human echovirus 30"  
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5'UTR  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 57  
AF521448

LOCUS Human coxsackievirus B5 isolate BE00-31 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AF521448

VERSION AF521448.1 GI:31790790

KEYWORDS Human coxsackievirus B5  
SOURCE Human coxsackievirus B5

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

REFERENCE 12767006

2 (bases 1 to 185)  
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers

1. .185  
/organism="Human coxsackievirus B5"  
/viroion  
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/isolate="BE00-31"  
/isolation\_source="patient 31 - zipcode Belgium 9320"  
/db\_xref="taxon:12074"  
<1. .>185

5'UTR  
ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 58  
AF521449

LOCUS Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.  
DEFINITION  
ACCESSION AF521449

VERSION AF521449.1 GI:31790791

KEYWORDS Human echovirus 30  
SOURCE Human echovirus 30

ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)

AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 185)

**AUTHORS** Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

**FEATURES** Location/Qualifiers

**source**

1..185

/organism="Human echovirus 30"

/virion

/mol\_type="genomic RNA"

/isolate="BE00-32"

/isolation\_source="patient 32 - zipcode Belgium 1703"

/db\_xref="taxon:41846"

<1..>185

**5'UTR**

**ORIGIN**

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CCCCTGAATCGGCTAATC 19

**Db** 14 CCCCTGAATCGGCTAATC 32

**RESULT** 59

**AF521450**

**LOCUS**

**DEFINITION** Human echovirus 30 isolate BE00-33 5' UTR, partial sequence.

**ACCESSION** AF521450

**VERSION** AF521450.1 GI:31790792

**KEYWORDS**

**SOURCE**

**ORGANISM**

Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 185)

**AUTHORS** Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

**FEATURES** Location/Qualifiers

**source**

1..185

/organism="Human echovirus 30"

/virion

/mol\_type="genomic RNA"

/isolate="BE00-33"

/isolation\_source="patient 33 - zipcode Belgium 1745"

/db\_xref="taxon:41846"

<1..>185

**5'UTR**

**ORIGIN**

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CCCCTGAATCGGCTAATC 19

**Db** 14 CCCCTGAATCGGCTAATC 32

**RESULT** 60

**AF521451**

**LOCUS**

**DEFINITION** Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.

**ACCESSION** AF521451

**VERSION** AF521451.1 GI:31790793

**KEYWORDS**

**SOURCE**

**ORGANISM**

Human echovirus 30

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 185)

**AUTHORS** Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

**FEATURES** Location/Qualifiers

**source**

1..185

/organism="Human echovirus 30"

/virion

/mol\_type="genomic RNA"

/isolate="BE00-34"

/isolation\_source="patient 34 - zipcode Belgium 1770"

/db\_xref="taxon:41846"

<1..>185

**5'UTR**

**ORIGIN**

Query Match 100.0%; Score 19; DB 13; Length 185;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 CCCCTGAATCGGCTAATC 19

**Db** 14 CCCCTGAATCGGCTAATC 32

**RESULT** 61

**AF521452**

**LOCUS**

**DEFINITION** Human echovirus 6 isolate BE00-35 5' UTR, partial sequence.

**ACCESSION** AF521452

**VERSION** AF521452.1 GI:31790794

**KEYWORDS**

**SOURCE**

**ORGANISM**

Human echovirus 6

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

1 (bases 1 to 185)

Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

```

REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
    source
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                /viral
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                /isolation_source="patient 35 - zipcode Belgium 3270"
                /db_xref="taxon:12062"
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 62
AF521453
LOCUS AF521453 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-36 5' UTR, partial sequence.
ACCESSION AF521453
VERSION AF521453.1 GI:31790795
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
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        Location/Qualifiers
            1..185
                /organism="Human echovirus 6"
                /viral
                /mol_type="genomic RNA"
                /isolate="BE00-36"
                /isolation_source="patient 36 - zipcode Belgium 2310"
                /db_xref="taxon:12062"
                <1..>185
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ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

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RESULT 63
AF521455
LOCUS AF521455 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-39 5' UTR, partial sequence.
ACCESSION AF521455
VERSION AF521455.1 GI:31790797
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
    source
        Location/Qualifiers
            1..185
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                /viral
                /mol_type="genomic RNA"
                /isolate="BE00-39"
                /isolation_source="patient 39 - zipcode Belgium 3290"
                /db_xref="taxon:12062"
                <1..>185
5'UTR
ORIGIN
Query Match 100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    |||||
Db 14 CCCCTGAATGCGGCTAATC 32

RESULT 64
AF521456
LOCUS AF521456 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 6 isolate BE00-41 5' UTR, partial sequence.
ACCESSION AF521456
VERSION AF521456.1 GI:31790798
KEYWORDS
SOURCE Human echovirus 6
ORGANISM Human echovirus 6
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
        Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological

```

Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

# FEATURES

source  
1. .185  
/organism="Human echovirus 6"  
/virion  
/mol\_type="genomic RNA"  
/isolate="BE00-41"  
/isolation\_source="patient 41 - zipcode Belgium 3390"  
/db\_xref="taxon:12062"  
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# 5'UTR ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

# RESULT 65

AF521457 185 bp RNA linear VRL 17-JUN-2003  
LOCUS Human echovirus 6 isolate BE00-42 5' UTR, partial sequence.  
DEFINITION Human echovirus 6 isolate BE00-42 5' UTR, partial sequence.  
ACCESSION AF521457  
VERSION AF521457.1 GI:31790799

# KEYWORDS

SOURCE Human echovirus 6

# ORGANISM

Human echovirus 6  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

J2767006

# REFERENCE

2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

# TITLE

Location/Qualifiers

# FEATURES

source  
1. .185  
/organism="Human echovirus 6"  
/virion  
/mol\_type="genomic RNA"  
/isolate="BE00-42"  
/isolation\_source="patient 42 - zipcode Belgium 3593"  
/db\_xref="taxon:12062"  
<1. .>185

# 5'UTR ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

# RESULT 66

AF521458 185 bp RNA linear VRL 17-JUN-2003  
LOCUS Human echovirus 6 isolate BE00-44 5' UTR, partial sequence.

# DEFINITION

Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.

# ACCESSION

AF521458

# VERSION

AF521458.1 GI:31790800

# KEYWORDS

Human echovirus 30

# SOURCE

Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

# JOURNAL

# PUBMED

12767006

# REFERENCE

2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

# TITLE

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

# JOURNAL

# PUBMED

12767006

# REFERENCE

1. .185  
/organism="Human echovirus 30"  
/virion  
/mol\_type="genomic RNA"  
/isolate="BE00-43"  
/isolation\_source="patient 43 - zipcode Belgium 9402"  
/db\_xref="taxon:41846"  
<1. .>185

# 5'UTR ORIGIN

Query Match 100.0%; Score 19; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 9.5;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 14 CCCCTGAATCGGCTAATC 32

# RESULT 67

# LOCUS

AF521459

# DEFINITION

Human echovirus 6 isolate BE00-44 5' UTR, partial sequence.

# ACCESSION

AF521459

# VERSION

AF521459.1 GI:31790801

# KEYWORDS

Human echovirus 6  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

# JOURNAL

# PUBMED

12767006

# REFERENCE

2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.

# AUTHORS

# TITLE

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

# JOURNAL

# PUBMED

12767006

# REFERENCE

1. .185  
/organism="Human echovirus 30"  
/virion  
/mol\_type="genomic RNA"  
/isolate="BE00-44"  
/isolation\_source="patient 44 - zipcode Belgium 9402"  
/db\_xref="taxon:41846"  
<1. .>185

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/organism="Human echovirus 6"
/virion
/mol_type="genomic RNA"
/isolate="BE00-44"
/isolation_source="patient 44 - zipcode Belgium 1910"
/db_xref="taxon:12062"
<!.>185

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
    |||||
Db 14 CCCCTGAATGGCGCTAATC 32

RESULT 68
AF521460
LOCUS      AF521460      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-47 5' UTR, partial sequence.
ACCESSION  AF521460
VERSION     AF521460.1 GI:31790802
KEYWORDS
SOURCE      Human coxsackievirus B5
ORGANISM    Human coxsackievirus B5
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS   Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE     Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE     Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
FEATURES   Location/Qualifiers
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                /virion
                /mol_type="genomic RNA"
                /isolate="BE00-47"
                /db_xref="taxon:12074"
                <!.>185

5'UTR
ORIGIN
Query Match      100.0%; Score 19; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
    |||||
Db 14 CCCCTGAATGGCGCTAATC 32

RESULT 69
AF521461
LOCUS      AF521461      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-48 5' UTR, partial sequence.
ACCESSION  AF521461
VERSION     AF521461.1 GI:31790803
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS   Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE     Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE     Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
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ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS   Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE     Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE     Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
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DEFINITION Human echovirus 6 isolate BE00-49 5' UTR, partial sequence.
ACCESSION  AF521462
VERSION     AF521462.1 GI:31790804
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM    Human echovirus 6
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS   Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
          Lindberg,A.M. and Van Ranst,M.
TITLE     Molecular typing and epidemiology of enteroviruses identified from
          an outbreak of aseptic meningitis in Belgium during the summer of
          2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
          Lindberg,M.A. and Van Ranst,M.
TITLE     Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
          Virology, Department of Microbiology and Immunology, Rega Institute
          for Medical Research, University of Leuven, Minderbroedersstraat
          10, Leuven BE-3000, Belgium
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RESULT 71
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DEFINITION      Human echovirus 6 isolate BE00-50 5' UTR, partial sequence.
ACCESSION      AF521463
VERSION      AF521463.1 GI:31790805
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM      Human echovirus 6
                Viruses; ssRNA positive-strand viruses, no DNA stage;
                Picornaviridae; Enterovirus.
REFERENCE
AUTHORS      Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
                Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
                an outbreak of aseptic meningitis in Belgium during the summer of
                2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
AUTHORS      Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
                Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
                Virology, Department of Microbiology and Immunology, Rega Institute
                for Medical Research, University of Leuven, Minderbroedersstraat
                10, Leuven BE-3000, Belgium
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DEFINITION      Human echovirus 13 isolate BE00-51 5' UTR, partial sequence.
ACCESSION      AF521464
VERSION      AF521464.1 GI:31790806
KEYWORDS
SOURCE      Human echovirus 13
ORGANISM      Human echovirus 13
                Viruses; ssRNA positive-strand viruses, no DNA stage;
                Picornaviridae; Enterovirus.
REFERENCE
AUTHORS      Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
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Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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RESULT 73
AF521465 LOCUS      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION      Human echovirus 6 isolate BE00-52 5' UTR, partial sequence.
ACCESSION      AF521465
VERSION      AF521465.1 GI:31790807
KEYWORDS
SOURCE      Human echovirus 6
ORGANISM      Human echovirus 6
                Viruses; ssRNA positive-strand viruses, no DNA stage;
                Picornaviridae; Enterovirus.
REFERENCE
AUTHORS      Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
                Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
                an outbreak of aseptic meningitis in Belgium during the summer of
                2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
AUTHORS      Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
                Lindberg,M.A. and Van Ranst,M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
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Db 14 CCCCTGAATCGGCTAATC 32

RESULT 74
AF521466 LOCUS      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION      Human echovirus 13 isolate BE00-53 5' UTR, partial sequence.
ACCESSION      AF521466
VERSION      AF521466.1 GI:31790808
KEYWORDS
SOURCE      Human echovirus 13
ORGANISM      Human echovirus 13
                Viruses; ssRNA positive-strand viruses, no DNA stage;
                Picornaviridae; Enterovirus.
REFERENCE
AUTHORS      Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
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Best Local Similarity 100.0%; Pred. No. 9.5; Mismatches 0; Indels 0; Gaps 0;  
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Db 14 CCCCTGAATGCGCTAATC 32  
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RESULT 74  
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DEFINITION AF521467  
ACCESSION AF521467.1 GI:31790809  
VERSION AF521467.1  
KEYWORDS Human coxsackievirus B5  
SOURCE Human coxsackievirus B5  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL PUBLISHED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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RESULT 75  
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ACCESSION AF521469.1 GI:31790811  
VERSION AF521469.1  
KEYWORDS Human echovirus 6  
SOURCE Human echovirus 6  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006  
2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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Db 14 CCCCTGAATGCGCTAATC 32  
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RESULT 76  
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VERSION AF521471.1  
KEYWORDS Human coxsackievirus B5  
SOURCE Human coxsackievirus B5  
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL PUBLISHED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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JOURNAL	Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
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LOCUS	AF521475 185 bp RNA linear VRL 17-JUN-2003
DEFINITION	Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
ACCESSION	AF521475
VERSION	AF521475.1 GI:31790817
KEYWORDS	Human echovirus 30
SOURCE	Human echovirus 30
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Ranst,M.
TITLE	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL	J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED	12767006
REFERENCE	2 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K., Lindberg,M.A. and Van Ranst,M.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
FEATURES	Location/Qualifiers source 1..185 /organism="Human coxsackievirus B5" /viralon /mol_type="genomic RNA" /isolate="BE00-29" /isolation_source="patient 29 - zipcode Belgium 9041" /db_xref="taxon:12074" <1..>185
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LOCUS	AF521474 185 bp RNA linear VRL 17-JUN-2003
DEFINITION	Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
ACCESSION	AF521474
VERSION	AF521474.1 GI:31790816
KEYWORDS	Human coxsackievirus 30
SOURCE	Human echovirus 30
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Ranst,M.
TITLE	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL	J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED	12767006
REFERENCE	2 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K., Lindberg,M.A. and Van Ranst,M.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
FEATURES	Location/Qualifiers source 1..185 /organism="Human coxsackievirus B5" /viralon /mol_type="genomic RNA" /isolate="BE00-29" /isolation_source="patient 29 - zipcode Belgium 9041" /db_xref="taxon:12074" <1..>185
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LOCUS	AF521473 185 bp RNA linear VRL 17-JUN-2003
DEFINITION	Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
ACCESSION	AF521473
VERSION	AF521473.1 GI:31790815
KEYWORDS	Human coxsackievirus B5
SOURCE	Human coxsackievirus B5
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Ranst,M.
TITLE	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL	J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED	12767006
REFERENCE	2 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K., Lindberg,M.A. and Van Ranst,M.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
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DEFINITION	Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
ACCESSION	AF521476
VERSION	AF521476.1 GI:31790816
KEYWORDS	Human coxsackievirus 30
SOURCE	Human coxsackievirus 30
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	1 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K., Lindberg,A.M. and Van Ranst,M.
TITLE	Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000
JOURNAL	J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED	12767006
REFERENCE	2 (bases 1 to 185)
AUTHORS	Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K., Lindberg,M.A. and Van Ranst,M.
TITLE	Direct Submission
JOURNAL	Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroederstraat 10, Leuven BE-3000, Belgium
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RESULT 80	AF521476 Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
LOCUS	AF521476 185 bp RNA linear VRL 17-JUN-2003
DEFINITION	Human coxsackievirus B5 isolate BE00-29 5' UTR, partial sequence.
ACCESSION	AF521476
VERSION	AF521476.1 GI:31790816
KEYWORDS	Human coxsackievirus 30
SOURCE	Human coxsackievirus 30
ORGANISM	Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
REFERENCE	

LOCUS AF521476 185 bp RNA linear VRL 17-JUN-2003  
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ACCESSION AF521476  
VERSION AF521476.1 GI:31790818  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
VIRUSES; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
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KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
VIRUSES; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
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DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.  
ACCESSION AF521478  
VERSION AF521478.1 GI:31790820  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
VIRUSES; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
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DEFINITION Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.  
ACCESSION AF521480  
VERSION AF521480.1 GI:31790822  
KEYWORDS

LOCUS AF521476 185 bp RNA linear VRL 17-JUN-2003  
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VIRUSES; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
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ORGANISM Human echovirus 30  
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Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
KEYWORDS Location/Qualifiers  
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VERSION AF521478.1 GI:31790820  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
VIRUSES; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium  
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DEFINITION Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.  
ACCESSION AF521480  
VERSION AF521480.1 GI:31790822  
KEYWORDS

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SOURCE      Human coxsackievirus B5
ORGANISM    Human coxsackievirus B5
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AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
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REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
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ACCESSION  AF521481
VERSION     AF521481.1 GI:31790823
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REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
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TITLE      Molecular typing and epidemiology of enteroviruses identified from
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JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
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TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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TITLE      Molecular typing and epidemiology of enteroviruses identified from
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JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
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REFERENCE   2 (bases 1 to 185)
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TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
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REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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VERSION     AF521483.1 GI:31790825
KEYWORDS
SOURCE     Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
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REFERENCE   1 (bases 1 to 185)

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AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
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JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
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REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
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for Medical Research, University of Leuven, Minderbroedersstraat  
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DEFINITION AF521484  
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AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
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JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
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AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
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SOURCE Human echovirus 30  
ORGANISM  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
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JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
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AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
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JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
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Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
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J. Med. Virol. 70 (3), 420-429 (2003)  
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 Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
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 SOURCE Human echovirus 13  
 ORGANISM Human echovirus 13  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
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 Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 Direct Submission  
 Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
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 VERSION AF521488.1 GI:31790830  
 KEYWORDS  
 SOURCE Human echovirus 16  
 ORGANISM Human echovirus 16  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.  
 1 (bases 1 to 185)  
 Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000  
 J. Med. Virol. 70 (3), 420-429 (2003)  
 12767006  
 2 (bases 1 to 185)  
 Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 Direct Submission  
 Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
 Virology, Department of Microbiology and Immunology, Rega Institute  
 for Medical Research, University of Leuven, Minderbroedersstraat  
 10, Leuven BE-3000, Belgium  
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 ACCESSION AF521490  
 VERSION AF521490.1 GI:31790832  
 KEYWORDS  
 SOURCE Human echovirus 6  
 ORGANISM Human echovirus 6  
 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.  
 1 (bases 1 to 185)  
 Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.  
 Molecular typing and epidemiology of enteroviruses identified from  
 an outbreak of aseptic meningitis in Belgium during the summer of  
 2000  
 J. Med. Virol. 70 (3), 420-429 (2003)  
 12767006  
 2 (bases 1 to 185)  
 Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
 Lindberg, M.A. and Van Ranst, M.

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TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
           Virology, Department of Microbiology and Immunology, Rega Institute
           for Medical Research, University of Leuven, Minderbroedersstraat
           10, Leuven BE-3000, Belgium
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Db 14 CCCCTGAATGCGGCTAATC 32

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DEFINITION
ACCESSION  AF521492
VERSION    AF521492.1 GI:31790834
KEYWORDS
SOURCE    Human echovirus 30
ORGANISM  Human echovirus 30
           Viruses; ssRNA positive-strand viruses, no DNA stage;
           Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
           Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
           an outbreak of aseptic meningitis in Belgium during the summer of
           2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
           Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
           Virology, Department of Microbiology and Immunology, Rega Institute
           for Medical Research, University of Leuven, Minderbroedersstraat
           10, Leuven BE-3000, Belgium
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ORGANISM  Human coxsackievirus B5
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AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
           Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
           an outbreak of aseptic meningitis in Belgium during the summer of
           2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
           Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
           Virology, Department of Microbiology and Immunology, Rega Institute
           for Medical Research, University of Leuven, Minderbroedersstraat
           10, Leuven BE-3000, Belgium
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ORGANISM  Human coxsackievirus B5
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AUTHORS    Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
           Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
           an outbreak of aseptic meningitis in Belgium during the summer of
           2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
           Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
           Virology, Department of Microbiology and Immunology, Rega Institute
           for Medical Research, University of Leuven, Minderbroedersstraat
           10, Leuven BE-3000, Belgium

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VERSION AF521498.1 GI:31790840
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SOURCE Human echovirus 6
ORGANISM Human echovirus 6
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

REFERENCE
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

FEATURES
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SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.

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REFERENCE
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium

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Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Gapop 10.0 , Gapext 1.0

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34	17	89.5	17	9	US-10-829-474-13	Sequence 13, Appl
35	17	89.5	24	8	US-10-938-005-2	Sequence 2, Appl
36	17	89.5	1216	7	US-10-767-701-7988	Sequence 7988, Ap
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38	16	84.2	16	9	US-10-829-474-12	Sequence 12, Appl
39	16	84.2	359	8	US-10-425-115-173355	Sequence 173355,
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92	14.8	77.9	2079	7	US-10-437-963-11634	Sequence 11634, A
93	14.8	77.9	2258	7	US-10-437-963-81682	Sequence 81682, A
94	14.8	77.9	2506	7	US-10-437-963-68811	Sequence 68811, A
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C 106	14.8	77.9	3501	7	US-10-437-963-25720	Sequence 25720, A	179	14.4	75.8	8397	7	US-10-282-122A-29380	Sequence 29380, A
C 107	14.8	77.9	3631	10	US-11-097-143-12547	Sequence 12547, A	180	14.4	75.8	8742	7	US-10-773-714-18	Sequence 18, Appl
C 108	14.8	77.9	3918	7	US-10-437-963-12519	Sequence 12519, A	181	14.4	75.8	49914	9	US-10-915-740A-19	Sequence 19, Appl
C 109	14.8	77.9	3964	7	US-10-437-963-14828	Sequence 14828, A	C 182	14.4	75.8	347814	7	US-10-322-696-76	Sequence 76, Appl
C 110	14.8	77.9	4086	8	US-10-793-639-478	Sequence 478, App	C 183	14.4	75.8	2242716	9	US-10-915-740A-1068	Sequence 1068, Ap
C 111	14.8	77.9	4089	7	US-10-437-963-23472	Sequence 23472, A	C 184	14.4	75.8	2256646	7	US-10-470-565-1	Sequence 1, Appl
C 112	14.8	77.9	4089	7	US-10-437-963-57049	Sequence 57049, A	185	14.2	74.7	25	9	US-10-956-157-251088	Sequence 251088, A
C 113	14.8	77.9	4365	7	US-10-437-963-81494	Sequence 81494, A	186	14.2	74.7	60	3	US-09-908-975-17345	Sequence 17345, A
C 114	14.8	77.9	4563	7	US-10-437-963-99438	Sequence 99438, A	C 187	14.2	74.7	201	8	US-10-719-993-26408	Sequence 26408, A
C 115	14.8	77.9	4605	7	US-10-437-963-87169	Sequence 87169, A	188	14.2	74.7	319	8	US-10-425-115-80672	Sequence 80672, A
C 116	14.8	77.9	4611	7	US-10-437-963-77761	Sequence 77761, A	C 189	14.2	74.7	335	7	US-10-424-599-25498	Sequence 25498, A
C 117	14.8	77.9	4802	7	US-10-437-963-54022	Sequence 54022, A	C 190	14.2	74.7	387	7	US-10-021-323-4630	Sequence 4630, Ap
C 118	14.8	77.9	4803	7	US-10-437-963-6155	Sequence 6155, Ap	C 191	14.2	74.7	451	4	US-09-925-065A-84313	Sequence 84313, A
C 119	14.8	77.9	4949	7	US-10-437-963-23468	Sequence 23468, A	C 192	14.2	74.7	457	7	US-10-424-599-54682	Sequence 54682, A
C 120	14.8	77.9	5007	7	US-10-437-963-23478	Sequence 23478, A	193	14.2	74.7	468	3	US-09-918-995-16031	Sequence 16031, A
C 121	14.8	77.9	5043	7	US-10-437-963-14832	Sequence 14832, A	194	14.2	74.7	487	9	US-10-779-543-19189	Sequence 19189, A
C 122	14.8	77.9	5091	7	US-10-437-963-14813	Sequence 14813, A	C 195	14.2	74.7	512	4	US-10-779-543-20843	Sequence 20843, A
C 123	14.8	77.9	5164	7	US-10-437-963-14824	Sequence 14824, A	C 196	14.2	74.7	514	4	US-09-925-065A-740536	Sequence 740536, A
C 124	14.8	77.9	5173	7	US-10-437-963-52988	Sequence 52988, A	C 197	14.2	74.7	514	5	US-10-027-632-141008	Sequence 141008, A
C 125	14.8	77.9	5257	7	US-10-437-963-53931	Sequence 53931, A	C 198	14.2	74.7	514	6	US-10-027-632-141008	Sequence 141008, A
C 126	14.8	77.9	5469	7	US-10-437-963-23465	Sequence 23465, A	C 199	14.2	74.7	524	7	US-10-021-323-12567	Sequence 12567, A
C 127	14.8	77.9	5802	7	US-10-437-963-23467	Sequence 23467, A	C 200	14.2	74.7	530	7	US-10-021-323-16847	Sequence 16847, A
C 128	14.8	77.9	6032	7	US-10-437-963-5378	Sequence 5378, Ap	201	14.2	74.7	534	4	US-09-925-065A-84290	Sequence 84290, A
C 129	14.8	77.9	6154	7	US-10-437-963-53951	Sequence 53951, A	202	14.2	74.7	535	4	US-09-925-065A-380735	Sequence 380735, A
C 130	14.8	77.9	6357	10	US-11-097-143-15112	Sequence 15112, A	C 203	14.2	74.7	535	4	US-09-925-065A-605576	Sequence 605576, A
C 131	14.8	77.9	6468	7	US-10-437-963-43858	Sequence 43858, A	C 204	14.2	74.7	543	4	US-09-925-065A-153402	Sequence 153402, A
C 132	14.8	77.9	6929	7	US-10-437-963-90023	Sequence 90023, A	205	14.2	74.7	548	4	US-09-925-065A-430404	Sequence 430404, A
C 133	14.8	77.9	6953	7	US-10-437-963-43833	Sequence 43833, A	C 206	14.2	74.7	548	4	US-09-925-065A-430405	Sequence 430405, A
C 134	14.8	77.9	7605	7	US-10-437-963-9963	Sequence 9963, Ap	C 207	14.2	74.7	577	4	US-09-925-065A-442742	Sequence 442742, A
C 135	14.8	77.9	7708	7	US-10-437-963-53032	Sequence 53032, A	C 208	14.2	74.7	583	3	US-09-764-877-2972	Sequence 2972, Ap
C 136	14.8	77.9	8279	7	US-10-437-963-14820	Sequence 14820, A	C 209	14.2	74.7	583	6	US-10-242-515-2972	Sequence 2972, Ap
C 137	14.8	77.9	9057	5	US-10-114-170-194	Sequence 170194, A	C 210	14.2	74.7	586	7	US-10-021-323-16484	Sequence 16484, A
C 138	14.8	77.9	9807	7	US-10-437-963-48751	Sequence 48751, A	C 211	14.2	74.7	587	4	US-09-925-065A-740537	Sequence 740537, A
C 139	14.8	77.9	9972	6	US-10-085-959-167	Sequence 167, App	C 212	14.2	74.7	592	4	US-09-925-065A-123839	Sequence 123839, A
C 140	14.8	77.9	9974	6	US-10-238-075-379	Sequence 379, App	C 213	14.2	74.7	592	7	US-10-437-963-54393	Sequence 54393, A
C 141	14.8	77.9	10549	7	US-10-437-963-89620	Sequence 89620, A	C 214	14.2	74.7	597	7	US-10-021-323-5517	Sequence 5517, Ap
C 142	14.8	77.9	11647	7	US-10-437-963-53268	Sequence 53268, A	C 215	14.2	74.7	608	8	US-10-653-047-1622	Sequence 361613, A
C 143	14.8	77.9	16929	7	US-10-437-963-43835	Sequence 43835, A	C 216	14.2	74.7	609	4	US-09-925-065A-361614	Sequence 361614, A
C 144	14.8	77.9	25235	6	US-10-164-230-2	Sequence 2, Appl	C 217	14.2	74.7	609	4	US-09-925-065A-361614	Sequence 361614, A
C 145	14.8	77.9	37672	6	US-10-004-113-49	Sequence 49, Appl	C 218	14.2	74.7	618	7	US-10-663-561-17	Sequence 17, Appl
C 146	14.8	77.9	55050	7	US-10-467-752-4	Sequence 4, Appl	C 219	14.2	74.7	628	7	US-10-424-599-14673	Sequence 14673, A
C 147	14.8	77.9	93483	6	US-10-034-650-49	Sequence 49, Appl	C 220	14.2	74.7	648	4	US-09-925-065A-390368	Sequence 390368, A
C 148	14.8	77.9	114280	8	US-10-719-993-6808	Sequence 6808, Ap	C 221	14.2	74.7	649	4	US-09-925-065A-530535	Sequence 530535, A
C 149	14.8	77.9	137935	8	US-10-741-600-17667	Sequence 17667, A	C 222	14.2	74.7	665	4	US-09-925-065A-93414	Sequence 93414, A
C 150	14.8	77.9	160921	5	US-10-087-192-1672	Sequence 1672, Ap	C 223	14.2	74.7	669	4	US-09-925-065A-778189	Sequence 778189, A
C 151	14.8	77.9	161334	5	US-10-087-192-730	Sequence 730, App	C 224	14.2	74.7	683	5	US-10-027-632-141009	Sequence 141009, A
C 152	14.8	77.9	263852	8	US-10-812-232-6	Sequence 6, Appl	C 225	14.2	74.7	683	6	US-10-027-632-141009	Sequence 141009, A
C 153	14.8	77.9	713059	5	US-10-027-632-174581	Sequence 174581, A	C 226	14.2	74.7	721	8	US-10-425-115-126748	Sequence 126748, A
C 154	14.8	77.9	713059	6	US-10-027-632-174581	Sequence 174581, A	C 227	14.2	74.7	771	4	US-09-925-065A-68422	Sequence 68422, A
C 155	14.4	75.8	145	3	US-09-736-457-1724	Sequence 1724, Ap	C 228	14.2	74.7	771	4	US-09-925-065A-68423	Sequence 68423, A
C 156	14.4	75.8	145	3	US-09-902-941-1724	Sequence 1724, Ap	C 229	14.2	74.7	796	5	US-10-027-632-1515	Sequence 1515, Ap
C 157	14.4	75.8	145	3	US-09-849-626-1724	Sequence 1724, Ap	C 230	14.2	74.7	796	5	US-10-027-632-1515	Sequence 1515, Ap
C 158	14.4	75.8	145	5	US-10-017-754-1724	Sequence 1724, Ap	C 231	14.2	74.7	796	6	US-10-027-632-1515	Sequence 1515, Ap
C 159	14.4	75.8	145	6	US-10-113-872-1724	Sequence 1724, Ap	C 232	14.2	74.7	796	6	US-10-027-632-1515	Sequence 1515, Ap
C 160	14.4	75.8	145	6	US-10-283-017-1724	Sequence 1724, Ap	C 233	14.2	74.7	817	5	US-10-066-543-88	Sequence 88, Appl
C 161	14.4	75.8	243	8	US-10-425-115-126798	Sequence 126798, A	C 234	14.2	74.7	864	8	US-10-425-115-165688	Sequence 165688, A
C 162	14.4	75.8	265	7	US-10-437-963-65910	Sequence 65910, A	C 235	14.2	74.7	866	10	US-11-097-143-15347	Sequence 15347, A
C 163	14.4	75.8	360	8	US-10-425-115-114899	Sequence 114899, A	C 236	14.2	74.7	875	7	US-10-424-599-111894	Sequence 111894, A
C 164	14.4	75.8	364	7	US-10-424-599-84676	Sequence 84676, A	C 237	14.2	74.7	926	9	US-10-450-763-29760	Sequence 29760, A
C 165	14.4	75.8	459	4	US-09-925-065A-259192	Sequence 259192, A	C 238	14.2	74.7	939	7	US-10-282-122A-22841	Sequence 22841, A
C 166	14.4	75.8	485	4	US-10-388-934-541	Sequence 541, App	C 239	14.2	74.7	1095	3	US-09-738-626-1791	Sequence 1791, Ap
C 167	14.4	75.8	585	4	US-09-925-065A-692313	Sequence 692313, A	C 240	14.2	74.7	1095	5	US-10-029-180-61	Sequence 61, Appl
C 168	14.4	75.8	715	8	US-10-425-115-178047	Sequence 178047, A	C 241	14.2	74.7	1095	9	US-10-952-045-61	Sequence 61, Appl
C 169	14.4	75.8	810	7	US-10-282-122A-12875	Sequence 12875, A	C 242	14.2	74.7	1099	7	US-10-282-122A-10642	Sequence 10642, A

243	14.2	74.7	1104	5	US-10-011-445-38	Sequence 38, Appl	316	14.2	74.7	12908	6	US-10-270-846-1	Sequence 1, Appl
244	14.2	74.7	1135	5	US-10-282-122A-10392	Sequence 1092, A	317	14.2	74.7	16181	8	US-10-723-860-1452	Sequence 1452, Ap
245	14.2	74.7	1221	6	US-10-156-761-6592	Sequence 6592, Ap	318	14.2	74.7	166181	8	US-10-723-860-3281	Sequence 3281, Ap
246	14.2	74.7	1232	7	US-10-424-598-124847	Sequence 124847, A	319	14.2	74.7	203132	7	US-10-322-281-459	Sequence 459, App
247	14.2	74.7	1297	4	US-09-925-065A-31739	Sequence 31739, A	c 320	14.2	74.7	519599	9	US-10-737-082-73	Sequence 73, Appl
248	14.2	74.7	1297	4	US-09-925-065A-31740	Sequence 31740, A	c 321	14.2	74.7	519599	9	US-10-737-082-73	Sequence 73, Appl
249	14.2	74.7	1297	5	US-10-027-633-254358	Sequence 254358, A	c 322	14.2	74.7	78452	8	US-10-719-933-6822	Sequence 6822, Ap
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251	14.2	74.7	1346	4	US-09-925-065A-86422	Sequence 86422, A	324	14.2	74.7	1601042	6	US-10-027-632-59064	Sequence 59064, A
252	14.2	74.7	1346	4	US-09-925-065A-86422	Sequence 86422, A	325	14.2	74.7	2731748	7	US-10-297-465A-1	Sequence 1, Appl
253	14.2	74.7	1400	9	US-10-956-157-5885	Sequence 5885, Ap	326	14.2	74.7	3309400	3	US-09-738-626-1	Sequence 1, Appl
254	14.2	74.7	1477	7	US-10-767-701-13331	Sequence 13331, A	c 327	14.2	74.7	9025608	6	US-10-156-761-1	Sequence 3, Appl
255	14.2	74.7	1503	3	US-09-974-300-1681	Sequence 1681, Ap	328	14	73.7	14	9	US-10-760-048-3	Sequence 3, Appl
256	14.2	74.7	1612	10	US-11-097-143-3351	Sequence 3351, Ap	c 329	14	73.7	25	7	US-10-719-956-300284	Sequence 300284, A
257	14.2	74.7	1665	8	US-10-780-002-44	Sequence 44, Appl	c 330	14	73.7	430	7	US-10-424-599-56607	Sequence 56607, A
258	14.2	74.7	1755	10	US-11-097-143-28781	Sequence 28781, A	c 331	14	73.7	440	7	US-10-424-599-15745	Sequence 15745, A
259	14.2	74.7	1985	6	US-10-341-961A-241	Sequence 241, App	332	14	73.7	502	7	US-10-424-599-140730	Sequence 140730, A
260	14.2	74.7	2063	5	US-10-011-445-39	Sequence 39, Appl	333	14	73.7	591	3	US-09-917-800A-117	Sequence 117, App
261	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	c 334	14	73.7	966	7	US-10-282-122A-41793	Sequence 41793, A
262	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	c 335	14	73.7	1356	7	US-10-282-122A-41793	Sequence 41793, A
263	14.2	74.7	2136	3	US-09-938-842A-803	Sequence 803, App	c 336	14	73.7	1473	3	US-09-815-242-4616	Sequence 4616, Ap
264	14.2	74.7	2217	10	US-11-069-633-13	Sequence 13, Appl	337	14	73.7	1515	3	US-09-815-242-4616	Sequence 4616, Ap
265	14.2	74.7	2255	8	US-09-925-065A-699467	Sequence 699467, A	c 338	14	73.7	1536	7	US-10-282-122A-8244	Sequence 8244, Ap
266	14.2	74.7	2445	7	US-10-425-115-37954	Sequence 37954, A	c 339	14	73.7	1660	9	US-10-764-420-539	Sequence 539, App
267	14.2	74.7	2445	7	US-10-425-115-37954	Sequence 37954, A	c 340	14	73.7	1660	9	US-10-764-420-539	Sequence 539, App
268	14.2	74.7	2535	7	US-10-424-598-42490	Sequence 42490, A	c 341	14	73.7	2465	10	US-11-097-143-24463	Sequence 24463, A
269	14.2	74.7	2592	3	US-09-828-846-444	Sequence 444, App	c 342	14	73.7	2465	10	US-11-097-143-24463	Sequence 24463, A
270	14.2	74.7	2688	10	US-11-097-143-34972	Sequence 34972, A	c 343	14	73.7	2465	10	US-11-097-143-24463	Sequence 24463, A
271	14.2	74.7	2910	6	US-10-745-237-317	Sequence 317, App	c 344	13.8	72.6	25	7	US-10-719-956-360997	Sequence 360997, A
272	14.2	74.7	2944	10	US-10-094-749-539	Sequence 539, App	c 345	13.8	72.6	25	7	US-10-719-956-360997	Sequence 360997, A
273	14.2	74.7	3036	7	US-10-425-114-33141	Sequence 33141, A	c 346	13.8	72.6	25	7	US-10-719-956-360997	Sequence 360997, A
274	14.2	74.7	3080	10	US-11-097-143-4339	Sequence 4339, Ap	c 347	13.8	72.6	25	8	US-10-719-900-11080	Sequence 11080, A
275	14.2	74.7	3080	10	US-11-097-143-4339	Sequence 4339, Ap	c 348	13.8	72.6	25	8	US-10-719-900-11080	Sequence 11080, A
276	14.2	74.7	3094	10	US-11-097-143-5329	Sequence 5329, Ap	c 349	13.8	72.6	25	8	US-10-719-900-11080	Sequence 11080, A
277	14.2	74.7	3111	8	US-10-437-963-47196	Sequence 47196, A	c 350	13.8	72.6	25	9	US-10-956-157-289056	Sequence 289056, A
278	14.2	74.7	3140	8	US-10-425-115-22365	Sequence 22365, A	c 351	13.8	72.6	129	6	US-10-392-808-19	Sequence 19, Appl
279	14.2	74.7	3165	6	US-10-108-260A-1501	Sequence 1501, Ap	c 352	13.8	72.6	142	8	US-10-425-115-56593	Sequence 56593, A
280	14.2	74.7	3344	6	US-10-172-118-636	Sequence 636, App	c 353	13.8	72.6	201	8	US-10-425-115-56593	Sequence 56593, A
281	14.2	74.7	3344	6	US-10-342-887-636	Sequence 636, App	c 354	13.8	72.6	201	8	US-10-425-115-56593	Sequence 56593, A
282	14.2	74.7	3344	9	US-10-831-704-73	Sequence 73, Appl	c 355	13.8	72.6	254	3	US-09-923-876-225	Sequence 225, App
283	14.2	74.7	3344	9	US-10-831-704-73	Sequence 73, Appl	c 356	13.8	72.6	254	3	US-09-923-876-225	Sequence 225, App
284	14.2	74.7	3505	9	US-10-956-157-650	Sequence 650, App	c 357	13.8	72.6	270	7	US-10-437-963-43091	Sequence 43091, A
285	14.2	74.7	3810	10	US-10-765-700-63	Sequence 63, Appl	c 358	13.8	72.6	296	9	US-10-779-543-921	Sequence 921, App
286	14.2	74.7	3810	10	US-11-097-143-3350	Sequence 3350, Ap	c 359	13.8	72.6	298	3	US-09-294-093B-4990	Sequence 4990, Ap
287	14.2	74.7	4281	10	US-11-097-143-3350	Sequence 3350, Ap	c 360	13.8	72.6	298	3	US-09-294-093B-4990	Sequence 4990, Ap
288	14.2	74.7	4519	7	US-10-467-685-33	Sequence 33, Appl	c 361	13.8	72.6	303	7	US-10-242-535A-20448	Sequence 20448, A
289	14.2	74.7	4557	7	US-10-467-685-33	Sequence 33, Appl	c 362	13.8	72.6	303	7	US-10-242-535A-20448	Sequence 20448, A
290	14.2	74.7	4667	8	US-10-618-941-52	Sequence 10388, A	c 363	13.8	72.6	329	8	US-10-085-783A-20448	Sequence 20448, A
291	14.2	74.7	4771	10	US-11-097-143-8512	Sequence 8512, Ap	c 364	13.8	72.6	430	3	US-09-764-891-6469	Sequence 6469, Ap
292	14.2	74.7	5165	8	US-10-425-115-108158	Sequence 108158, A	c 365	13.8	72.6	432	3	US-10-783-590-2730	Sequence 2730, Ap
293	14.2	74.7	5549	6	US-10-354-358-23	Sequence 23, Appl	c 366	13.8	72.6	442	8	US-10-674-124A-10837	Sequence 10837, A
294	14.2	74.7	5549	9	US-10-490-592-1	Sequence 1, Appl	c 367	13.8	72.6	462	3	US-09-918-995-831	Sequence 831, App
295	14.2	74.7	5549	9	US-10-490-592-1	Sequence 1, Appl	c 368	13.8	72.6	462	3	US-09-918-995-831	Sequence 831, App
296	14.2	74.7	5577	9	US-10-499-065A-384	Sequence 384, App	c 369	13.8	72.6	463	3	US-09-796-692-2606	Sequence 2606, Ap
297	14.2	74.7	6587	10	US-11-097-143-1099	Sequence 1099, Ap	c 370	13.8	72.6	463	5	US-10-040-862-2606	Sequence 2606, Ap
298	14.2	74.7	7005	10	US-11-097-143-20273	Sequence 85, Appl	c 371	13.8	72.6	463	6	US-10-057-475B-2606	Sequence 2606, Ap
299	14.2	74.7	8201	6	US-10-240-485-63	Sequence 63, Appl	c 372	13.8	72.6	463	6	US-10-154-884B-2606	Sequence 2606, Ap
300	14.2	74.7	13075	10	US-11-097-143-20272	Sequence 20272, A	c 373	13.8	72.6	463	8	US-10-764-324-2606	Sequence 2606, Ap
301	14.2	74.7	16929	3	US-09-984-429-725	Sequence 725, App	c 374	13.8	72.6	467	8	US-10-674-124A-6772	Sequence 6772, Ap
302	14.2	74.7	19802	10	US-11-097-143-16666	Sequence 16666, A	c 375	13.8	72.6	469	3	US-09-918-995-7115	Sequence 7115, Ap
303	14.2	74.7	22111	7	US-10-212-993-11	Sequence 11, Appl	c 376	13.8	72.6	471	7	US-10-242-535A-43397	Sequence 43397, A
304	14.2	74.7	26933	7	US-10-322-281-541	Sequence 541, App	c 377	13.8	72.6	471	7	US-10-085-783A-43397	Sequence 43397, A
305	14.2	74.7	33393	7	US-10-322-281-238	Sequence 238, App	c 378	13.8	72.6	493	7	US-10-424-599-113911	Sequence 113911, A
306	14.2	74.7	44413	8	US-10-741-600-17915	Sequence 17915, A	c 379	13.8	72.6	500	4	US-09-925-065A-487214	Sequence 487214, A
307	14.2	74.7	54334	8	US-10-719-993-6790	Sequence 6790, Ap	c 380	13.8	72.6	508	4	US-09-925-065A-213946	Sequence 213946, A
308	14.2	74.7	69770	6	US-10-292-798-1323	Sequence 1323, Ap	c 381	13.8	72.6	519	3	US-09-974-300-1460	Sequence 1460, Ap
309	14.2	74.7	96598	3	US-09-997-722-137	Sequence 127, App	c 382	13.8	72.6	535	7	US-10-437-963-2381	Sequence 2381, Ap
310	14.2	74.7	119057	5	US-10-270-875-1	Sequence 1, Appl	c 383	13.8	72.6	542	8	US-09-925-065A-494214	Sequence 494214, A
311	14.2	74.7	129908	5	US-10-270-875-1	Sequence 1, Appl	c 384	13.8	72.6	545	8	US-10-425-115-121776	Sequence 121776, A
312	14.2	74.7	129908	5	US-10-270-875-1	Sequence 1, Appl	c 385	13.8	72.6	547	4	US-09-925-065A-251345	Sequence 251345, A
313	14.2	74.7	129908	5	US-10-270-786-1	Sequence 1, Appl	c 386	13.8	72.6	548	4	US-09-925-065A-19336	Sequence 19336, A
314	14.2	74.7	129908	5	US-10-270-786-1	Sequence 1, Appl	c 387	13.8	72.6	548	4	US-09-925-065A-19337	Sequence 19337, A
315	14.2	74.7	129908	5	US-10-270-859-1	Sequence 1, Appl	c 388	13.8	72.6	548	4	US-09-925-065A-19938	Sequence 19938, A

C 389	13.8	72.6	550	4	US-09-925-065A-374022	Sequence 374022,	462	13.8	72.6	1034	9	US-10-450-763-6388	Sequence 6388, Ap
C 390	13.8	72.6	558	5	US-10-106-698-1875	Sequence 1875, Ap	C 463	13.8	72.6	1053	9	US-10-450-763-28412	Sequence 28412, A
C 391	13.8	72.6	558	5	US-10-487-901-166	Sequence 166, App	C 464	13.8	72.6	1099	7	US-10-282-122A-40036	Sequence 40036, A
C 392	13.8	72.6	560	5	US-10-027-632-142053	Sequence 142053,	C 465	13.8	72.6	1102	3	US-09-974-300-2671	Sequence 2671, Ap
C 393	13.8	72.6	560	6	US-10-027-632-142053	Sequence 142053,	C 466	13.8	72.6	1103	7	US-10-282-122A-37102	Sequence 37102, A
C 394	13.8	72.6	564	4	US-09-925-065A-157232	Sequence 157232,	C 467	13.8	72.6	1155	7	US-10-425-114-14768	Sequence 14768, A
C 395	13.8	72.6	569	4	US-09-925-065A-434002	Sequence 434002,	C 468	13.8	72.6	1218	7	US-10-282-122A-10923	Sequence 10923, A
C 396	13.8	72.6	573	4	US-09-925-065A-274574	Sequence 274574,	C 469	13.8	72.6	1218	7	US-10-282-122A-19434	Sequence 19434, A
C 397	13.8	72.6	576	4	US-09-925-065A-163903	Sequence 163903,	C 470	13.8	72.6	1218	7	US-10-424-599-49257	Sequence 49257, A
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C 399	13.8	72.6	581	4	US-09-925-065A-440004	Sequence 440004,	C 472	13.8	72.6	1302	2	US-08-945-038-5	Sequence 5, Appli
C 400	13.8	72.6	583	4	US-09-925-065A-440005	Sequence 440005,	C 473	13.8	72.6	1302	7	US-10-335-977-3738	Sequence 3738, Ap
C 401	13.8	72.6	583	7	US-10-430-201-303	Sequence 303, App	C 474	13.8	72.6	1314	7	US-10-335-977-3739	Sequence 3739, Ap
C 402	13.8	72.6	583	7	US-10-430-201-304	Sequence 304, App	C 475	13.8	72.6	1326	7	US-10-282-122A-23449	Sequence 23449, A
C 403	13.8	72.6	591	4	US-09-925-065A-530517	Sequence 530517,	C 476	13.8	72.6	1335	7	US-10-282-122A-42127	Sequence 42127, A
C 404	13.8	72.6	595	7	US-10-767-701-3936	Sequence 3936, Ap	C 477	13.8	72.6	1356	5	US-10-270-333-80	Sequence 80, Appl
C 405	13.8	72.6	599	9	US-10-972-079-34027	Sequence 34027, A	C 478	13.8	72.6	1356	9	US-10-745-237-187	Sequence 187, App
C 406	13.8	72.6	599	9	US-10-972-079-34028	Sequence 34028, A	C 479	13.8	72.6	1356	10	US-11-097-143-16259	Sequence 16259, A
C 407	13.8	72.6	599	9	US-10-972-079-34033	Sequence 34033, A	C 480	13.8	72.6	1395	6	US-10-369-493-43591	Sequence 43591, A
C 408	13.8	72.6	600	9	US-10-956-157-7272	Sequence 7272, Ap	C 481	13.8	72.6	1404	3	US-09-804-551B-9	Sequence 9, Appli
C 409	13.8	72.6	602	4	US-09-925-065A-296301	Sequence 296301,	C 482	13.8	72.6	1451	6	US-10-283-423-19	Sequence 19, Appl
C 410	13.8	72.6	606	4	US-09-925-065A-436624	Sequence 436624,	C 483	13.8	72.6	1451	6	US-10-213-821-19	Sequence 19, Appl
C 411	13.8	72.6	607	4	US-09-925-065A-817644	Sequence 817644,	C 484	13.8	72.6	1451	7	US-10-736-048-19	Sequence 19, Appl
C 412	13.8	72.6	620	4	US-09-925-065A-646609	Sequence 646609,	C 485	13.8	72.6	1452	8	US-10-489-425-59	Sequence 59, Appl
C 413	13.8	72.6	638	5	US-10-027-632-209545	Sequence 209545,	C 486	13.8	72.6	1554	7	US-10-425-114-1363	Sequence 1363, Ap
C 414	13.8	72.6	638	6	US-10-027-632-209545	Sequence 209545,	C 487	13.8	72.6	1575	9	US-10-450-763-7099	Sequence 7099, Ap
C 415	13.8	72.6	644	7	US-10-424-539-91398	Sequence 91398, A	C 488	13.8	72.6	1589	5	US-10-087-192-1751	Sequence 1751, Ap
C 416	13.8	72.6	645	9	US-10-487-901-826	Sequence 826, App	C 489	13.8	72.6	1627	8	US-10-425-115-66930	Sequence 66930, A
C 417	13.8	72.6	646	4	US-09-925-065A-60501	Sequence 60501, A	C 490	13.8	72.6	1630	7	US-10-403-571-89	Sequence 89, Appl
C 418	13.8	72.6	650	5	US-10-027-632-242742	Sequence 242742,	C 491	13.8	72.6	1665	9	US-10-450-763-28569	Sequence 28569, A
C 419	13.8	72.6	650	5	US-10-027-632-242743	Sequence 242743,	C 492	13.8	72.6	1690	8	US-10-425-115-19149	Sequence 19149, A
C 420	13.8	72.6	650	6	US-10-027-632-242742	Sequence 242742,	C 493	13.8	72.6	1755	6	US-10-369-493-24301	Sequence 24301, A
C 421	13.8	72.6	650	6	US-10-027-632-242743	Sequence 242743,	C 494	13.8	72.6	1956	3	US-09-854-761-13883	Sequence 13883, A
C 422	13.8	72.6	654	5	US-10-106-698-1453	Sequence 1453, Ap	C 495	13.8	72.6	2011	3	US-09-825-489-11	Sequence 11, Appl
C 423	13.8	72.6	655	5	US-10-027-632-257853	Sequence 257853,	C 496	13.8	72.6	2103	7	US-10-437-963-31475	Sequence 31475, A
C 424	13.8	72.6	663	5	US-10-027-632-257853	Sequence 257853,	C 497	13.8	72.6	2128	7	US-10-437-963-86520	Sequence 86520, A
C 425	13.8	72.6	663	5	US-10-027-632-230356	Sequence 230356,	C 498	13.8	72.6	2202	4	US-09-925-065A-725286	Sequence 725286,
C 426	13.8	72.6	663	6	US-10-027-632-230356	Sequence 230356,	C 499	13.8	72.6	2202	4	US-09-925-065A-725287	Sequence 725287,
C 427	13.8	72.6	668	4	US-09-925-065A-719915	Sequence 719915,	C 500	13.8	72.6	2210	5	US-10-027-632-263144	Sequence 263144,
C 428	13.8	72.6	668	4	US-09-925-065A-719916	Sequence 719916,							
C 429	13.8	72.6	672	4	US-09-925-065A-922842	Sequence 922842,							
C 430	13.8	72.6	672	4	US-09-925-065A-947181	Sequence 947181,							
C 431	13.8	72.6	672	8	US-10-653-047-6637	Sequence 6637, Ap							
C 432	13.8	72.6	673	3	US-09-764-891-1670	Sequence 1670, Ap							
C 433	13.8	72.6	673	5	US-10-205-428-146	Sequence 146, App							
C 434	13.8	72.6	693	7	US-10-335-977-3737	Sequence 3737, Ap							
C 435	13.8	72.6	704	6	US-10-369-493-37060	Sequence 37060, A							
C 436	13.8	72.6	705	9	US-10-487-901-2979	Sequence 2979, Ap							
C 437	13.8	72.6	719	7	US-10-398-221-1377	Sequence 1377, Ap							
C 438	13.8	72.6	726	5	US-10-027-632-123918	Sequence 123918,							
C 439	13.8	72.6	726	6	US-10-027-632-123918	Sequence 123918,							
C 440	13.8	72.6	735	9	US-10-487-901-6744	Sequence 6744, Ap							
C 441	13.8	72.6	756	8	US-10-425-115-19151	Sequence 19151, A							
C 442	13.8	72.6	756	4	US-09-925-065A-8622	Sequence 8622, Ap							
C 443	13.8	72.6	796	4	US-09-925-065A-8623	Sequence 8623, Ap							
C 444	13.8	72.6	796	4	US-09-925-065A-8624	Sequence 8624, Ap							
C 445	13.8	72.6	846	7	US-10-282-122A-31040	Sequence 31040, A							
C 446	13.8	72.6	872	7	US-10-425-114-14918	Sequence 14918, A							
C 447	13.8	72.6	889	3	US-09-764-891-8360	Sequence 8360, Ap							
C 448	13.8	72.6	889	3	US-09-764-891-8361	Sequence 8361, Ap							
C 449	13.8	72.6	889	5	US-10-205-428-785	Sequence 785, App							
C 450	13.8	72.6	889	5	US-10-205-428-786	Sequence 786, App							
C 451	13.8	72.6	903	5	US-10-027-632-121510	Sequence 121510,							
C 452	13.8	72.6	903	5	US-10-027-632-121511	Sequence 121511,							
C 453	13.8	72.6	903	6	US-10-027-632-121510	Sequence 121510,							
C 454	13.8	72.6	903	6	US-10-027-632-121511	Sequence 121511,							
C 455	13.8	72.6	929	7	US-10-424-599-63357	Sequence 63357, A							
C 456	13.8	72.6	957	5	US-10-027-632-121435	Sequence 121435,							
C 457	13.8	72.6	957	6	US-10-027-632-121435	Sequence 121435,							
C 458	13.8	72.6	969	6	US-10-369-493-24179	Sequence 24179, A							
C 459	13.8	72.6	993	6	US-10-188-359-86	Sequence 86, Appl							
C 460	13.8	72.6	993	9	US-10-956-157-2037	Sequence 2037, Ap							
C 461	13.8	72.6	1031	8	US-10-425-115-73200	Sequence 73200, A							

ALIGNMENTS

RESULT 1  
US-10-352-806A-2  
; Sequence 2, Application US/10352806A  
; Publication No. US20030170617A1  
; GENERAL INFORMATION:  
; APPLICANT: PASIOSKE, BRITAN L.  
; TITLE OF INVENTION: CRUDE BIOLOGICAL DERIVATIVES COMPETENT FOR NUCLEIC ACID  
; TITLE OF INVENTION: DETECTION  
; FILE REFERENCE: AMBI:0790US  
; CURRENT APPLICATION NUMBER: US/10352,806A  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2003-01-28  
; PRIOR FILING DATE: 2002-01-28  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Primer  
US-10-352-806A-2  
Query Match 100.0%; Score 19; DB 6; Length 19;  
Best Local Similarity 100.0%; Pred. NO. 2.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 CCCCGAATCGGCTAATC 19

Db 1 CCCCTGAATGCGGCTAATC 19  
|||||

## RESULT 2

US-10-829-474-1  
; Sequence 1, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-1

Query Match 100.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
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Db 1 CCCCTGAATGCGGCTAATC 19  
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## RESULT 3

US-10-829-474-14  
; Sequence 14, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 14  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-14

Query Match 100.0%; Score 19; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
|||||

Db 1 CCCCTGAATGCGGCTAATC 19  
|||||

## RESULT 4

US-10-829-474-15  
; Sequence 15, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.

; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 15  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-15

Query Match 100.0%; Score 19; DB 9; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
|||||

Db 2 CCCCTGAATGCGGCTAATC 20  
|||||

## RESULT 5

US-10-829-474-16  
; Sequence 16, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 16  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-16

Query Match 100.0%; Score 19; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 2.4;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
|||||

Db 7 CCCCTGAATGCGGCTAATC 25  
|||||

## RESULT 6

US-10-332-123-70  
; Sequence 70, Application US/10332123  
; Publication No. US20040072239A1  
; GENERAL INFORMATION:  
; APPLICANT: RENAUD, Patricia  
; APPLICANT: GUILLOT, Emmanuelle  
; APPLICANT: MABILAT, Claude  
; APPLICANT: VACHON, Carole  
; APPLICANT: LACROIX, Bruno  
; APPLICANT: VERNET, Guy  
; APPLICANT: ARMAND, Marie-Astrid  
; APPLICANT: LAFFAIRE, Philippe  
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
; FILE REFERENCE: 114502  
; CURRENT APPLICATION NUMBER: US/10/332,123  
; CURRENT FILING DATE: 2003-09-24

; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: FR00-08839  
 ; PRIOR FILING DATE: 2000-07-06  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 70  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Poliovirus type 2  
 US-10-332-123-70

Query Match 100.0%; Score 19; DB 7; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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 Db 7 CCCCTGAATGGGCTAATC 25

RESULT 7  
 US-10-332-123-72  
 ; Sequence 72, Application US/10332123  
 ; Publication No. US20040072239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RENAUD, Patricia  
 ; APPLICANT: GUILLLOT, Emmanuelle  
 ; APPLICANT: MABILAT, Claude  
 ; APPLICANT: VACHON, Carole  
 ; APPLICANT: LACROIX, Bruno  
 ; APPLICANT: VERNET, Guy  
 ; APPLICANT: ARMAND, Marie-Astrid  
 ; APPLICANT: LAFFAIRE, Philippe  
 ; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
 ; FILE REFERENCE: 114502  
 ; CURRENT APPLICATION NUMBER: US/10/332,123  
 ; PRIOR FILING DATE: 2003-09-24  
 ; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR FILING DATE: 2000-07-06  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 72  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Coxsackievirus A21  
 US-10-332-123-72

Query Match 100.0%; Score 19; DB 7; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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 Db 6 CCCCTGAATGGGCTAATC 24

RESULT 8  
 US-10-332-123-74  
 ; Sequence 74, Application US/10332123  
 ; Publication No. US20040072239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RENAUD, Patricia  
 ; APPLICANT: GUILLLOT, Emmanuelle  
 ; APPLICANT: MABILAT, Claude  
 ; APPLICANT: VACHON, Carole  
 ; APPLICANT: LACROIX, Bruno  
 ; APPLICANT: VERNET, Guy  
 ; APPLICANT: ARMAND, Marie-Astrid  
 ; APPLICANT: LAFFAIRE, Philippe

; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
 ; FILE REFERENCE: 114502  
 ; CURRENT APPLICATION NUMBER: US/10/332,123  
 ; CURRENT FILING DATE: 2003-09-24  
 ; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: FR00-08839  
 ; PRIOR FILING DATE: 2000-07-06  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: Patent in version 3.2  
 ; SEQ ID NO 74  
 ; LENGTH: 30  
 ; TYPE: DNA  
 ; ORGANISM: Echovirus 12  
 US-10-332-123-74

Query Match 100.0%; Score 19; DB 7; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 2.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
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 Db 11 CCCCTGAATGGGCTAATC 29

RESULT 9  
 US-10-408-519-1  
 ; Sequence 1, Application US/10408519  
 ; Publication No. US20030228683A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Kan-Hung  
 ; APPLICANT: Shih, Yu-Hau  
 ; APPLICANT: Tsai, Chuan-Mei  
 ; APPLICANT: Wang, Yih-Weng  
 ; APPLICANT: Hsiao, Hsiung  
 ; APPLICANT: Bair, Chi-Horng  
 ; APPLICANT: Wang, Shin-Hwan  
 ; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES  
 ; FILE REFERENCE: 12674-002002  
 ; CURRENT APPLICATION NUMBER: US/10/408,519  
 ; CURRENT FILING DATE: 2003-04-07  
 ; PRIOR APPLICATION NUMBER: US 09/522,417  
 ; PRIOR FILING DATE: 2000-03-09  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 1  
 ; LENGTH: 52  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Probe from 5' ends of enterovirus genes  
 US-10-408-519-1

Query Match 100.0%; Score 19; DB 6; Length 52;  
 Best Local Similarity 100.0%; Pred. No. 2.5;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19  
 |||||  
 Db 34 CCCCTGAATGGGCTAATC 52

RESULT 10  
 US-10-332-123-54  
 ; Sequence 54, Application US/10332123  
 ; Publication No. US20040072239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RENAUD, Patricia  
 ; APPLICANT: GUILLLOT, Emmanuelle  
 ; APPLICANT: MABILAT, Claude  
 ; APPLICANT: VACHON, Carole  
 ; APPLICANT: LACROIX, Bruno



```

; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; PRIOR FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; TYPE: DNA
; ORGANISM: Coxsackievirus (D00538)
US-10-332-123-54

Query Match      100.0%; Score 19; DB 7; Length 520;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 386 CCCCTGAATCGGCTAATC 404

RESULT 11
US-10-332-123-53
; Sequence 53, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 53
; LENGTH: 521
; TYPE: DNA
; ORGANISM: Poliovirus (X00595)
US-10-332-123-53

Query Match      100.0%; Score 19; DB 7; Length 521;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 387 CCCCTGAATCGGCTAATC 405

RESULT 12
US-10-332-123-55
; Sequence 55, Application US/10332123
; Publication No. US20040072239A1
; GENERAL INFORMATION:
; APPLICANT: RENAUD, Patricia
; APPLICANT: GUILLOT, Emmanuelle
; APPLICANT: MABILAT, Claude
; APPLICANT: VACHON, Carole
; APPLICANT: LACROIX, Bruno
; APPLICANT: VERNET, Guy
; APPLICANT: ARMAND, Marie-Astrid
; APPLICANT: LAFFAIRE, Philippe
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS
; FILE REFERENCE: 114502
; CURRENT APPLICATION NUMBER: US/10/332,123
; CURRENT FILING DATE: 2003-09-24
; PRIOR APPLICATION NUMBER: PCT/FR01/02191
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: FR00-08839
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 525
; TYPE: DNA
; ORGANISM: Echovirus (X77708)
US-10-332-123-55

Query Match      100.0%; Score 19; DB 7; Length 525;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 391 CCCCTGAATCGGCTAATC 409

RESULT 13
US-10-760-048-67
; Sequence 67, Application US/10760048
; Publication No. US20050159710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 67
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-760-048-67

Query Match      100.0%; Score 19; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 373 CCCCTGAATCGGCTAATC 391

RESULT 14
US-10-614-283-1
; Sequence 1, Application US/10614283
; Publication No. US20050112095A1
; GENERAL INFORMATION:
; APPLICANT: HSU, TSU-AN
; APPLICANT: WU, TZONG-YUAN
; APPLICANT: LEE, JIN-CHING
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
; GENERAL INFORMATION:

```

APPLICANT: RENAUD, Patricia  
APPLICANT: GUILLOT, Emmanuelle  
APPLICANT: MABILAT, Claude  
APPLICANT: VACHON, Carole  
APPLICANT: LACROIX, Bruno  
APPLICANT: VERNET, Guy  
APPLICANT: ARMAND, Marie-Astrid  
APPLICANT: LAFFAIRE, Philippe  
TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
FILE REFERENCE: 114502  
CURRENT APPLICATION NUMBER: US/10/332,123  
CURRENT FILING DATE: 2003-09-24  
PRIOR APPLICATION NUMBER: PCT/FR01/02191  
PRIOR FILING DATE: 2001-07-06  
PRIOR APPLICATION NUMBER: FR00-08839  
PRIOR FILING DATE: 2000-07-06  
NUMBER OF SEQ ID NOS: 108  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 55  
LENGTH: 525  
TYPE: DNA  
ORGANISM: Echovirus (X77708)  
US-10-332-123-55

Query Match 100.0%; Score 19; DB 7; Length 525;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
Db 391 CCCCTGAATCGGCTAATC 409

RESULT 13  
US-10-760-048-67  
; Sequence 67, Application US/10760048  
; Publication No. US20050159710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 67  
; LENGTH: 660  
; TYPE: DNA  
; ORGANISM: Coxsackievirus B3  
US-10-760-048-67

Query Match 100.0%; Score 19; DB 9; Length 660;  
Best Local Similarity 100.0%; Pred. No. 3;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
Db 373 CCCCTGAATCGGCTAATC 391

RESULT 14  
US-10-614-283-1  
; Sequence 1, Application US/10614283  
; Publication No. US20050112095A1  
; GENERAL INFORMATION:  
; APPLICANT: HSU, TSU-AN  
; APPLICANT: WU, TZONG-YUAN  
; APPLICANT: LEE, JIN-CHING  
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN  
; GENERAL INFORMATION:

```
; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614.283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 1
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-10-614-283-1

Query Match      100.0%; Score 19; DB 9; Length 709;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 420 CCCCTGAATCGGCTAATC 438

RESULT 15
US-10-839-729-21
; Sequence 21, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21

Query Match      100.0%; Score 19; DB 8; Length 743;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 448 CCCCTGAATCGGCTAATC 466

RESULT 16
US-10-489-136-10
; Sequence 10, Application US/10489136
; Publication No. US20050014150A1
; GENERAL INFORMATION:
; APPLICANT: Atabekov, Joseph
; APPLICANT: Dorokhov, Yuri
; APPLICANT: Skulachev, Maxim
; APPLICANT: Ivanov, Peter
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
; FILE REFERENCE: 9286.30
; CURRENT APPLICATION NUMBER: US/10/489,136
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: PCT/EP02/09844
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: DE 101 43 238.0
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 10
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Poliovirus
US-10-489-136-10

Query Match      100.0%; Score 19; DB 8; Length 745;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 454 CCCCTGAATCGGCTAATC 472

RESULT 17
US-09-884-586A-3
; Sequence 3, Application US/09884586A
; Publication No. US20030046716A1
; GENERAL INFORMATION:
; APPLICANT: Echelard, Yann
; APPLICANT: Meade, Harry M.
; APPLICANT: Eichner, Wolfram
; APPLICANT: Sommermeyer, Klaus
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED PLATELET DERIVED
; TITLE OF INVENTION: GROWTH FACTOR
; FILE REFERENCE: 10275-120001
; CURRENT APPLICATION NUMBER: US/09/884,586A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/212,406
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-586A-3

Query Match      100.0%; Score 19; DB 3; Length 2076;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
Db 1203 CCCCTGAATCGGCTAATC 1221

RESULT 18
US-10-136-819-7
; Sequence 7, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
; FILE REFERENCE: 6627-Pat198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 7399
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7

Query Match      100.0%; Score 19; DB 6; Length 7399;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCCCTGAATGCGGCTAATC 19  
Db 454 CCCCTGAATGCGGCTAATC 472

RESULT 19  
US-10-408-456-4  
; Sequence 4, Application US/10408456  
; Publication No. US20040013648A1  
; GENERAL INFORMATION:  
; APPLICANT: Oxford Biomedica (UK) Limited  
; TITLE OF INVENTION: Vector System  
; FILE REFERENCE: 674523-2016  
; CURRENT APPLICATION NUMBER: US/10/408,456  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB01/04433  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 0024550.6  
; PRIOR FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 4  
; LENGTH: 10448  
; TYPE: DNA  
; ORGANISM: Equine Infectious Anemia Virus  
US-10-408-456-4

Query Match 100.0%; Score 19; DB 6; Length 10448;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
Db 1427 CCCCTGAATGCGGCTAATC 1445

RESULT 20  
US-10-408-456-5  
; Sequence 5, Application US/10408456  
; Publication No. US20040013648A1  
; GENERAL INFORMATION:  
; APPLICANT: Oxford Biomedica (UK) Limited  
; TITLE OF INVENTION: Vector System  
; FILE REFERENCE: 674523-2016  
; CURRENT APPLICATION NUMBER: US/10/408,456  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB01/04433  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 0024550.6  
; PRIOR FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 5  
; LENGTH: 11058  
; TYPE: DNA  
; ORGANISM: Equine Infectious Anemia Virus  
US-10-408-456-5

Query Match 100.0%; Score 19; DB 6; Length 11058;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
Db 3699 CCCCTGAATGCGGCTAATC 3717

RESULT 21  
US-10-408-456-34  
; Sequence 34, Application US/10408456  
; Publication No. US20040013648A1

; GENERAL INFORMATION:  
; APPLICANT: Oxford Biomedica (UK) Limited  
; TITLE OF INVENTION: Vector System  
; FILE REFERENCE: 674523-2016  
; CURRENT APPLICATION NUMBER: US/10/408,456  
; PRIOR FILING DATE: 2003-04-08  
; PRIOR APPLICATION NUMBER: PCT/GB01/04433  
; PRIOR FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 0024550.6  
; PRIOR FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 34  
; LENGTH: 11622  
; TYPE: DNA  
; ORGANISM: Equine Infectious Anemia Virus  
US-10-408-456-34

Query Match 100.0%; Score 19; DB 6; Length 11622;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
Db 7130 CCCCTGAATGCGGCTAATC 7148

RESULT 22  
US-10-873-573-7  
; Sequence 7, Application US/10873573  
; Publication No. US20050002907A1  
; GENERAL INFORMATION:  
; APPLICANT: ROHL, JONATHAN  
; APPLICANT: MITRAPHANOUS, KYRI  
; APPLICANT: MISKIN, JAMES  
; APPLICANT: KINGSMAN, SUSAN MARIE  
; TITLE OF INVENTION: VECTOR SYSTEM  
; FILE REFERENCE: 674523-2016.1  
; CURRENT APPLICATION NUMBER: US/10/873,573  
; CURRENT FILING DATE: 2004-06-21  
; PRIOR APPLICATION NUMBER: 10/408,456  
; PRIOR FILING DATE: 2003-04-07  
; PRIOR APPLICATION NUMBER: PCT/GB01/04433  
; PRIOR FILING DATE: 2001-10-05  
; PRIOR APPLICATION NUMBER: GB 0024550.6  
; PRIOR FILING DATE: 2000-10-06  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 7  
; LENGTH: 11622  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: nucleotide sequence  
US-10-873-573-7

Query Match 100.0%; Score 19; DB 8; Length 11622;  
Best Local Similarity 100.0%; Pred. No. 3.6;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGCGGCTAATC 19  
Db 7130 CCCCTGAATGCGGCTAATC 7148

RESULT 23  
US-10-829-474-10  
; Sequence 10, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF

APPLICANT: MARIANI, Brian D.  
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
FILE REFERENCE: 043956-0121  
CURRENT APPLICATION NUMBER: US/10/829,474  
CURRENT FILING DATE: 2004-04-22  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 10  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
OTHER INFORMATION: RNA  
US-10-829-474-10

Query Match 94.7%; Score 18; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
|||||  
Db 1 CCCTGAATGCGGCTAATC 18

## RESULT 24

US-10-829-474-11  
Sequence 11, Application US/10829474  
Publication No. US20050239055A1  
GENERAL INFORMATION:  
APPLICANT: Genetics & IVF  
APPLICANT: MARIANI, Brian D.  
TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
FILE REFERENCE: 043956-0121  
CURRENT APPLICATION NUMBER: US/10/829,474  
CURRENT FILING DATE: 2004-04-22  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 11  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
OTHER INFORMATION: RNA  
US-10-829-474-11

Query Match 94.7%; Score 18; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 8.5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAAT 18  
|||||  
Db 1 CCCTGAATGCGGCTAAT 18

## RESULT 25

US-09-802-110B-105  
Sequence 105, Application US/09802110B  
Publication No. US20030082535A1  
GENERAL INFORMATION:  
APPLICANT: Leushner, James  
Dunn, May  
LaCroix, Jean-Michel  
TITLE OF INVENTION: METHOD, COMPOSITIONS AND KIT FOR  
DETECTION AND IDENTIFICATION OF MICROORGANISMS  
NUMBER OF SEQUENCES: 189  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Oppedahl & Larson LLP  
STREET: PO Box 5068  
CITY: Dillon  
STATE: CO

COUNTRY: US  
ZIP: 80435  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage  
COMPUTER: IBM compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Word Perfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/802,110B  
FILING DATE: 07-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: <Unknown>  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Larson, Marina T.  
REGISTRATION NUMBER: 32,038  
REFERENCE/DOCKET NUMBER: VGEN.P-058-2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (970) 468-6600  
TELEFAX: (970) 468-0104  
TELEX: <Unknown>  
INFORMATION FOR SEQ ID NO: 105:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 25  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHETICAL: no  
ANTI-SENSE: yes  
FRAGMENT TYPE: internal  
SEQUENCE DESCRIPTION: SEQ ID NO: 105:  
US-09-802-110B-105

Query Match 94.7%; Score 18; DB 3; Length 25;  
Best Local Similarity 100.0%; Pred. No. 8.7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAAT 18  
|||||  
Db 8 CCCTGAATGCGGCTAAT 25

## RESULT 26

US-10-104-611-31  
Sequence 31, Application US/10104611  
Publication No. US20020160976A1  
GENERAL INFORMATION:  
APPLICANT: Miles, Vincent J.  
Mathews, Michael B.  
Katze, Michael G.  
Witherell, Gary  
Watson, Julia C.  
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/104,611  
FILING DATE: 22-Mar-2002  
CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/221,816B  
 ; FILING DATE: 01-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7960-030  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 627 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: RNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
 US-10-104-611-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;  
 Best Local Similarity 78.9%; Pred. No. 23;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19  
 |||:||||:||||:|  
 DB 457 CCCUGAAGCGGCUAAC 475

RESULT 27  
 US-10-112-547-31  
 ; Sequence 31, Application US/10112547  
 ; Publication No. US20020160977A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miles, Vincent J.  
 ; Mathews, Michael B.  
 ; Katze, Michael G.  
 ; Witherell, Gary  
 ; Watson, Julia C.  
 ; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
 ; OF VIRAL REPLICATION  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036/2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/112,547  
 ; FILING DATE: 28-Mar-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/221,816B  
 ; FILING DATE: 01-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7960-030  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 627 base pairs

Query Match 91.6%; Score 17.4; DB 5; Length 627;  
 Best Local Similarity 78.9%; Pred. No. 23;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19  
 |||:||||:||||:|  
 DB 457 CCCUGAAGCGGCUAAC 475

; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: RNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
 US-10-112-547-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;  
 Best Local Similarity 78.9%; Pred. No. 23;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19  
 |||:||||:||||:|  
 DB 457 CCCUGAAGCGGCUAAC 475

RESULT 28  
 US-10-112-241-31  
 ; Sequence 31, Application US/10112241  
 ; Publication No. US20020165194A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Miles, Vincent J.  
 ; Mathews, Michael B.  
 ; Katze, Michael G.  
 ; Witherell, Gary  
 ; Watson, Julia C.  
 ; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
 ; OF VIRAL REPLICATION  
 ; NUMBER OF SEQUENCES: 33  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Pennie & Edmonds  
 ; STREET: 1155 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: USA  
 ; ZIP: 10036/2711  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/10/112,241  
 ; FILING DATE: 28-Mar-2002  
 ; CLASSIFICATION: <Unknown>  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/221,816B  
 ; FILING DATE: 01-APR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Coruzzi, Laura A  
 ; REGISTRATION NUMBER: 30,742  
 ; REFERENCE/DOCKET NUMBER: 7960-030  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (212) 790-9090  
 ; TELEFAX: (212) 869-8864  
 ; TELEX: 66141 PENNIE  
 ; INFORMATION FOR SEQ ID NO: 31:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 627 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: RNA  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
 US-10-112-241-31

Query Match 91.6%; Score 17.4; DB 5; Length 627;  
 Best Local Similarity 78.9%; Pred. No. 23;  
 Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGTAATC 19  
 |||:||||:||||:|  
 DB 457 CCCUGAAGCGGCUAAC 475

## RESULT 29

US-10-109-368-31  
; Sequence 31, Application US/10109368  
; Publication No. US20030144226A1  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/109,368  
FILING DATE: 27-Mar-2002  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816  
FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-109-368-31

Query Match 91.6%; Score 17.4; DB 6; Length 627;  
Best Local Similarity 78.9%; Pred. No. 23;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGCTAATC 19  
|||:||||:||||:|  
Db 457 CCCUGAUGCGCUAAC 475

## RESULT 30

US-10-867-798-31  
; Sequence 31, Application US/10867798  
; Publication No. US20040254140A1  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/867,798  
FILING DATE: 14-Jun-2004  
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/10/109,368  
FILING DATE: 27-Mar-2002

APPLICATION NUMBER: US/08/221,816  
FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-867-798-31

Query Match 91.6%; Score 17.4; DB 8; Length 627;  
Best Local Similarity 78.9%; Pred. No. 23;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGCTAATC 19  
|||:||||:||||:|  
Db 457 CCCUGAUGCGCUAAC 475

## RESULT 31

US-10-829-474-6  
; Sequence 6, Application US/10829474  
; Publication No. US2005023905A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 6  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-6

Query Match 89.5%; Score 17; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17  
Db 1 CCCCTGAATGCGGCTAA 17

## RESULT 32

US-10-829-474-7  
; Sequence 7, Application US/10829474  
; Publication No. US20050239055A1

## GENERAL INFORMATION:

; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 7

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA

US-10-829-474-7

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAATC 19  
Db 1 CCTGAATGCGGCTAATC 17

## RESULT 33

US-10-829-474-9

; Sequence 9, Application US/10829474

; Publication No. US20050239055A1

## GENERAL INFORMATION:

; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 9

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral

; OTHER INFORMATION: RNA

US-10-829-474-9

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCCTGAATGCGGCTAAT 18  
Db 1 CCCCTGAATGCGGCTAAT 17

## RESULT 34

US-10-829-474-13

; Sequence 13, Application US/10829474

; Publication No. US20050239055A1

## GENERAL INFORMATION:

; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 13

; LENGTH: 17

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-13

Query Match 89.5%; Score 17; DB 9; Length 17;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCCTGAATGCGGCTAAT 18  
Db 1 CCCCTGAATGCGGCTAAT 17

## RESULT 35

US-10-938-005-2

; Sequence 2, Application US/10938005

; Publication No. US20050048475A1

## GENERAL INFORMATION:

; APPLICANT: Paul, John H.  
; APPLICANT: Casper, Erica T.  
; APPLICANT: Patterson, Stacey S.  
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus  
; FILE REFERENCE: USF-114XC621

; CURRENT APPLICATION NUMBER: US/10/938,005

; CURRENT FILING DATE: 2004-09-10

; PRIOR APPLICATION NUMBER: 10/857,109

; PRIOR FILING DATE: 2004-05-28

; PRIOR APPLICATION NUMBER: 10/179,082

; PRIOR FILING DATE: 2002-06-25

; PRIOR APPLICATION NUMBER: 60/301,218

; PRIOR FILING DATE: 2001-06-27

; NUMBER OF SEQ ID NOS: 10

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 2

; LENGTH: 24

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Primer Ent P2 (JP128)

US-10-938-005-2

Query Match

Best Local Similarity 89.5%; Score 17; DB 8; Length 24;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17  
Db 8 CCCCTGAATGCGGCTAA 24

## RESULT 36

US-10-767-701-7988

; Sequence 7988, Application US/10767701

; Publication No. US20040172684A1

## GENERAL INFORMATION:

; APPLICANT: Kovalic, David K.

; APPLICANT: Zhou, Yihua

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With





```
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||| |||||
Db 538 CCCCTGAGTGCAGCTAATC 556

RESULT 41
US-10-437-963-33913/c
; Sequence 33913, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 33913
; LENGTH: 1275
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_37980C.1
; US-10-437-963-33913

Query Match 83.2%; Score 15.8; DB 7; Length 1275;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||| |||||
Db 411 CCCCTGAGTGCAGCTAATC 393

RESULT 42
US-10-282-122A-19830/c
; Sequence 19830, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06

Best Local Similarity 83.2%; Score 15.8; DB 7; Length 1275;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||| |||||
Db 411 CCCCTGAGTGCAGCTAATC 393

RESULT 43
US-10-179-082A-2
; Sequence 2, Application US/10179082A
; Publication No. US20030186222A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H
; TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASB
; FILE REFERENCE: USF-114XC6
; CURRENT APPLICATION NUMBER: US/10/179,082A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Enterovirus sp.
; US-10-179-082A-2

Query Match 81.1%; Score 15.4; DB 6; Length 24;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
    ||||| ||||| |||||
Db 8 CCCCGGAATCGGCTAA 24

RESULT 44
US-09-974-300-5975
; Sequence 5975, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
```

```
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19830
; LENGTH: 1326
; TYPE: DNA
; ORGANISM: Enterobacter cloacae
; US-10-282-122A-19830
```

```
Query Match 83.2%; Score 15.8; DB 7; Length 1326;
Best Local Similarity 89.5%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATGCGGCTAATC 19
    ||||| ||||| |||||
Db 621 CACCTGAATGCGGCAATC 603
```

```
RESULT 43
US-10-179-082A-2
; Sequence 2, Application US/10179082A
; Publication No. US20030186222A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H
; TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASB
; FILE REFERENCE: USF-114XC6
; CURRENT APPLICATION NUMBER: US/10/179,082A
; CURRENT FILING DATE: 2002-11-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Enterovirus sp.
; US-10-179-082A-2
```

```
Query Match 81.1%; Score 15.4; DB 6; Length 24;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATGCGGCTAA 17
    ||||| ||||| |||||
Db 8 CCCCGGAATCGGCTAA 24
```

```
RESULT 44
US-09-974-300-5975
; Sequence 5975, Application US/09974300
; Patent No. US20020146721A1
; GENERAL INFORMATION:
; APPLICANT: Berka, Randy M.
; APPLICANT: Clausen, Ib Groth
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE OF INVENTION: Expression
; FILE REFERENCE: 10085.500-US
; CURRENT APPLICATION NUMBER: US/09/974,300
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/680,598
; PRIOR FILING DATE: 2000-10-06
; PRIOR APPLICATION NUMBER: 60/279,526
; PRIOR FILING DATE: 2001-03-27
```



```
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2003-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-847-1549

Query Match      81.1%; Score 15.4; DB 3; Length 32193;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
   |||||
Db 2571 CCCCTGAATGCGGCTAA 2555

RESULT 50
US-10-154-1549/c
; Sequence 1549, Application US/10092154
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009C1
; CURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1549
; LENGTH: 32193
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1549

Query Match      81.1%; Score 15.4; DB 5; Length 32193;
Best Local Similarity 94.1%; Pred. No. 4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAA 17
   |||||
Db 2571 CCCCTGAATGCGGCTAA 2555

RESULT 51
US-10-829-474-8
; Sequence 8, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 8
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized forward primer for amplifying enteroviral
; RNA

US-10-829-474-8
Query Match      78.9%; Score 15; DB 9; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAA 17
   |||||
Db 1 CCTGAATGCGGCTAA 15

RESULT 52
US-10-424-599-90608
; Sequence 90608, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 90608
; LENGTH: 197
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_52831C.1
US-10-424-599-90608

Query Match      78.9%; Score 15; DB 7; Length 197;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 TGAATGCGGCTAATC 19
   |||||
Db 65 TGAATGCGGCTAATC 79

RESULT 53
US-10-425-115-89087
; Sequence 89087, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 89087
; LENGTH: 415
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_181248C.1
US-10-425-115-89087

Query Match      78.9%; Score 15; DB 8; Length 415;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAA 17
   |||||
Db 174 CCTGAATGCGGCTAA 188
```



```

: GENERAL INFORMATION:
: APPLICANT: Wang, David G.
: TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
: TITLE OF INVENTION: Polymorphisms in the Human Genome
: FILE REFERENCE: 108827, 129
: CURRENT APPLICATION NUMBER: US/10/027,632
: CURRENT FILING DATE: 2002-04-30
: PRIOR APPLICATION NUMBER: US 60/218,006
: PRIOR FILING DATE: 2000-07-12
: PRIOR APPLICATION NUMBER: US 60/198,676
: PRIOR FILING DATE: 2000-04-20
: PRIOR APPLICATION NUMBER: US 60/193,483
: PRIOR FILING DATE: 2000-03-29
: PRIOR APPLICATION NUMBER: US 60/185,218
: PRIOR FILING DATE: 2000-02-24
: PRIOR APPLICATION NUMBER: US 60/167,363
: PRIOR FILING DATE: 1999-11-23
: PRIOR APPLICATION NUMBER: US 60/156,358
: PRIOR FILING DATE: 1999-09-28
: PRIOR APPLICATION NUMBER: US 60/146,002
: PRIOR FILING DATE: 1999-08-09
: NUMBER OF SEQ ID NOS: 325720
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 261980
: LENGTH: 969
: TYPE: DNA
: ORGANISM: Human
: US-10-027-632-261980

```

```

Query Match      78.9%; Score 15; DB 5; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  CTGAATCGGCTAAT 18
          |||||
Db      81  CTGAATCGGCTAAT 95

```

```

RESULT 58
US-10-027-632-261981
; Sequence 261981, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261981
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261981

```

Query Match	78.9%;	Score 15;	DB 5;	Length 969;
Best Local Similarity	100.0%;	Pred. No. 5.2e+02;		

```

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CTGAATGGCGCTAAT 18
      |||||
      |||||
Db 81 CTGAATGGCGCTAAT 95

RESULT 59
US-10-027-632-261979
; Sequence 261979, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TYPE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 261979
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261979

```

```

Query Match          78.9%;   Score 15;   DB 6;   Length 969;
Best Local Similarity 100.0%;   Pred. NO. 5.2e+02;
Matches 15;   Conservative 0;   Mismatches 0;   Indels 0;   Gaps 0;

Qy      4   CTGAATCGCGCTAAT 18
          |||||
Db      81   CTGAATCGCGCTAAT 95

RESULT 60
US-10-027-632-261980
; Sequence 261980, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002

```

```
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261980
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261980

Query Match      78.9%; Score 15; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CTGAATCGCGCTAAT 18
      |||||
Db      81 CTGAATCGCGCTAAT 95

RESULT 61
US-10-027-632-261981
; Sequence 261981, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261981
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261981

Query Match      78.9%; Score 15; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CTGAATCGCGCTAAT 18
      |||||
Db      81 CTGAATCGCGCTAAT 95

RESULT 62
US-10-437-963-38285
; Sequence 38285, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 261980
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-261980

Query Match      78.9%; Score 15; DB 6; Length 969;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CTGAATCGCGCTAAT 18
      |||||
Db      81 CTGAATCGCGCTAAT 95

RESULT 63
US-10-450-763-29581
; Sequence 29581, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 29581
; LENGTH: 2780
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1409)..(2074)
; OTHER INFORMATION: 94% homologous to Escherichia coli L-asparagine permease (L-
; OTHER INFORMATION: asparagine transport protein), accession number D90785, Smith-
; OTHER INFORMATION: Waterman Score=1059.
US-10-450-763-29581

Query Match      78.9%; Score 15; DB 9; Length 2780;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5 TGAATCGCGCTAATC 19
      |||||
Db      239 TGAATCGCGCTAATC 253

RESULT 64
US-10-719-900-576555
; Sequence 576555, Application US/10719900
; Publication No. US20050026164A1
; GENERAL INFORMATION:
; APPLICANT: Xue Mei Zhou
; TITLE OF INVENTION: Methods of Genetic Analysis of Mouse
; FILE REFERENCE: 3528.1
; CURRENT APPLICATION NUMBER: US/10/719,900
; CURRENT FILING DATE: 2003-11-20
; PRIOR APPLICATION NUMBER: 60/427,808
```

```

: PRIOR FILING DATE: 2002 11 20
: NUMBER OF SEQ ID NOS: 982914
: SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
: SEQ ID NO 576555
: LENGTH: 25
: TYPE: DNA
: ORGANISM: Mus musculus
US-10-719-900-576555

```

```
Query Match      77.9%; Score 14.8; DB 8; Length 25;
Best Local Similarity 88.9%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```

RESULT 65
US-10-719-993-17666
; Sequence 17666, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17666
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-17666

```

```
Query Match      77.9%; Score 14.8; DB 8; Length 201;
Best Local Similarity 88.9%; Pred. No. 6.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

RESULT 66  
US-10-741-600-37330/c  
; Sequence 37330, Application US/10741600  
; Publication No. US20050026169A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001499  
; CURRENT APPLICATION NUMBER: US/10/741,600  
; CURRENT FILING DATE: 2003-12-22  
; NUMBER OF SEQ ID NOS: 73397  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 37330  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-741-600-37330

Query Match	77.9%	Score 14.8;	DB 8;	Length 201;
Best Local Similarity	88.9%;	Pred. No. 6.1e+03;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;
Qy	2	CCCTGAATGCGGTAATC	19	
Dd	21	CCCTGAATGCGCCAATC	4	

```

RESULT 67
US-09-864-408A-4133/c
; Sequence 4133, Application US/09864408A
; Publication No. US20040009474A1
; GENERAL INFORMATION:
; APPLICANT: Leach, Martin D.
; APPLICANT: Shmkets, Richard A.
; TITLE OF INVENTION: No. US20040009474A1 Human Polynucleotides and Polypeptides Ence
; FILE REFERENCE: 21402-012
; CURRENT APPLICATION NUMBER: US/09/864,408A
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: 60/206,690
; PRIOR FILING DATE: 2000-05-24
; NUMBER OF SEQ ID NOS: 9068
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4133
; LENGTH: 293
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Wherein n may be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (286)..(286)
; OTHER INFORMATION: Wherein n may be a, c, g or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (289)..(289)
; OTHER INFORMATION: Wherein n may be a, c, g or t
US-09-864-408A-4133

```

```

Query Match      77.9%; Score 14.8; DB 3; Length 293;
Best Local Similarity 88.9%; Pred. No. 6.3e+03;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy  2  CCCTGATGCGGCTAATC 19
      ||| ||||| ||||| |||
Db  257  CC CGGAATGCGGCTAGTC 240

```

```

RESULT 68
US-10-674-124A-10734/c
; Sequence 10734, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GEN MAPING METHOD USING MICROSATELLITE
; TYPE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674, 124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 10734
; LENGTH: 295
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: chr6.fa.07frz.115276001
; FEATURE:

```

; OTHER INFORMATION: Located on chromosome 6  
; FEATURE:  
; OTHER INFORMATION: Distance between a terminus base of telomere on  
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base  
; OTHER INFORMATION: sequence : 112298313  
; FEATURE:  
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of  
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and  
; OTHER INFORMATION: 5'-terminus of this base sequence : 96016  
US-10-674-124A-10734

Query Match 77.9%; Score 14.8; DB 8; Length 295;  
Best Local Similarity 88.9%; Pred. No. 6.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 27 CCCTGAATGCACTAAT 10

## RESULT 69

US-10-437-963-66461/c  
; Sequence 66461, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 66461  
; LENGTH: 354  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_6740C.1  
US-10-437-963-66461

Query Match 77.9%; Score 14.8; DB 7; Length 354;  
Best Local Similarity 88.9%; Pred. No. 6.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 92 CCCTCAATGGGCTAAT 75

## RESULT 70

US-10-424-599-81916  
; Sequence 81916, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 81916  
; LENGTH: 405

; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(405)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_44988C.1  
US-10-424-599-81916

Query Match 77.9%; Score 14.8; DB 7; Length 405;  
Best Local Similarity 88.9%; Pred. No. 6.4e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGGGCTAAT 18  
| | | | | | | | | | | | | | | | | | | | | |  
Db 380 CCCTGAATGGGCGAAT 397

## RESULT 71

US-10-240-425-991/c  
; Sequence 991, Application US/10240425  
; Publication No. US20040033502A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Amanda  
; APPLICANT: Boland, Joseph F.  
; APPLICANT: Lord, Reginald V.  
; APPLICANT: Alvarez, Chris  
; APPLICANT: Wetzel, Jon C.  
; APPLICANT: Scherf, Uwe  
; APPLICANT: Vockley, Joseph G.  
; TITLE OF INVENTION: Gene Expression Profiles in Esophageal Tissue  
; FILE REFERENCE: 44921-5026  
; CURRENT APPLICATION NUMBER: US/10/240,425  
; CURRENT FILING DATE: 2002-09-30  
; PRIOR APPLICATION NUMBER: PCT/US01/09847  
; PRIOR FILING DATE: 2001-03-28  
; PRIOR APPLICATION NUMBER: US 60/193,446  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 1588  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 991  
; LENGTH: 537  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: Genbank Accession No. US20040033502A1 AI922821  
US-10-240-425-991

Query Match 77.9%; Score 14.8; DB 7; Length 537;  
Best Local Similarity 88.9%; Pred. No. 6.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 162 CCCTGAACGGCGCTAATC 145

## RESULT 72

US-09-925-065A-152961/c  
; Sequence 152961, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20



; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 152961  
 ; LENGTH: 595  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-152961

Query Match 77.9%; Score 14.8; DB 4; Length 595;  
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
 Db 433 CACTGAATGGGCTAATC 416

RESULT 73  
 US-09-925-065A-886331/c  
 ; Sequence 886331, Application US/09925065A  
 ; Publication No. US20050228172A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US/09/925,065A  
 ; CURRENT FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 886331  
 ; LENGTH: 612  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-886331

Query Match 77.9%; Score 14.8; DB 4; Length 612;  
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
 Db 445 CCCTGAGGCGAGCTAATC 428

RESULT 74  
 US-10-425-115-112682/c  
 ; Sequence 112682, Application US/10425115  
 ; Publication No. US20040214272A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants  
 ; FILE REFERENCE: 38-21(53222)B

; CURRENT APPLICATION NUMBER: US/10/425,115  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 369326  
 ; SEQ ID NO 112682  
 ; LENGTH: 635  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: MRT4577\_34256C.1  
 US-10-425-115-112682

Query Match 77.9%; Score 14.8; DB 8; Length 635;  
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
 Db 527 CCCTGAAGCGGCTAACC 510

RESULT 75  
 US-10-238-075-384  
 ; Sequence 384, Application US/10238075  
 ; Publication No. US20030148324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: I.N.S.E.R.M.  
 ; TITLE OF INVENTION: Polynucleotides which are of nature B2/D+ A- and which are isolat  
 ; TITLE OF INVENTION: E.coli, and biological uses of these polynucleotides and of thei  
 ; FILE REFERENCE: BLANDINE  
 ; CURRENT APPLICATION NUMBER: US/10/238,075  
 ; CURRENT FILING DATE: 2002-09-10  
 ; PRIOR APPLICATION NUMBER: 0003145  
 ; PRIOR FILING DATE: 2000-03-10  
 ; NUMBER OF SEQ ID NOS: 1576  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 384  
 ; LENGTH: 708  
 ; TYPE: DNA  
 ; ORGANISM: Escherichia coli  
 US-10-238-075-384

Query Match 77.9%; Score 14.8; DB 6; Length 708;  
 Best Local Similarity 88.9%; Pred. No. 6.6e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTAAT 18  
 Db 643 GCCTGAATGCGGCAAT 660

RESULT 76  
 US-10-437-963-80579/c  
 ; Sequence 80579, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with  
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 80579  
 ; LENGTH: 714  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa

```

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 18639
; LENGTH: 719
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-18639

Query Match          77.9%   Score 14.8; DB 6; Length 719;
Best Local Similarity 88.9%   Pred. No. 6.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CCCTGAATGCGGCTAATC 19
          |||||
DB      160 CCCTGAATGCGCTGATC 177

RESULT 79
US-10-006-285-246/c
; Sequence 246, Application US/10006285
; Publication No. US20030165854A1
; GENERAL INFORMATION:
; APPLICANT: Mary Jane Cunningham
; APPLICANT: Matthew R. Kaser
; TITLE OF INVENTION: MARKER GENES RESPONDING TO TREATMENT WITH TOXINS
; FILE REFERENCE: PA-0039 US
; CURRENT APPLICATION NUMBER: US/10/006,285
; CURRENT FILING DATE: 2001-12-05
; NUMBER OF SEQ ID NOS: 514
; SOFTWARE: PERL Program
; SEQ ID NO 246
; LENGTH: 767
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030165854A1 211417_Rn.1
US-10-006-285-246

Query Match          77.9%   Score 14.8; DB 6; Length 767;
Best Local Similarity 88.9%   Pred. No. 6.7e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2  CCCTGAATGCGGCTAATC 19
          |||||
DB      476 CCCTGACTGTGGCTAATC 459

RESULT 80
US-10-027-632-154375/c
; Sequence 154375, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

```

;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 154375  
;; LENGTH: 810  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-154375

Query Match 77.9%; Score 14.8; DB 5; Length 810;  
Best Local Similarity 88.9%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 575 CCCTGAATGCGGCTAATC 558

RESULT 81  
US-10-027-632-154375/c  
;; Sequence 154375, Application US/10027632  
;; Publication No. US20030204075A9  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; TITLE OF INVENTION: Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 154375  
;; LENGTH: 810  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-154375

Query Match 77.9%; Score 14.8; DB 6; Length 810;  
Best Local Similarity 88.9%; Pred. No. 6.7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 575 CCCTGAATGCGGCTAATC 558

RESULT 82  
US-11-097-143-12548  
;; Sequence 12548, Application US/11097143  
;; Publication No. US20050208558A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Venter, J. Craig  
;; APPLICANT: et al.

;; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
;; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
;; FILE REFERENCE: CLO00728  
;; CURRENT APPLICATION NUMBER: US/11/097,143  
;; CURRENT FILING DATE: 2005-04-04  
;; PRIOR APPLICATION NUMBER: 60/157,832  
;; PRIOR FILING DATE: 1999-10-05  
;; PRIOR APPLICATION NUMBER: 60/160,191  
;; PRIOR FILING DATE: 1999-10-19  
;; PRIOR APPLICATION NUMBER: 60/161,932  
;; PRIOR FILING DATE: 1999-10-28  
;; PRIOR APPLICATION NUMBER: 60/164,769  
;; PRIOR FILING DATE: 1999-11-12  
;; PRIOR APPLICATION NUMBER: 60/173,383  
;; PRIOR FILING DATE: 1999-12-28  
;; PRIOR APPLICATION NUMBER: 60/175,693  
;; PRIOR FILING DATE: 2000-01-12  
;; PRIOR APPLICATION NUMBER: 60/184,831  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: 60/191,637  
;; PRIOR FILING DATE: 2000-03-23  
;; NUMBER OF SEQ ID NOS: 43008  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 12548  
;; LENGTH: 925  
;; TYPE: DNA  
;; ORGANISM: DROSOPHILA  
US-11-097-143-12548

Query Match 77.9%; Score 14.8; DB 10; Length 925;  
Best Local Similarity 88.9%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 675 CTCTGAATGCGGCTAATC 692

RESULT 83  
US-10-027-632-262260  
;; Sequence 262260, Application US/10027632  
;; Publication No. US20020198371A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
;; TITLE OF INVENTION: Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.129  
;; CURRENT APPLICATION NUMBER: US/10/027,632  
;; CURRENT FILING DATE: 2002-04-30  
;; PRIOR APPLICATION NUMBER: US 60/218,006  
;; PRIOR FILING DATE: 2000-07-12  
;; PRIOR APPLICATION NUMBER: US 60/198,676  
;; PRIOR FILING DATE: 2000-04-20  
;; PRIOR APPLICATION NUMBER: US 60/193,483  
;; PRIOR FILING DATE: 2000-03-29  
;; PRIOR APPLICATION NUMBER: US 60/185,218  
;; PRIOR FILING DATE: 2000-02-24  
;; PRIOR APPLICATION NUMBER: US 60/167,363  
;; PRIOR FILING DATE: 1999-11-23  
;; PRIOR APPLICATION NUMBER: US 60/156,358  
;; PRIOR FILING DATE: 1999-09-28  
;; PRIOR APPLICATION NUMBER: US 60/146,002  
;; PRIOR FILING DATE: 1999-08-09  
;; NUMBER OF SEQ ID NOS: 325720  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 262260  
;; LENGTH: 926  
;; TYPE: DNA  
;; ORGANISM: Human  
US-10-027-632-262260

Query Match 77.9%; Score 14.8; DB 5; Length 926;

Best Local Similarity 88.9%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 84

US-10-027-632-262261  
; Sequence 262261, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027.632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 262261  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-262261

Query Match 77.9%; Score 14.8; DB 5; Length 926;  
Best Local Similarity 88.9%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 85

US-10-027-632-262260  
; Sequence 262260, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027.632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146,002  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 262260  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-262260

Query Match 77.9%; Score 14.8; DB 6; Length 926;  
Best Local Similarity 88.9%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 86

US-10-027-632-262261  
; Sequence 262261, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT APPLICATION NUMBER: US/10/027.632  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR APPLICATION NUMBER: US 60/218,006  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR APPLICATION NUMBER: US 60/198,676  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR APPLICATION NUMBER: US 60/193,483  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR APPLICATION NUMBER: US 60/185,218  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/167,363  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR APPLICATION NUMBER: US 60/156,358  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR APPLICATION NUMBER: US 60/146,002  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 262261  
; LENGTH: 926  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-262261

Query Match 77.9%; Score 14.8; DB 6; Length 926;  
Best Local Similarity 88.9%; Pred. No. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19  
Db 311 CCCTGAAAGCGGCTTATC 328

RESULT 87

US-10-437-963-56313/c  
; Sequence 56313, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

```

: APPLICANT: Li, Ping
: TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
: TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
: FILE REFERENCE: 38-21(53221) B
: CURRENT APPLICATION NUMBER: US/10/437,963
: CURRENT FILING DATE: 2003-05-14
: NUMBER OF SEQ ID NOS: 204966
: SEQ ID NO 56313
: LENGTH: 1026
: TYPE: DNA
: ORGANISM: Oryza sativa
: FEATURE:
: NAME/KEY: unsure
: LOCATION: (1)..(1026)
: OTHER INFORMATION: unsure at all n locations
: FEATURE:
: OTHER INFORMATION: Clone ID: PAT_MRT4530_58236C.1
: US-10-437-963-56313

```

Query Match 77.9%; Score 14.8; DB 7; Length 1026;  
Best Local Similarity 88.9%; Pred. NO. 6.8e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18  
Db 767 CCCTTCAATGCGGCTAAT 750

RESULT 88  
US-10-268-441-13/c  
; Sequence 13, Application US/10268441  
; Publication No. US20030084475A1

```

: ORGANISM: Cancon, Edgar B.
: APPLICANT: Coughlan, Sean J.
: APPLICANT: Helentjaris, Timothy George
: APPLICANT: Jung, Rudolf
: APPLICANT: Li, Chun Ping
: APPLICANT: Nichols, Scott
: APPLICANT: Ripp, Kevin
: APPLICANT: Zheng, Peizhong
: TITLE OF INVENTION: NUCLEIC ACID FRAGMENT
: TITLE OF INVENTION: ORGANELLE
: TITLE OF INVENTION: FORMATION AND METHOD
: FILE REFERENCE: BB1392 US NA
: CURRENT APPLICATION NUMBER: US/10/268,441-13
: CURRENT FILING DATE: 2002-10-09
: PRIOR APPLICATION NUMBER: US/09/672,607
: PRIOR FILING DATE: 2000-09-28
: PRIOR APPLICATION NUMBER: 60/157209
: PRIOR FILING DATE: 1999-09-30
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 13
: LENGTH: 1468
: TYPE: DNA
: ORGANISM: Triticum aestivum
: US-10-268-441-13

```

Query Match	77.9%	Score 14.8;	DB 5;	Length 1468;
Best Local Similarity	88.9%	Pred. No. 7e+02;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 2 CCTGAATCGGCTAATC 19  
Db 554 CCCTGAAAGCGGCTAACC 537

RESULT 89  
US-10-437-963-56310/c  
; Sequence 56310, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:

? APPLICANT: La Rosa, Thomas J.  
 ? APPLICANT: Kovalic, David K.  
 ? APPLICANT: Zhou, Yihua  
 ? APPLICANT: Cao, Yongwei  
 ? APPLICANT: Wu, Wei  
 ? APPLICANT: Boukharov, Andrey A.  
 ? APPLICANT: Barbasuk, Brad  
 ? APPLICANT: Li, Ping  
 ? TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ? TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
 ? FILE REFERENCE: 38-21(53221)B  
 ? CURRENT APPLICATION NUMBER: US/10/437,963  
 ? CURRENT FILING DATE: 2003-05-14  
 ? NUMBER OF SEQ ID NOS: 204966  
 ? SEQ ID NO 56310  
 ? LENGTH: 1551  
 ? TYPE: DNA  
 ? ORGANISM: Oryza sativa  
 ? FEATURE:  
 ? OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58233C.1  
 ? US-10-437-963-56310

Query Match 77.9%; Score 14.8; DB 7; Length 1551;  
Best Local Similarity 88.9%; Pred. NO. 7e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAAT 18  
||| | ||||| |||||  
Db 1292 CCCTTCAATGCGGCTAAT 1275

```

RESULT 90
US-10-027-632-257412
; Sequence 257412, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 257412
; LENGTH: 1929
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-257412

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Query Match	77.9%	Score 14.8;	DB 5;	Length 1929;
Best Local Similarity	88.9%	Pred. No. 7.1e+02;		
Matches 16; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

QY 1 CCCCTGAATGGGCTAAT 18  
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Db 1751 CCCCTGAAAGCAGCTAAT 1768

RESULT 91  
 US-10-632-257412  
 ; Sequence 257412, Application US/10027632  
 ; Publication No. US20030204075A9  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
 ; Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.129  
 ; CURRENT APPLICATION NUMBER: US/10/027,632  
 ; CURRENT FILING DATE: 2002-04-30  
 ; PRIOR APPLICATION NUMBER: US 60/218,006  
 ; PRIOR FILING DATE: 2000-07-12  
 ; PRIOR APPLICATION NUMBER: US 60/198,676  
 ; PRIOR FILING DATE: 2000-04-20  
 ; PRIOR APPLICATION NUMBER: US 60/193,483  
 ; PRIOR FILING DATE: 2000-03-29  
 ; PRIOR APPLICATION NUMBER: US 60/185,218  
 ; PRIOR FILING DATE: 2000-02-24  
 ; PRIOR APPLICATION NUMBER: US 60/167,363  
 ; PRIOR FILING DATE: 1999-11-23  
 ; PRIOR APPLICATION NUMBER: US 60/156,358  
 ; PRIOR FILING DATE: 1999-09-28  
 ; PRIOR APPLICATION NUMBER: US 60/146,002  
 ; PRIOR FILING DATE: 1999-08-09  
 ; NUMBER OF SEQ ID NOS: 325720  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 257412  
 ; LENGTH: 1929  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-027-632-257412

Query Match 77.9%; Score 14.8; DB 6; Length 1929;  
 Best Local Similarity 88.9%; Pred. No. 7.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAAT 18  
 |||||  
 DB 1751 CCCCTGAATCGGCTAAT 1768

RESULT 92  
 US-10-437-963-11634/c  
 ; Sequence 11634, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 11634  
 ; LENGTH: 2079  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_1783C.1  
 US-10-437-963-11634

Query Match 77.9%; Score 14.8; DB 7; Length 2079;  
 Best Local Similarity 88.9%; Pred. No. 7.1e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAAT 18  
 |||||  
 DB 530 CCCTTCATCGGCTAAT 513

RESULT 93  
 US-10-437-963-81682/c  
 ; Sequence 81682, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 81682  
 ; LENGTH: 2256  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_81184C.1  
 US-10-437-963-81682

Query Match 77.9%; Score 14.8; DB 7; Length 2256;  
 Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAAT 18  
 |||||  
 DB 1991 CCCTTCATCGGCTAAT 1974

RESULT 94  
 US-10-437-963-68811/c  
 ; Sequence 68811, Application US/10437963  
 ; Publication No. US20040123343A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: La Rosa, Thomas J.  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Cao, Yongwei  
 ; APPLICANT: Wu, Wei  
 ; APPLICANT: Boukharov, Andrey A.  
 ; APPLICANT: Barbazuk, Brad  
 ; APPLICANT: Li, Ping  
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
 ; Title of Invention: Plants and Uses Thereof for Plant Improvement  
 ; FILE REFERENCE: 38-21(53221)B  
 ; CURRENT APPLICATION NUMBER: US/10/437,963  
 ; CURRENT FILING DATE: 2003-05-14  
 ; NUMBER OF SEQ ID NOS: 204966  
 ; SEQ ID NO 68811  
 ; LENGTH: 2508  
 ; TYPE: DNA  
 ; ORGANISM: Oryza sativa  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_6953C.1  
 US-10-437-963-68811

Query Match 77.9%; Score 14.8; DB 7; Length 2508;  
 Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
 Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAAT 18

Db 806 CCCTCAATGGCGCTAAT 789  
|||||

RESULT 95  
US-10-437-963-87164/c  
; Sequence 87164, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 87164  
; LENGTH: 2525  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_86136C.1  
US-10-437-963-87164

Query Match 77.9%; Score 14.8; DB 7; Length 2525;  
Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy .1 CCCCTGAATGGCGCTAAT 18  
|||||

Db 1363 CCCTCAATGGCGCTAAT 1346

RESULT 96  
US-11-097-143-35308  
; Sequence 35308, Application US/11097143  
; Publication No. US20050208558A1  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig  
; APPLICANT: et al.  
; TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
; TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
; FILE REFERENCE: CL000728  
; CURRENT APPLICATION NUMBER: US/11/097,143  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: 60/157,832  
; PRIOR FILING DATE: 1999-10-05  
; PRIOR APPLICATION NUMBER: 60/160,191  
; PRIOR FILING DATE: 1999-10-19  
; PRIOR APPLICATION NUMBER: 60/161,932  
; PRIOR FILING DATE: 1999-10-28  
; PRIOR APPLICATION NUMBER: 60/164,769  
; PRIOR FILING DATE: 1999-11-12  
; PRIOR APPLICATION NUMBER: 60/173,383  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: 60/175,693  
; PRIOR FILING DATE: 2000-01-12  
; PRIOR APPLICATION NUMBER: 60/184,831  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: 60/191,637  
; PRIOR FILING DATE: 2000-03-23  
; NUMBER OF SEQ ID NOS: 43008  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35308  
; LENGTH: 2534

; TYPE: DNA  
; ORGANISM: DROSOPHILA  
US-11-097-143-35308

Query Match 77.9%; Score 14.8; DB 10; Length 2534;  
Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGGCGCTAAT 18  
|||||

Db 1922 CGCTTGAATGGCGCTAAT 1939

RESULT 97  
US-10-437-963-56314/c  
; Sequence 56314, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 56314  
; LENGTH: 2549  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_58237C.1  
US-10-437-963-56314

Query Match 77.9%; Score 14.8; DB 7; Length 2549;  
Best Local Similarity 88.9%; Pred. No. 7.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CCCCTGAATGGCGCTAAT 18  
|||||

Db 2404 CCCTCAATGGCGCTAAT 2387

RESULT 98  
US-10-437-963-58797/c  
; Sequence 58797, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 58797  
; LENGTH: 2775  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:





GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:29:05 ; Search time 413.942 Seconds  
(Without alignments)  
105.905 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 cccctgaatggcggtatc 19

Scoring table: IDENTITY\_NUC

Gapop 10.0., Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database: Published Applications NA New:

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 6: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
- 7: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 8: /cgn2\_6/ptodata/2/pubpna/US10\_NEW\_PUB.seq.\*
- 9: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	100.0	20	12	US-11-119-231-99
2	19	100.0	25	12	US-11-119-231-98
3	19	100.0	28	12	US-11-119-231-47
4	19	100.0	28	12	US-11-119-231-95
5	19	100.0	72	7	US-10-886-517A-3
6	19	100.0	117	7	US-10-886-517A-41
7	19	100.0	117	7	US-10-886-517A-49
8	19	100.0	117	7	US-10-886-517A-59
9	19	100.0	117	7	US-10-886-517A-61
10	19	100.0	117	7	US-10-886-517A-65
11	19	100.0	118	7	US-10-886-517A-62
12	19	100.0	118	7	US-10-886-517A-63
13	19	100.0	118	7	US-10-886-517A-64
14	19	100.0	118	7	US-10-886-517A-66
15	19	100.0	118	7	US-10-886-517A-67
16	19	100.0	118	7	US-10-886-517A-68
17	19	100.0	118	7	US-10-886-517A-69
18	19	100.0	118	7	US-10-886-517A-70
19	19	100.0	118	7	US-10-886-517A-71
20	19	100.0	810	12	US-11-155-478A-137
					Sequence 137, App
					Sequence 99, Appl
					Sequence 98, Appl
					Sequence 47, Appl
					Sequence 35, Appl
					Sequence 3, Appl
					Sequence 41, Appl
					Sequence 49, Appl
					Sequence 59, Appl
					Sequence 61, Appl
					Sequence 65, Appl
					Sequence 62, Appl
					Sequence 63, Appl
					Sequence 66, Appl
					Sequence 67, Appl
					Sequence 68, Appl
					Sequence 69, Appl
					Sequence 70, Appl
					Sequence 71, Appl
					Sequence 137, App

21	18	94.7	73	7	US-10-886-517A-4	Sequence 4, Appl
22	18	94.7	73	7	US-10-886-517A-5	Sequence 5, Appl
23	18	94.7	73	7	US-10-886-517A-6	Sequence 6, Appl
24	18	94.7	73	7	US-10-886-517A-11	Sequence 11, Appl
25	17.4	91.6	72	7	US-10-886-517A-1	Sequence 1, Appl
26	17.4	91.6	72	7	US-10-886-517A-2	Sequence 2, Appl
27	17.4	91.6	118	7	US-10-886-517A-29	Sequence 29, Appl
28	17.4	91.6	118	7	US-10-886-517A-30	Sequence 30, Appl
29	17.4	91.6	118	7	US-10-886-517A-31	Sequence 31, Appl
30	17.4	91.6	118	7	US-10-886-517A-33	Sequence 33, Appl
31	17.4	91.6	118	7	US-10-886-517A-34	Sequence 34, Appl
32	17.4	91.6	118	7	US-10-886-517A-36	Sequence 36, Appl
33	17.4	91.6	118	7	US-10-886-517A-37	Sequence 37, Appl
34	17.4	91.6	119	7	US-10-886-517A-28	Sequence 28, Appl
35	17.4	91.6	119	7	US-10-886-517A-35	Sequence 35, Appl
36	17.4	91.6	119	7	US-10-886-517A-39	Sequence 39, Appl
37	17.4	91.6	119	7	US-10-886-517A-42	Sequence 42, Appl
38	17.4	91.6	119	7	US-10-886-517A-44	Sequence 44, Appl
39	17.4	91.6	119	7	US-10-886-517A-47	Sequence 47, Appl
40	17.4	91.6	119	7	US-10-886-517A-51	Sequence 51, Appl
41	17.4	91.6	119	7	US-10-886-517A-55	Sequence 55, Appl
42	17.4	91.6	119	7	US-10-886-517A-56	Sequence 56, Appl
43	17.4	91.6	119	7	US-10-886-517A-58	Sequence 58, Appl
44	17.4	91.6	120	7	US-10-886-517A-60	Sequence 60, Appl
45	17.4	91.6	120	7	US-10-886-517A-53	Sequence 53, Appl
46	17.4	91.6	415	7	US-10-886-517A-21	Sequence 21, Appl
47	17.4	91.6	627	12	US-11-195-109-31	Sequence 31, Appl
48	17	89.5	73	7	US-10-886-517A-7	Sequence 7, Appl
49	17	89.5	73	7	US-10-886-517A-12	Sequence 12, Appl
50	16.4	86.3	118	7	US-10-886-517A-48	Sequence 48, Appl
51	15.8	83.2	118	7	US-10-886-517A-32	Sequence 32, Appl
52	15.8	83.2	118	7	US-10-886-517A-38	Sequence 38, Appl
53	15.8	83.2	118	7	US-10-886-517A-40	Sequence 40, Appl
54	15.8	83.2	118	7	US-10-886-517A-43	Sequence 43, Appl
55	15.8	83.2	118	7	US-10-886-517A-45	Sequence 45, Appl
56	15.8	83.2	118	7	US-10-886-517A-46	Sequence 46, Appl
57	15.8	83.2	118	7	US-10-886-517A-50	Sequence 50, Appl
58	15.8	83.2	118	7	US-10-886-517A-52	Sequence 52, Appl
59	15.8	83.2	118	7	US-10-886-517A-57	Sequence 57, Appl
60	15.8	83.2	119	7	US-10-886-517A-54	Sequence 54, Appl
61	15.4	81.1	175673	12	US-11-121-086-55	Sequence 55, Appl
62	14.8	77.9	32	8	US-10-939-294A-8358	Sequence 8358, Ap
63	14.8	77.9	32	8	US-10-939-294A-20728	Sequence 20728, A
64	14.8	77.9	48	8	US-10-939-294A-332	Sequence 332, App
65	14.8	77.9	48	8	US-10-939-294A-1620	Sequence 1620, Ap
66	14.8	77.9	64	8	US-10-939-294A-2653	Sequence 2653, Ap
67	14.8	77.9	64	8	US-10-939-294A-2701	Sequence 2701, Ap
68	14.8	77.9	201	8	US-10-995-561-38314	Sequence 38314, A
69	14.8	77.9	595	6	US-09-925-065A-152961	Sequence 152961, A
70	14.8	77.9	612	6	US-09-925-065A-886331	Sequence 886331, A
71	14.8	77.9	1946	8	US-10-750-185-37125	Sequence 37125, A
72	14.8	77.9	1946	8	US-10-750-623-37125	Sequence 37125, A
73	14.8	77.9	2139	7	US-10-932-182A-80809	Sequence 80809, A
74	14.8	77.9	2139	7	US-10-932-182A-80809	Sequence 80809, A
75	14.8	77.9	137935	8	US-10-995-561-13278	Sequence 13278, A
76	14.8	77.9	150481	12	US-11-112-908-37	Sequence 37, Appl
77	14.8	77.9	171162	12	US-11-112-908-38	Sequence 38, Appl
78	14.8	77.9	358847	7	US-10-330-773-305	Sequence 305, App
79	14.4	75.8	459	6	US-09-925-065A-259192	Sequence 259192, A
80	14.4	75.8	585	6	US-09-925-065A-692313	Sequence 692313, A
81	14.4	75.8	1638	8	US-10-750-185-50407	Sequence 50407, A
82	14.4	75.8	1638	8	US-10-750-623-50407	Sequence 50407, A
83	14.4	75.8	70549	7	US-10-330-773-413	Sequence 413, App
84	14.4	75.8	173120	9	US-11-114-798-55	Sequence 55, Appl
85	14.4	75.8	182303	12	US-11-121-086-45	Sequence 45, Appl
86	14.2	74.7	451	6	US-09-925-065A-84313	Sequence 84313, A
87	14.2	74.7	534	6	US-09-925-065A-740536	Sequence 740536, A
88	14.2	74.7	534	6	US-09-925-065A-84290	Sequence 84290, A
89	14.2	74.7	535	6	US-09-925-065A-380735	Sequence 380735, A
90	14.2	74.7	535	6	US-09-925-065A-605576	Sequence 605576, A
91	14.2	74.7	543	6	US-09-925-065A-153402	Sequence 153402, A
92	14.2	74.7	548	6	US-09-925-065A-430404	Sequence 430404, A
93	14.2	74.7	548	6	US-09-925-065A-430405	Sequence 430405, A

C 94	14.2	74.7	573	9	US-11-096-568A-8418	Sequence 8418, Ap	C 167	13.8	72.6	2202	6	US-09-925-065A-725287	Sequence 725287,
C 95	14.2	74.7	577	6	US-09-925-065A-442742	Sequence 442742,	168	13.8	72.6	2226	7	US-10-932-182A-5447	Sequence 5447, Ap
C 96	14.2	74.7	587	6	US-09-925-065A-740537	Sequence 740537,	169	13.8	72.6	2226	7	US-10-932-182A-5447	Sequence 5447, Ap
C 97	14.2	74.7	592	6	US-09-925-065A-123839	Sequence 123839,	170	13.8	72.6	2266	6	US-09-925-065A-23650	Sequence 23650, A
C 98	14.2	74.7	609	6	US-09-925-065A-361613	Sequence 361613,	C 171	13.8	72.6	2817	6	US-09-925-065A-669289	Sequence 669289,
C 99	14.2	74.7	609	6	US-09-925-065A-361614	Sequence 361614,	C 172	13.8	72.6	2817	6	US-09-925-065A-669289	Sequence 669289,
C 100	14.2	74.7	648	6	US-09-925-065A-390368	Sequence 390368,	C 173	13.8	72.6	3594	8	US-10-775-169-317	Sequence 317, App
C 101	14.2	74.7	649	6	US-09-925-065A-390368	Sequence 390368,	C 174	13.8	72.6	4261	12	US-11-122-329-112	Sequence 112, App
C 102	14.2	74.7	665	6	US-09-925-065A-93414	Sequence 93414, A	C 175	13.8	72.6	4261	9	US-11-253-881-7	Sequence 7, Appli
C 103	14.2	74.7	669	6	US-09-925-065A-778189	Sequence 778189,	C 176	13.8	72.6	5605	9	US-10-330-773-597	Sequence 597, App
C 104	14.2	74.7	771	6	US-09-925-065A-68422	Sequence 68422, A	C 177	13.8	72.6	34603	7	US-10-330-773-597	Sequence 738, App
C 105	14.2	74.7	771	6	US-09-925-065A-68422	Sequence 68422, A	C 178	13.8	72.6	71594	7	US-10-330-773-597	Sequence 738, App
C 106	14.2	74.7	1218	8	US-10-454-437-393	Sequence 393, App	C 179	13.8	72.6	91576	8	US-10-995-561-13461	Sequence 13461, A
C 107	14.2	74.7	1248	7	US-10-932-182A-39	Sequence 39, Appl	C 180	13.8	72.6	204803	7	US-10-330-773-325	Sequence 325, App
C 108	14.2	74.7	1248	7	US-10-932-182A-39	Sequence 39, Appl	C 181	13.8	72.6	218821	12	US-11-121-086-31	Sequence 31, Appl
C 109	14.2	74.7	1297	6	US-09-925-065A-31739	Sequence 31739, A	C 182	13.8	72.6	348101	7	US-10-330-773-122	Sequence 122, App
C 110	14.2	74.7	1297	6	US-09-925-065A-31739	Sequence 31739, A	C 183	13.8	72.6	645179	8	US-10-995-561-13293	Sequence 13293, A
C 111	14.2	74.7	1346	6	US-09-925-065A-31740	Sequence 31740, A	C 184	13.8	72.6	1080000	8	US-10-928-446A-1	Sequence 1, Appli
C 112	14.2	74.7	1346	6	US-09-925-065A-86422	Sequence 86422, A	C 185	13.8	72.6	1080000	8	US-10-928-446A-181	Sequence 181, App
C 113	14.2	74.7	1672	8	US-10-750-185-59975	Sequence 59975, A	C 186	13.8	72.6	1080000	8	US-10-928-446A-185	Sequence 185, App
C 114	14.2	74.7	1672	8	US-10-750-185-59975	Sequence 59975, A	C 187	13.8	72.6	1080000	8	US-10-928-446A-187	Sequence 187, App
C 115	14.2	74.7	2217	6	US-09-925-065A-699467	Sequence 699467,	C 188	13.8	72.6	1080000	8	US-10-928-446A-189	Sequence 189, App
C 116	14.2	74.7	2732	8	US-10-750-185-41642	Sequence 41642, A	C 189	13.8	72.6	1080000	8	US-10-928-446A-191	Sequence 191, App
C 117	14.2	74.7	2732	8	US-10-750-623-41642	Sequence 41642, A	C 190	13.8	72.6	1080000	8	US-10-928-446A-193	Sequence 193, App
C 118	14.2	74.7	2906	8	US-10-750-185-43438	Sequence 43438, A	C 191	13.8	72.6	1080000	8	US-10-928-446A-195	Sequence 195, App
C 119	14.2	74.7	2906	8	US-10-750-623-43438	Sequence 43438, A	C 192	13.8	72.6	1080000	8	US-10-928-446A-197	Sequence 197, App
C 120	14.2	74.7	3769	8	US-10-750-185-25076	Sequence 25076, A	C 193	13.8	72.6	1080000	8	US-10-928-446A-199	Sequence 199, App
C 121	14.2	74.7	3769	8	US-10-750-623-25076	Sequence 25076, A	C 194	13.8	72.6	1080000	8	US-10-928-446A-201	Sequence 201, App
C 122	14.2	74.7	48986	12	US-11-124-367A-5003	Sequence 5003, Ap	C 195	13.4	70.5	25	7	US-10-932-182A-141074	Sequence 141074,
C 123	14.2	74.7	75782	7	US-10-330-773-772	Sequence 772, App	C 196	13.4	70.5	25	7	US-10-932-182A-141074	Sequence 141074,
C 124	14.2	74.7	146733	7	US-10-330-773-387	Sequence 387, App	C 197	13.4	70.5	25	12	US-11-121-849-465224	Sequence 465224,
C 125	14.2	74.7	156297	12	US-11-121-086-65	Sequence 65, Appl	C 198	13.4	70.5	231	7	US-10-932-182A-80546	Sequence 80546, A
C 126	13.8	72.6	500	6	US-09-925-065A-487214	Sequence 487214,	C 199	13.4	70.5	231	7	US-10-932-182A-80546	Sequence 80546, A
C 127	13.8	72.6	508	6	US-09-925-065A-213946	Sequence 213946,	C 200	13.4	70.5	332	6	US-09-925-065A-160447	Sequence 160447,
C 128	13.8	72.6	542	6	US-09-925-065A-494214	Sequence 494214,	C 201	13.4	70.5	358	6	US-09-925-065A-192455	Sequence 192455,
C 129	13.8	72.6	547	6	US-09-925-065A-251345	Sequence 251345,	C 202	13.4	70.5	376	6	US-09-925-065A-791376	Sequence 791376,
C 130	13.8	72.6	548	6	US-09-925-065A-199315	Sequence 199315, A	C 203	13.4	70.5	379	6	US-09-925-065A-746414	Sequence 746414,
C 131	13.8	72.6	548	6	US-09-925-065A-199316	Sequence 199316, A	C 204	13.4	70.5	380	6	US-09-925-065A-112583	Sequence 112583,
C 132	13.8	72.6	548	6	US-09-925-065A-199317	Sequence 199317, A	C 205	13.4	70.5	417	6	US-09-925-065A-917514	Sequence 917514,
C 133	13.8	72.6	548	6	US-09-925-065A-199318	Sequence 199318, A	C 206	13.4	70.5	417	6	US-09-925-065A-917515	Sequence 917515,
C 134	13.8	72.6	550	6	US-09-925-065A-175232	Sequence 175232,	C 207	13.4	70.5	444	6	US-09-925-065A-426571	Sequence 426571,
C 135	13.8	72.6	564	6	US-09-925-065A-374022	Sequence 374022,	C 208	13.4	70.5	445	6	US-09-925-065A-754703	Sequence 754703,
C 136	13.8	72.6	569	6	US-09-925-065A-434002	Sequence 434002,	C 209	13.4	70.5	451	6	US-10-623-155-211	Sequence 211, App
C 137	13.8	72.6	573	6	US-09-925-065A-274574	Sequence 274574,	C 210	13.4	70.5	471	6	US-09-925-065A-252379	Sequence 252379,
C 138	13.8	72.6	576	6	US-09-925-065A-163903	Sequence 163903,	C 211	13.4	70.5	485	6	US-09-925-065A-852158	Sequence 852158,
C 139	13.8	72.6	581	6	US-09-925-065A-440003	Sequence 440003,	C 212	13.4	70.5	491	6	US-09-925-065A-852912	Sequence 852912,
C 140	13.8	72.6	581	6	US-09-925-065A-440004	Sequence 440004,	C 213	13.4	70.5	528	6	US-09-925-065A-599766	Sequence 599766,
C 141	13.8	72.6	581	6	US-09-925-065A-440005	Sequence 440005,	C 214	13.4	70.5	561	6	US-09-925-065A-437247	Sequence 437247,
C 142	13.8	72.6	591	6	US-09-925-065A-530517	Sequence 530517,	C 215	13.4	70.5	577	6	US-09-925-065A-437902	Sequence 437902,
C 143	13.8	72.6	602	6	US-09-925-065A-296301	Sequence 296301,	C 216	13.4	70.5	577	6	US-09-925-065A-437903	Sequence 437903,
C 144	13.8	72.6	602	6	US-10-750-185-1025	Sequence 1025, Ap	C 217	13.4	70.5	577	6	US-09-925-065A-905595	Sequence 905595,
C 145	13.8	72.6	602	8	US-10-750-185-3591	Sequence 3591, Ap	C 218	13.4	70.5	581	6	US-09-925-065A-873888	Sequence 873888,
C 146	13.8	72.6	602	8	US-10-750-623-1025	Sequence 1025, Ap	C 219	13.4	70.5	585	6	US-09-925-065A-577662	Sequence 577662,
C 147	13.8	72.6	602	8	US-10-750-623-3591	Sequence 3591, Ap	C 220	13.4	70.5	586	6	US-09-925-065A-46637	Sequence 46637, A
C 148	13.8	72.6	606	6	US-09-925-065A-436624	Sequence 436624,	C 221	13.4	70.5	609	6	US-09-925-065A-813607	Sequence 813607,
C 149	13.8	72.6	606	6	US-09-925-065A-817644	Sequence 817644,	C 222	13.4	70.5	618	6	US-09-925-065A-128964	Sequence 128964,
C 150	13.8	72.6	620	6	US-09-925-065A-646609	Sequence 646609,	C 223	13.4	70.5	620	6	US-09-925-065A-492503	Sequence 492503,
C 151	13.8	72.6	646	6	US-09-925-065A-60501	Sequence 60501, A	C 224	13.4	70.5	630	6	US-09-925-065A-427568	Sequence 427568,
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C 153	13.8	72.6	672	6	US-09-925-065A-719916	Sequence 719916,	C 226	13.4	70.5	643	6	US-09-925-065A-863075	Sequence 863075,
C 154	13.8	72.6	672	6	US-09-925-065A-922842	Sequence 922842,	C 227	13.4	70.5	810	6	US-09-925-065A-23114	Sequence 23114, A
C 155	13.8	72.6	672	6	US-09-925-065A-947181	Sequence 947181,	C 228	13.4	70.5	810	6	US-09-925-065A-23115	Sequence 23115, A
C 156	13.8	72.6	796	6	US-09-925-065A-8662	Sequence 8622, Ap	C 229	13.4	70.5	913	6	US-09-925-065A-709534	Sequence 709534,
C 157	13.8	72.6	796	6	US-09-925-065A-86623	Sequence 8623, Ap	C 230	13.4	70.5	913	6	US-09-925-065A-709535	Sequence 709535,
C 158	13.8	72.6	796	6	US-09-925-065A-8624	Sequence 8624, Ap	C 231	13.4	70.5	1290	9	US-11-096-568A-10052	Sequence 10052, A
C 159	13.8	72.6	1249	6	US-09-925-065A-715166	Sequence 715166,	C 232	13.4	70.5	1587	7	US-10-932-182A-82256	Sequence 82256, A
C 160	13.8	72.6	1728	8	US-10-750-185-39169	Sequence 39169, A	C 233	13.4	70.5	1587	7	US-10-932-182A-82256	Sequence 82256, A
C 161	13.8	72.6	1728	8	US-10-750-185-39169	Sequence 39169, A	C 234	13.4	70.5	1798	8	US-10-750-623-37688	Sequence 37688, A
C 162	13.8	72.6	1896	8	US-10-750-185-44889	Sequence 44889, A	C 235	13.4	70.5	1798	8	US-10-750-623-37688	Sequence 37688, A
C 163	13.8	72.6	1896	8	US-10-750-623-44889	Sequence 44889, A	C 236	13.4	70.5	3171	7	US-10-501-035-189	Sequence 2, Appli
C 164	13.8	72.6	2186	8	US-10-750-185-36969	Sequence 36969, A	C 237	13.4	70.5	3171	9	US-11-264-046-2	Sequence 7, Appli
C 165	13.8	72.6	2186	8	US-10-750-623-36969	Sequence 36969, A	C 238	13.4	70.5	3205	7	US-10-649-591-7	Sequence 121, App
C 166	13.8	72.6	2202	6	US-09-925-065A-725286	Sequence 725286,	C 239	13.4	70.5	3205	12	US-11-090-739-121	Sequence 121, App

C 240	13.4	70.5	3705	12	US-11-186-284-17	Sequence 17, Appl	C 313	13.2	69.5	533	6	US-09-925-065A-9569	Sequence 9569, Ap
C 241	13.4	70.5	3705	9	US-11-096-568A-33272	Sequence 33272, A	C 314	13.2	69.5	533	6	US-09-925-065A-9570	Sequence 9570, Ap
C 242	13.4	70.5	4405	8	US-10-750-185-58770	Sequence 58770, A	C 315	13.2	69.5	536	6	US-09-925-065A-188708	Sequence 188708, Ap
C 243	13.4	70.5	4405	8	US-10-750-623-58770	Sequence 58770, A	C 316	13.2	69.5	537	6	US-09-925-065A-490381	Sequence 490381, Ap
C 244	13.4	70.5	12561	12	US-11-124-367A-5110	Sequence 5110, Ap	C 317	13.2	69.5	537	6	US-09-925-065A-490382	Sequence 490382, Ap
C 245	13.4	70.5	24458	7	US-10-330-773-450	Sequence 450, App	C 318	13.2	69.5	537	6	US-09-925-065A-490383	Sequence 490383, Ap
C 246	13.4	70.5	38059	9	US-11-129-861-4	Sequence 4, Appl	C 319	13.2	69.5	537	6	US-09-925-065A-490384	Sequence 490384, Ap
C 247	13.4	70.5	69885	8	US-10-995-561-13490	Sequence 13490, A	C 320	13.2	69.5	542	6	US-09-925-065A-40661	Sequence 40661, A
C 248	13.4	70.5	61361	8	US-10-995-561-13501	Sequence 13501, A	C 321	13.2	69.5	542	6	US-09-925-065A-40662	Sequence 40662, A
C 249	13.4	70.5	81463	7	US-10-330-773-659	Sequence 659, App	C 322	13.2	69.5	542	6	US-09-925-065A-177100	Sequence 177100, Ap
C 250	13.4	70.5	90572	12	US-11-124-368A-2900	Sequence 2900, Ap	C 323	13.2	69.5	542	6	US-09-925-065A-342552	Sequence 342552, Ap
C 251	13.4	70.5	165857	12	US-11-121-086-34	Sequence 34, Appl	C 324	13.2	69.5	545	6	US-09-925-065A-408690	Sequence 408690, Ap
C 252	13.2	69.5	19	8	US-10-310-914A-404459	Sequence 404459, A	C 325	13.2	69.5	549	6	US-09-925-065A-333337	Sequence 333337, Ap
C 253	13.2	69.5	19	8	US-10-310-914A-404459	Sequence 404459, A	C 326	13.2	69.5	549	6	US-09-925-065A-333338	Sequence 333338, Ap
C 254	13.2	69.5	22	8	US-10-310-914A-404459	Sequence 404459, A	C 327	13.2	69.5	550	6	US-09-925-065A-500379	Sequence 500379, Ap
C 255	13.2	69.5	24	8	US-10-310-914A-502424	Sequence 502424, A	C 328	13.2	69.5	550	6	US-09-925-065A-500380	Sequence 500380, Ap
C 256	13.2	69.5	25	7	US-10-932-182A-33573	Sequence 33573, A	C 329	13.2	69.5	552	6	US-09-925-065A-423173	Sequence 423173, Ap
C 257	13.2	69.5	25	7	US-10-932-182A-33573	Sequence 33573, A	C 330	13.2	69.5	553	6	US-09-925-065A-592720	Sequence 592720, Ap
C 258	13.2	69.5	25	12	US-11-121-849-593941	Sequence 593941, A	C 331	13.2	69.5	553	6	US-09-925-065A-733253	Sequence 733253, Ap
C 259	13.2	69.5	25	12	US-11-121-849-593942	Sequence 593942, A	C 332	13.2	69.5	554	6	US-09-925-065A-201959	Sequence 201959, Ap
C 260	13.2	69.5	41	8	US-10-834-397-111	Sequence 11, Appl	C 333	13.2	69.5	555	6	US-09-925-065A-96461	Sequence 96461, A
C 261	13.2	69.5	180	12	US-11-096-622-12	Sequence 12, Appl	C 334	13.2	69.5	555	6	US-09-925-065A-424255	Sequence 424255, Ap
C 262	13.2	69.5	201	8	US-10-995-561-16485	Sequence 16485, A	C 335	13.2	69.5	556	6	US-09-925-065A-424256	Sequence 424256, Ap
C 263	13.2	69.5	201	8	US-10-995-561-38324	Sequence 38324, A	C 336	13.2	69.5	557	6	US-09-925-065A-482550	Sequence 482550, Ap
C 264	13.2	69.5	201	8	US-10-995-561-58889	Sequence 58889, A	C 337	13.2	69.5	558	6	US-09-925-065A-188709	Sequence 188709, Ap
C 265	13.2	69.5	201	8	US-10-995-561-58889	Sequence 58889, A	C 338	13.2	69.5	558	6	US-09-925-065A-230898	Sequence 230898, Ap
C 266	13.2	69.5	201	8	US-10-995-561-58889	Sequence 58889, A	C 339	13.2	69.5	558	6	US-09-925-065A-230899	Sequence 230899, Ap
C 267	13.2	69.5	201	12	US-11-124-367A-7674	Sequence 7674, Ap	C 340	13.2	69.5	562	6	US-09-925-065A-200654	Sequence 200654, Ap
C 268	13.2	69.5	320	6	US-09-925-065A-26382	Sequence 26382, A	C 341	13.2	69.5	562	6	US-09-925-065A-653471	Sequence 653471, Ap
C 269	13.2	69.5	321	8	US-10-834-397-54	Sequence 54, Appl	C 342	13.2	69.5	563	6	US-09-925-065A-132831	Sequence 132831, Ap
C 270	13.2	69.5	363	6	US-09-925-065A-474417	Sequence 474417, A	C 343	13.2	69.5	563	6	US-09-925-065A-132832	Sequence 132832, Ap
C 271	13.2	69.5	370	6	US-09-925-065A-570311	Sequence 570311, A	C 344	13.2	69.5	563	6	US-09-925-065A-466104	Sequence 466104, Ap
C 272	13.2	69.5	370	6	US-09-925-065A-570312	Sequence 570312, A	C 345	13.2	69.5	563	6	US-09-925-065A-466105	Sequence 466105, Ap
C 273	13.2	69.5	370	6	US-09-925-065A-570313	Sequence 570313, A	C 346	13.2	69.5	566	6	US-09-925-065A-455751	Sequence 455751, Ap
C 274	13.2	69.5	370	6	US-09-925-065A-570314	Sequence 570314, A	C 347	13.2	69.5	568	6	US-09-925-065A-386489	Sequence 386489, Ap
C 275	13.2	69.5	386	6	US-09-925-065A-109065	Sequence 109065, A	C 348	13.2	69.5	568	6	US-09-925-065A-386490	Sequence 386490, Ap
C 276	13.2	69.5	402	6	US-09-925-065A-186734	Sequence 186734, A	C 349	13.2	69.5	571	6	US-09-925-065A-160563	Sequence 160563, Ap
C 277	13.2	69.5	402	6	US-09-925-065A-186735	Sequence 186735, A	C 350	13.2	69.5	575	6	US-09-925-065A-799897	Sequence 799897, Ap
C 278	13.2	69.5	418	6	US-09-925-065A-481153	Sequence 481153, A	C 351	13.2	69.5	577	6	US-09-925-065A-790272	Sequence 790272, Ap
C 279	13.2	69.5	426	6	US-09-925-065A-148038	Sequence 148038, A	C 352	13.2	69.5	579	6	US-09-925-065A-149585	Sequence 149585, Ap
C 280	13.2	69.5	426	6	US-09-925-065A-148039	Sequence 148039, A	C 353	13.2	69.5	579	6	US-09-925-065A-149586	Sequence 149586, Ap
C 281	13.2	69.5	430	6	US-09-925-065A-495824	Sequence 495824, A	C 354	13.2	69.5	579	12	US-11-128-061-2894	Sequence 2894, Ap
C 282	13.2	69.5	430	6	US-09-925-065A-642090	Sequence 642090, A	C 355	13.2	69.5	579	12	US-11-128-049-2894	Sequence 2894, Ap
C 283	13.2	69.5	443	6	US-09-925-065A-181072	Sequence 181072, A	C 356	13.2	69.5	579	12	US-11-128-049-6536	Sequence 6536, Ap
C 284	13.2	69.5	455	6	US-09-925-065A-507703	Sequence 507703, A	C 357	13.2	69.5	579	12	US-11-128-049-6536	Sequence 6536, Ap
C 285	13.2	69.5	455	6	US-09-925-065A-507704	Sequence 507704, A	C 358	13.2	69.5	580	6	US-09-925-065A-365055	Sequence 365055, Ap
C 286	13.2	69.5	457	6	US-09-925-065A-143456	Sequence 143456, A	C 359	13.2	69.5	580	6	US-09-925-065A-365055	Sequence 365055, Ap
C 287	13.2	69.5	459	6	US-09-925-065A-602333	Sequence 602333, A	C 360	13.2	69.5	583	6	US-09-925-065A-723748	Sequence 723748, Ap
C 288	13.2	69.5	461	6	US-09-925-065A-599090	Sequence 599090, A	C 361	13.2	69.5	585	6	US-09-925-065A-772500	Sequence 772500, Ap
C 289	13.2	69.5	463	6	US-09-925-065A-602332	Sequence 602332, A	C 362	13.2	69.5	587	6	US-09-925-065A-455598	Sequence 455598, A
C 290	13.2	69.5	470	6	US-09-925-065A-508689	Sequence 508689, A	C 363	13.2	69.5	587	6	US-09-925-065A-251589	Sequence 251589, Ap
C 291	13.2	69.5	471	6	US-09-925-065A-508689	Sequence 508689, A	C 364	13.2	69.5	589	6	US-09-925-065A-941869	Sequence 941869, Ap
C 292	13.2	69.5	482	8	US-10-858-730-299	Sequence 299, App	C 365	13.2	69.5	589	6	US-09-925-065A-651693	Sequence 651693, Ap
C 293	13.2	69.5	488	6	US-09-925-065A-536192	Sequence 536192, A	C 366	13.2	69.5	596	6	US-09-925-065A-457997	Sequence 457997, Ap
C 294	13.2	69.5	499	6	US-09-925-065A-108240	Sequence 108240, A	C 367	13.2	69.5	596	6	US-09-925-065A-53494	Sequence 53494, A
C 295	13.2	69.5	499	6	US-09-925-065A-108241	Sequence 108241, A	C 368	13.2	69.5	596	6	US-09-925-065A-525001	Sequence 525001, Ap
C 296	13.2	69.5	499	6	US-09-925-065A-108242	Sequence 108242, A	C 369	13.2	69.5	599	6	US-09-925-065A-525002	Sequence 525002, Ap
C 297	13.2	69.5	499	6	US-09-925-065A-108243	Sequence 108243, A	C 370	13.2	69.5	600	6	US-09-925-065A-702468	Sequence 702468, Ap
C 298	13.2	69.5	499	6	US-09-925-065A-902048	Sequence 902048, A	C 371	13.2	69.5	600	6	US-09-925-065A-645743	Sequence 645743, Ap
C 299	13.2	69.5	501	6	US-09-925-065A-495017	Sequence 495017, A	C 372	13.2	69.5	600	6	US-09-925-065A-907559	Sequence 907559, Ap
C 300	13.2	69.5	501	6	US-09-925-065A-495018	Sequence 495018, A	C 373	13.2	69.5	600	8	US-10-750-185-893	Sequence 893, App
C 301	13.2	69.5	501	6	US-09-925-065A-798082	Sequence 798082, A	C 374	13.2	69.5	601	6	US-09-925-065A-792528	Sequence 792528, Ap
C 302	13.2	69.5	514	6	US-09-925-065A-146690	Sequence 146690, A	C 375	13.2	69.5	601	6	US-09-925-065A-792529	Sequence 792529, Ap
C 303	13.2	69.5	514	6	US-09-925-065A-146691	Sequence 146691, A	C 376	13.2	69.5	601	6	US-09-925-065A-792530	Sequence 792530, Ap
C 304	13.2	69.5	516	6	US-09-925-065A-146692	Sequence 146692, A	C 377	13.2	69.5	602	6	US-09-925-065A-117175	Sequence 117175, Ap
C 305	13.2	69.5	516	6	US-09-925-065A-146693	Sequence 146693, A	C 378	13.2	69.5	602	6	US-09-925-065A-117176	Sequence 117176, Ap
C 306	13.2	69.5	518	6	US-09-925-065A-489052	Sequence 489052, A	C 379	13.2	69.5	602	6	US-09-925-065A-117177	Sequence 117177, Ap
C 307	13.2	69.5	518	6	US-09-925-065A-652368	Sequence 652368, A	C 380	13.2	69.5	602	6	US-09-925-065A-768781	Sequence 768781, Ap
C 308	13.2	69.5	523	6	US-09-925-065A-352573	Sequence 352573, A	C 381	13.2	69.5	602	6	US-09-925-065A-768782	Sequence 768782, Ap
C 309	13.2	69.5	531	6	US-09-925-065A-733254	Sequence 733254, A	C 382	13.2	69.5	602	6	US-09-925-065A-768783	Sequence 768783, Ap
C 310	13.2	69.5	531	6	US-09-925-065A-812186	Sequence 812186, A	C 383	13.2	69.5	603	6	US-09-925-065A-654413	Sequence 654413, Ap
C 311	13.2	69.5	533	6	US-09-925-065A-20554	Sequence 20554, A	C 384	13.2	69.5	604	6	US-09-925-065A-601657	Sequence 601657, Ap
C 312	13.2	69.5	533	6	US-09-925-065A-9568	Sequence 9568, Ap	C 385	13.2	69.5	605	6	US-09-925-065A-727955	Sequence 727955, Ap



QY 1 CCCCTGAATGGCGCTAATC 19  
Db 1 CCCCTGAATGGCGCTAATC 19

## RESULT 2

US-11-119-231-98  
; Sequence 98, Application US/11119231  
; Publication No. US20060003352A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkin, W. Ian  
; APPLICANT: Jingyue, Ju  
; APPLICANT: Thomas, Briese  
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics  
; FILE REFERENCE: 0575/71310-A  
; CURRENT APPLICATION NUMBER: US/11/119,231  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 98  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: Forward Primer for Enterovirus A/B 702/495  
US-11-119-231-98

Query Match 100.0%; Score 19; DB 12; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.34;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19  
Db 6 CCCCTGAATGGCGCTAATC 24

## RESULT 3

US-11-119-231-47  
; Sequence 47, Application US/11119231  
; Publication No. US20060003352A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkin, W. Ian  
; APPLICANT: Jingyue, Ju  
; APPLICANT: Thomas, Briese  
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics  
; FILE REFERENCE: 0575/71310-A  
; CURRENT APPLICATION NUMBER: US/11/119,231  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: FORWARD PRIMER FOR ENTEROVIRUS  
US-11-119-231-47

Query Match 100.0%; Score 19; DB 12; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19  
Db 9 CCCCTGAATGGCGCTAATC 27

## RESULT 4

US-11-119-231-95  
; Sequence 95, Application US/11119231  
; Publication No. US20060003352A1  
; GENERAL INFORMATION:  
; APPLICANT: Lipkin, W. Ian

; APPLICANT: Jingyue, Ju  
; APPLICANT: Thomas, Briese  
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics  
; FILE REFERENCE: 0575/71310-A  
; CURRENT APPLICATION NUMBER: US/11/119,231  
; CURRENT FILING DATE: 2005-04-28  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 95  
; LENGTH: 28  
; TYPE: DNA  
; ORGANISM: ARTIFICIAL SEQUENCE  
; FEATURE:  
; OTHER INFORMATION: FORWARD PRIMER FOR ENTEROVIRUS  
US-11-119-231-95

Query Match 100.0%; Score 19; DB 12; Length 28;  
Best Local Similarity 100.0%; Pred. No. 0.35;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19  
Db 9 CCCCTGAATGGCGCTAATC 27

## RESULT 5

US-10-886-517A-3  
; Sequence 3, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 72  
; TYPE: DNA  
; ORGANISM: enterovirus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28)...(28)  
; OTHER INFORMATION: n = A, T, C or G  
US-10-886-517A-3

Query Match 100.0%; Score 19; DB 7; Length 72;  
Best Local Similarity 100.0%; Pred. No. 0.39;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19  
Db 41 CCCCTGAATGGCGCTAATC 59

## RESULT 6

US-10-886-517A-41  
; Sequence 41, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74

```
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 41
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-41

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 7
US-10-886-517A-49
; Sequence 49, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 49
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-49

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 8
US-10-886-517A-59
; Sequence 59, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-59

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 9
US-10-886-517A-61
; Sequence 61, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 117
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-61

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 10
US-10-886-517A-65
; Sequence 65, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 117
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-65

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78

RESULT 11
US-10-886-517A-62
; Sequence 62, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: KONG, LILLY
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 117
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-62

Query Match      100.0%; Score 19; DB 7; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 60 CCCCTGAATCGGCTAATC 78
```

```
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 62
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-62

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 12
US-10-886-517A-63
; Sequence 63, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-63

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 13
US-10-886-517A-64
; Sequence 64, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-64

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 14
US-10-886-517A-66
; Sequence 66, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: GROEN, JAN
; APPLICANT: KONG, LILLY
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-66

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 15
US-10-886-517A-67
; Sequence 67, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-67

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   |||||
Db 61 CCCCTGAATGCGGCTAATC 79

RESULT 16
US-10-886-517A-68
; Sequence 68, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
```

```
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 68
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-68

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 17
US-10-886-517A-69
; Sequence 69, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 69
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-69

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 18
US-10-886-517A-70
; Sequence 70, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
```

```
US-10-886-517A-70

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 19
US-10-886-517A-71
; Sequence 71, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 71
; LENGTH: 118
; TYPE: DNA
; ORGANISM: enterovirus
US-10-886-517A-71

Query Match      100.0%; Score 19; DB 7; Length 118;
Best Local Similarity 100.0%; Pred. No. 0.41;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
Db      61 CCCCTGAATCGGCTAATC 79

RESULT 20
US-11-155-478A-137
; Sequence 137, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 810
; TYPE: DNA
; ORGANISM: human Enterovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(810)
; OTHER INFORMATION: human Enterovirus
; OTHER INFORMATION: strain Coxsakiavirus B1
; OTHER INFORMATION: accession number ml6560
US-11-155-478A-137
```



Query Match 100.0%; Score 19; DB 12; Length 810;  
Best Local Similarity 100.0%; Pred. No. 0.51; 0; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 4 CCCCTGAATGCGGCTAATC 22

## RESULT 21

US-10-886-517A-4  
; Sequence 4, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 73  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: n = T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: n = G or C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (12)...(12)  
; OTHER INFORMATION: n = C or T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (14)...(14)  
; OTHER INFORMATION: n = A, C, or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15)...(15)  
; OTHER INFORMATION: n = C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (16)...(16)  
; OTHER INFORMATION: n = G or A  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (19)...(19)  
; OTHER INFORMATION: n = T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (28)...(28)  
; OTHER INFORMATION: n = A, T, C, or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (30)...(30)  
; OTHER INFORMATION: n = T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (31)...(31)  
; OTHER INFORMATION: n = G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (33)...(33)  
; OTHER INFORMATION: n = G  
; FEATURE:

; NAME/KEY: misc feature  
; LOCATION: (59)...(59)  
; OTHER INFORMATION: n = C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (61)...(61)  
; OTHER INFORMATION: n = T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (62)...(62)  
; OTHER INFORMATION: n = A or T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (65)...(65)  
; OTHER INFORMATION: n = A or C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (66)...(66)  
; OTHER INFORMATION: n = C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (67)...(67)  
; OTHER INFORMATION: n = C  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (68)...(68)  
; OTHER INFORMATION: n = C or T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (69)...(69)  
; OTHER INFORMATION: n = A or G  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (70)...(70)  
; OTHER INFORMATION: n = C or G  
US-10-886-517A-4

Query Match 94.7%; Score 18; DB 7; Length 73;  
Best Local Similarity 94.7%; Pred. No. 1.5;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 42 CCCCTGAATGCGGCTAATC 60

## RESULT 22

US-10-886-517A-5  
; Sequence 5, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 73  
; TYPE: DNA  
; ORGANISM: enterovirus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (5)...(5)  
; OTHER INFORMATION: n = C or T  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (11)...(11)  
; OTHER INFORMATION: n = G

```
FEATURE:
NAME/KEY: misc feature
LOCATION: (12)...(12)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (14)...(14)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (15)...(15)
OTHER INFORMATION: n = A
FEATURE:
NAME/KEY: misc feature
LOCATION: (16)...(16)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (19)...(19)
OTHER INFORMATION: n = A
FEATURE:
NAME/KEY: misc feature
LOCATION: (28)...(28)
OTHER INFORMATION: n = A, T, C or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (30)...(30)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (31)...(31)
OTHER INFORMATION: n = G or T
FEATURE:
NAME/KEY: misc feature
LOCATION: (33)...(33)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (59)...(59)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (61)...(61)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (62)...(62)
OTHER INFORMATION: n = T
FEATURE:
NAME/KEY: misc feature
LOCATION: (65)...(65)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (66)...(66)
OTHER INFORMATION: n = C or T
FEATURE:
NAME/KEY: misc feature
LOCATION: (67)...(67)
OTHER INFORMATION: n = A or G
FEATURE:
NAME/KEY: misc feature
LOCATION: (68)...(68)
OTHER INFORMATION: n = C
FEATURE:
NAME/KEY: misc feature
LOCATION: (69)...(69)
OTHER INFORMATION: n = G
FEATURE:
NAME/KEY: misc feature
LOCATION: (70)...(70)
OTHER INFORMATION: n = G
US-10-886-517A-5
```

```
Query Match 94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 42 CCCCTGAATCGGCTAANC 60

RESULT 23
US-10-886-517A-6
; Sequence 6, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = A, T, or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)...(11)
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = A, G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A, T, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = A, C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = T, G or C
```

```

; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = A, T or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)...(66)
; OTHER INFORMATION: n = A, G, or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = T, G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G
US-10-886-517A-6

```

```

Query Match      94.7%; Score 18; DB 7; Length 73;
Best Local Similarity 94.7%; Pred. No. 1.5;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 42 CCCCTGAATGCGGCTAANC 60

```

RESULT 24

```

US-10-886-517A-11
; Sequence 11, Application US/10886517A
; Publication No. US20060008910A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE OF INVENTION: RHINOVIROSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)...(11)

```

```

; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = G or A
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (28)...(28)
; OTHER INFORMATION: n = A, T, C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (66)...(66)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G

```

## US-10-886-517A-11

Query Match 94.7%; Score 18; DB 7; Length 73;  
Best Local Similarity 94.7%; Pred. No. 1.5;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 42 CCCCTGAATGGCGCTAACC 50

## RESULT 25

US-10-886-517A-1  
; Sequence 1, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 72  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: consensus sequence  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 28  
; OTHER INFORMATION: n = A,T,C or G  
US-10-886-517A-1

Query Match 91.6%; Score 17.4; DB 7; Length 72;  
Best Local Similarity 94.7%; Pred. No. 3.2;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 41 CCCCTGAATGGCGCTAACC 59

## RESULT 26

US-10-886-517A-2  
; Sequence 2, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 72  
; TYPE: RNA  
; ORGANISM: human rhinovirus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (28)...(28)  
; OTHER INFORMATION: n = A,U,C or G  
US-10-886-517A-2

Query Match 91.6%; Score 17.4; DB 7; Length 72;

Best Local Similarity 78.9%; Pred. No. 3.2;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 41 CCCUGAAGCGGCTAACC 59

## RESULT 27

US-10-886-517A-29  
; Sequence 29, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 29  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-29

Query Match 91.6%; Score 17.4; DB 7; Length 118;  
Best Local Similarity 94.7%; Pred. No. 3.4;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

## RESULT 28

US-10-886-517A-30  
; Sequence 30, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 30  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-30

Query Match 91.6%; Score 17.4; DB 7; Length 118;  
Best Local Similarity 94.7%; Pred. No. 3.4;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

## RESULT 29

US-10-886-517A-31  
; Sequence 31, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:

```
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-31

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 30
US-10-886-517A-33
; Sequence 33, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-33

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 31
US-10-886-517A-34
; Sequence 34, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 118
; TYPE: DNA
```

```
; ORGANISM: human rhinovirus
US-10-886-517A-34

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 22
US-10-886-517A-36
; Sequence 36, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-36

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 33
US-10-886-517A-37
; Sequence 37, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 37
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-37

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79

RESULT 34
US-10-886-517A-38
; Sequence 38, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-38

Query Match          91.6%; Score 17.4; DB 7; Length 118;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
Db 61 CCCCTGAATGCGGCTAACC 79
```

```
US-10-886-517A-28
; Sequence 28, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 28
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-28
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 62 CCCCTGAATCGGCTAACC 80

RESULT 35
US-10-886-517A-35
; Sequence 35, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-35
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-39
; Sequence 39, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-39
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-42
; Sequence 42, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-42
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 62 CCCCTGAATCGGCTAACC 80

US-10-886-517A-44
; Sequence 44, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 44
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-44
Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
   |||||
Db 62 CCCCTGAATCGGCTAACC 80
```

```

Db      62 CCCCTGAATCGGCTAACC 80

RESULT 39
US-10-886-517A-47
; Sequence 47, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-47

Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

RESULT 40
US-10-886-517A-51
; Sequence 51, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-51

Query Match          91.6%; Score 17.4; DB 7; Length 119;
Best Local Similarity 94.7%; Pred. No. 3.4;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 CCCCTGAATCGGCTAATC 19
        |||||
Db      62 CCCCTGAATCGGCTAACC 80

RESULT 41
US-10-886-517A-55
; Sequence 55, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES

```

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
Db 62 CCCCTGAATCGGCTAACC 80

## RESULT 44

US-10-886-517A-60

; Sequence 60, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; TITLE OF INVENTION: RHINOVIRUSES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886,517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 60

; LENGTH: 119

; TYPE: DNA

; ORGANISM: human rhinovirus

US-10-886-517A-60

Query Match 91.6%; Score 17.4; DB 7; Length 119;

Best Local Similarity 94.7%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
Db 62 CCCCTGAATCGGCTAACC 80

## RESULT 45

US-10-886-517A-53

; Sequence 53, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; TITLE OF INVENTION: RHINOVIRUSES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886,517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 53

; LENGTH: 120

; TYPE: DNA

; ORGANISM: human rhinovirus

US-10-886-517A-53

Query Match 91.6%; Score 17.4; DB 7; Length 120;

Best Local Similarity 94.7%; Pred. No. 3.4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
Db 62 CCCCTGAATCGGCTAACC 80

## RESULT 46

US-10-886-517A-21

; Sequence 21, Application US/10886517A

; Publication No. US20060008810A1

; GENERAL INFORMATION:

; APPLICANT: LEE, MING-CHOU

; APPLICANT: KONG, LILLY

; APPLICANT: GROEN, JAN

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING

; TITLE OF INVENTION: RHINOVIRUSES

; FILE REFERENCE: FOCs-003

; CURRENT APPLICATION NUMBER: US/10/886,517A

; CURRENT FILING DATE: 2004-07-06

; NUMBER OF SEQ ID NOS: 74

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 21

; LENGTH: 415

; TYPE: DNA

; ORGANISM: human rhinovirus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 35, 44, 60,

; LOCATION: 61, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,

; LOCATION: 284, 346, 390

; OTHER INFORMATION: n = A, T, C or G

US-10-886-517A-21

Query Match 91.6%; Score 17.4; DB 7; Length 415;

Best Local Similarity 94.7%; Pred. No. 4;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
Db 297 CCCCTGAATCGGCTAACC 315

## RESULT 47

US-11-195-109-31

; Sequence 31, Application US/11195109

; Publication No. US20050265975A1

; GENERAL INFORMATION:

; APPLICANT: Miles, Vincent J.

; APPLICANT: Mathews, Michael B.

; APPLICANT: Katze, Michael G.

; APPLICANT: Witherell, Gary

; APPLICANT: Watson, Julia C.

; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION

; TITLE OF INVENTION: OF VIRAL REPLICATION

; NUMBER OF SEQUENCES: 33

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036/2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSeq Version 2.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/11/195,109

; FILING DATE: 01-Aug-2005

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/10/867,798

; FILING DATE: 14-Jun-2004

; APPLICATION NUMBER: US/10/109,368

; FILING DATE: 27-Mar-2002

; APPLICATION NUMBER: US/08/221,816

; FILING DATE: 01-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Cotuzzi, Laura A

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7960-030

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-8864



TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-11-195-109-31

Query Match 91.6%; Score 17.4; DB 12; Length 627;  
Best Local Similarity 78.9%; Pred. No. 4.1;  
Matches 15; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||:||||:||||:|  
Db 457 CCCCTGAATGCGGCTAACC 475

RESULT 48  
US-10-886-517A-7  
; Sequence 7, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06

NUMBER OF SEQ ID NOS: 74  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 7  
LENGTH: 73  
TYPE: DNA  
ORGANISM: human rhinovirus

FEATURE:  
NAME/KEY: misc feature  
LOCATION: (5)...(5)  
OTHER INFORMATION: n = A, T or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (11)...(11)  
OTHER INFORMATION: n = G or C  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (12)...(12)  
OTHER INFORMATION: n = C or T  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (14)...(14)  
OTHER INFORMATION: n = A, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (15)...(15)  
OTHER INFORMATION: n = T, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (16)...(16)  
OTHER INFORMATION: n = A, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (19)...(19)  
OTHER INFORMATION: n = T  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (23)...(29)  
OTHER INFORMATION: n = A, C, T or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (30)...(30)

OTHER INFORMATION: n = A, C or T  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (31)...(31)  
OTHER INFORMATION: n = A, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (33)...(33)  
OTHER INFORMATION: n = T, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (52)...(52)  
OTHER INFORMATION: n = A, C, T or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (59)...(59)  
OTHER INFORMATION: n = A, G or C  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (61)...(61)  
OTHER INFORMATION: n = A, T or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (62)...(62)  
OTHER INFORMATION: n = A or T  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (65)...(65)  
OTHER INFORMATION: n = A or C  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (66)...(66)  
OTHER INFORMATION: n = A, C or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (67)...(67)  
OTHER INFORMATION: n = T, G or C  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (68)...(68)  
OTHER INFORMATION: n = C or T  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (69)...(69)  
OTHER INFORMATION: n = A or G  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (70)...(70)  
OTHER INFORMATION: n = C or G  
US-10-886-517A-7

Query Match 89.5%; Score 17; DB 7; Length 73;  
Best Local Similarity 89.5%; Pred. No. 5.5;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||:|||||:|||||  
Db 42 CCCCTGAATGCGGCTAANC 60

RESULT 49  
US-10-886-517A-12  
; Sequence 12, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06

```
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 73
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)...(5)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11)...(11)
; OTHER INFORMATION: n = G or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (12)...(12)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (14)...(14)
; OTHER INFORMATION: n = A, C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (15)...(15)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (16)...(16)
; OTHER INFORMATION: n = G or A
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)...(19)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (23)...(29)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (30)...(30)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (31)...(31)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (33)...(33)
; OTHER INFORMATION: n = G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (52)...(52)
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (59)...(59)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (61)...(61)
; OTHER INFORMATION: n = T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (62)...(62)
; OTHER INFORMATION: n = A or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (65)...(65)
; OTHER INFORMATION: n = A or C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (66)...(66)
```

```
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (67)...(67)
; OTHER INFORMATION: n = C
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (68)...(68)
; OTHER INFORMATION: n = C or T
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (69)...(69)
; OTHER INFORMATION: n = A or G
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (70)...(70)
; OTHER INFORMATION: n = C or G
; US-10-886-517A-12

Query Match      89.5%; Score 17; DB 7; Length 73;
Best Local Similarity 89.5%; Pred. No. 5.5;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
         |||||
Db      42 CCCCTGAATGCGCTAANC 60

RESULT 50
US-10-886-517A-48
; Sequence 48, Application US/10886517A
; Publication No. US200600810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 78, 89, 92, 110
; OTHER INFORMATION: n = A,T,C or G
; US-10-886-517A-48

Query Match      86.3%; Score 16.4; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 13;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 CCCCTGAATCGGCTAATC 19
         |||||
Db      61 CCCCTGAATGCGCTAANC 79

RESULT 51
US-10-886-517A-32
; Sequence 32, Application US/10886517A
; Publication No. US200600810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; FILE REFERENCE: FOCs-003
```

; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-32

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 52  
US-10-886-517A-38  
; Sequence 38, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-38

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 53  
US-10-886-517A-40  
; Sequence 40, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-40

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 32  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-32

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 52  
US-10-886-517A-38  
; Sequence 38, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-38

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 53  
US-10-886-517A-40  
; Sequence 40, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-40

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 54  
US-10-886-517A-43  
; Sequence 43, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 43  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-43

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 55  
US-10-886-517A-45  
; Sequence 45, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY  
; APPLICANT: GROEN, JAN  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING  
; FILE REFERENCE: FOCs-003  
; CURRENT APPLICATION NUMBER: US/10/886,517A  
; CURRENT FILING DATE: 2004-07-06  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 45  
; LENGTH: 118  
; TYPE: DNA  
; ORGANISM: human rhinovirus  
US-10-886-517A-45

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 61 CCCCTGAATGGCGCTAACC 79

RESULT 56  
US-10-886-517A-46  
; Sequence 46, Application US/10886517A  
; Publication No. US20060008810A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, MING-CHOU  
; APPLICANT: KONG, LILLY

```

; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOC5-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-46

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. NO.29;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGGCTAATC 19  
Db 61 CCCCTGAATGTGGCTAAC 79

```

RESULT 57
; Sequence 50, Application US/10886517A
; Publication No. US2006008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 1.0
; SEQ ID NO 50
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-50

```

Query Match 83.2%; Score 15.8; DB 7; Length 118;  
Best Local Similarity 89.5%; Pred. No. 29;  
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
|||||  
p'b 61 CCCCTGAATGTGGCTAAC 79

```

RESULT 58
US-10-886-517A-52
; Sequence 52, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F0CS-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-52

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGGCTAATC 19  
db 61 CCCCTGAATGTGGCTAACC 79

```

RESULT 59
US-10-886-517A-57
; Sequence 57, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: FOCs-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 118
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 92
; OTHER INFORMATION: n = A,T,C or G
US-10-886-517A-57

```

```
Query Match      83.2%; Score 15.8; DB 7; Length 118;
Best Local Similarity 89.5%; Pred. No. 29;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATGCGCTAATC 19  
|||  
Db 61 CCCCTGAATGTGGCTAAC 79

```

RESULT 60
US-10-886-517A-54
; Sequence 54, Application US/10886517A
; Publication No. US20060008810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: P0CS-003
; CURRENT APPLICATION NUMBER: US/10/886.517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 54
; LENGTH: 119
; TYPE: DNA
; ORGANISM: human rhinovirus
US-10-886-517A-54

```

Query Match	83.2%	Score 15.8;	DB 7;	Length 119;
Best Local Similarity	89.5%;	Pred. No. 29;		
Matches 17; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

**Qy**            1 CCCTGAATGCGGTAATC 19  
               |||||  
**Db**            62 CCCCAGATGCGGTAACC 80

RESULT 63  
US-10-939-294A-20728/c  
; Sequence 20728, Application US/10939294A  
; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingle, Maneesh

```

RESULT 65
US-10-939-294A-1620
; Sequence 1620, Application US/10939294A
; Publication No. US20050266417A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Turner, Daniel
; APPLICANT: Pingle, Maneesh
; APPLICANT: Pincas, Hanna
; TITLE OF INVENTION: Methods for identifying
; FILE REFERENCE: 19603/4131 (CRF D-2995)
; CURRENT APPLICATION NUMBER: US/10/939,
; CURRENT FILING DATE: 2004-09-10

```

; PRIOR APPLICATION NUMBER: US 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 38995  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 1620  
; LENGTH: 48  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-1620

Query Match 77.9%; Score 14.8; DB 8; Length 48;  
Best Local Similarity 88.9%; Pred. No. 98;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19  
||| ||||| ||||| |||||  
Db 26 CCCGGAATGCGCAATC 43

RESULT 66  
US-10-939-294A-2653/c  
; Sequence 2653, Application US/10939294A  
; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingle, Maneesh  
; APPLICANT: Pincas, Hanna  
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
; CURRENT APPLICATION NUMBER: US/10/939,294A  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: US 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 38995  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2653  
; LENGTH: 64  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-2653

Query Match 77.9%; Score 14.8; DB 8; Length 64;  
Best Local Similarity 88.9%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19  
||| ||||| ||||| |||||  
Db 39 CCCGGAATGCGCAATC 22

RESULT 67  
US-10-939-294A-2701/c  
; Sequence 2701, Application US/10939294A  
; Publication No. US20050266417A1  
; GENERAL INFORMATION:  
; APPLICANT: Barany, Francis  
; APPLICANT: Turner, Daniel  
; APPLICANT: Pingle, Maneesh  
; APPLICANT: Pincas, Hanna  
; TITLE OF INVENTION: Methods for identifying target nucleic acid molecules  
; FILE REFERENCE: 19603/4121 (CRF D-2995-02)  
; CURRENT APPLICATION NUMBER: US/10/939,294A  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: US 60/502/731  
; PRIOR FILING DATE: 2003-09-12  
; NUMBER OF SEQ ID NOS: 38995  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 2701

; LENGTH: 64  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: oligonucleotide probe  
US-10-939-294A-2701

Query Match 77.9%; Score 14.8; DB 8; Length 64;  
Best Local Similarity 88.9%; Pred. No. 1e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19  
||| ||||| ||||| |||||  
Db 55 CCCGGAATGCGCAATC 38

RESULT 68  
US-10-995-561-38314/c  
; Sequence 38314, Application US/109955561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 38314  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-38314

Query Match 77.9%; Score 14.8; DB 8; Length 201;  
Best Local Similarity 88.9%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19  
||| ||||| ||||| |||||  
Db 21 CCTGAATGCGCCAATC 4

RESULT 69  
US-09-925-065A-152961/c  
; Sequence 152961, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 152961  
; LENGTH: 595  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-152961

Query Match 77.9%; Score 14.8; DB 6; Length 595;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
DB 433 CACTGAATGGCGCTAATC 416

## RESULT 70

US-09-925-065A-886331/c  
; Sequence 886331, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 886331  
; LENGTH: 612  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-886331

Query Match 77.9%; Score 14.8; DB 6; Length 612;  
Best Local Similarity 88.9%; Pred. No. 1.3e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
DB 445 CCCTGAAGGCGAGCTAATC 428

## RESULT 71

US-10-750-185-37125/c  
; Sequence 37125, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37125  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: Bovine  
US-10-750-185-37125

Query Match 77.9%; Score 14.8; DB 8; Length 1946;  
Best Local Similarity 88.9%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
DB 933 CCCTGAATGGCGCTAATC 916

## RESULT 72

US-10-750-623-37125/c  
; Sequence 37125, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 37125  
; LENGTH: 1946  
; TYPE: DNA  
; ORGANISM: Bovine  
US-10-750-623-37125

Query Match 77.9%; Score 14.8; DB 8; Length 1946;  
Best Local Similarity 88.9%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | |  
DB 933 CCCTGAATGGCGCTAATC 916

## RESULT 73

US-10-932-182A-80809/c  
; Sequence 80809, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 80809  
; LENGTH: 2139  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-80809

Query Match 77.9%; Score 14.8; DB 7; Length 2139;  
Best Local Similarity 88.9%; Pred. No. 1.5e+02;  
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCCTGAATGGCGCTAATC 19  
| | | | | | | | | | | | | | | | | |

Db 408 CCTGAATGCGCAGATC 391

RESULT 74

US-10-932-182A-80809/c

; Sequence 80809, Application US/10932182A

; Publication No. US20060046253A1

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIKO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: 030685-043

; CURRENT APPLICATION NUMBER: US/10/932.182A

; CURRENT FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 80809

; LENGTH: 2139

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

US-10-932-182A-80809

Query Match 77.9%; Score 14.8; DB 7; Length 2139;

Best Local Similarity 88.9%; Pred. No. 1.5e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 408 CCTGAATGCGCAGATC 391

RESULT 75

US-10-995-561-13278/c

; Sequence 13278, Application US/10995561

; Publication No. US20050272054A1

; GENERAL INFORMATION:

; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF

; TITLE OF INVENTION: DETECTION AND USES THEREOF

; FILE REFERENCE: CL001559

; CURRENT APPLICATION NUMBER: US/10/995.561

; CURRENT FILING DATE: 2004-11-24

; NUMBER OF SEQ ID NOS: 85702

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13278

; LENGTH: 137935

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)...(137935)

; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-10-995-561-13278

Query Match 77.9%; Score 14.8; DB 8; Length 137935;

Best Local Similarity 88.9%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 67700 CCTGAATGCGCCCAATC 67683

RESULT 76

US-11-112-908-37/c

; Sequence 37, Application US/11112908

; Publication No. US20050260659A1

; GENERAL INFORMATION:

; APPLICANT: Harris, Cole

; APPLICANT: Davis, Lisa M.

; TITLE OF INVENTION: Breast Cancer Biomarkers

; FILE REFERENCE: 04-164-US

; CURRENT APPLICATION NUMBER: US/11/112.908

; CURRENT FILING DATE: 2005-04-22

; PRIOR APPLICATION NUMBER: US 60/564,758

; PRIOR FILING DATE: 2004-04-23

; PRIOR APPLICATION NUMBER: US 60/575,978

; PRIOR FILING DATE: 2004-06-01

; PRIOR APPLICATION NUMBER: US 60/631,702

; PRIOR FILING DATE: 2004-11-30

; PRIOR APPLICATION NUMBER: US 60/633,826

; PRIOR FILING DATE: 2004-12-07

; NUMBER OF SEQ ID NOS: 511

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 37

; LENGTH: 150481

; TYPE: DNA

; ORGANISM: Homo sapiens

US-11-112-908-37

Query Match 77.9%; Score 14.8; DB 12; Length 150481;

Best Local Similarity 88.9%; Pred. No. 2.4e+02;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAATC 19

Db 138554 CCTGAATGCGCCCAATC 138537

RESULT 78

US-10-330-773-305/c

; Sequence 305, Application US/10330773

; Publication No. US20060040262A1

; GENERAL INFORMATION:

; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro



```

: TITLE OF INVENTION: Novel Compositions and Methods in Cancer
:
: FILE REFERENCE: 529452001300
: CURRENT APPLICATION NUMBER: US/10/330,773
: CURRENT FILING DATE: 2002-12-27
:
: NUMBER OF SEQ ID NOS: 981
:
: SOFTWARE: FastSeq for Windows Version 4.0
:
: SEQ ID NO 305
: LENGTH: 358847
:
: TYPE: DNA
:
: ORGANISM: Mus musculus
:
: FEATURE:
:
: NAME/KEY: misc_feature
: LOCATION: (1)...(358847)
:
: OTHER INFORMATION: n = A,T,C or G
:
: US-10-330-773-305

```

```
Query Match      77.9%; Score 14.8; DB 7; Length 358847;
Best Local Similarity 88.9%; Pred. NO. 2.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0;
```

Qy 2 CCCTGAATGCGGCTAATC 19  
 Db 252910 CCCTGAATGCACCTAATC 252893

RESULT 79

```

US-09-925-065A-259192/c
; Sequence 259192, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 259192
; LENGTH: 459
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-259192

```

Query Match 75.8%; Score 14.4; DB 6; Length 459;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels

Qy 3 CTTGAATGCGGCTAAT 18  
Db 45 CTTGAATGCTGCTAAT 30

**RESULT 80**

```

US/09-925-065A-692313/C
; Sequence 692313, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108927.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

```

; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: fastSEQ for Windows Version 4.0
; SEQ ID NO 692313
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-692313

```

Query Match 75.8%; Score 14.4; DB 6; Length 585;  
Best Local Similarity 93.8%; Pred. No. 2.2e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels

Qy 1 CCCCTGAATGCGGCTA 16  
Db 473 CCCCTGAATGCGGCAA 458

## RESULT 81

```

US-10-750-185-50407
; Sequence 50407, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INVERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50407
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-50407

```

Query Match 75.8%; Score 14.4; DB 8; Length 1638;  
Best Local Similarity 93.8%; Pred. No. 2.5e+02;  
Matches 15; Conservative 0; Mismatches 1; Indels 0

Qy 1 CCCCTGAATCGGCTA 16  
Db 1503 CCCCTGAATGCTGCTA 1518

RESULT 82

```

US-10-750-623-50407
; Sequence 50407, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom

```

```
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50407
; LENGTH: 1638
; TYPE: DNA
; ORGANISM: Bovine 19866880379342
US-10-750-623-50407

Query Match 75.8%; Score 14.4; DB 8; Length 1638;
Best Local Similarity 93.8%; Pred. No. 2.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 1503 CCCCTGAATGCTGCTA 1518

RESULT 83
US-10-330-773-413/c
; Sequence 413, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: S29452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 70549
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(70549)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-413

Query Match 75.8%; Score 14.4; DB 7; Length 70549;
Best Local Similarity 93.8%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 CTGAATGCGGCTAATC 19
| | | | | | | | | | | | | | | |
Db 56056 CTGAATGCAGCTAATC 56041

RESULT 84
US-11-114-798-55
; Sequence 55, Application US/11114798
; Publication No. US20060035246A1
; GENERAL INFORMATION:
; APPLICANT: WU, RINA
; APPLICANT: MARQUEZ, ABBEY
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND
; TITLE OF INVENTION: COMPOSITIONS
; FILE REFERENCE: 0618.011.0004
; CURRENT APPLICATION NUMBER: US/11/114,798
; CURRENT FILING DATE: 2005-04-26
; PRIOR APPLICATION NUMBER: 10/173,525
; PRIOR FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: 09/952,851
; PRIOR FILING DATE: 2001-09-14
```

```
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 173120
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: nucleotide sequence
US-11-114-798-55

Query Match 75.8%; Score 14.4; DB 9; Length 173120;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 8805 CCCCTGAATGCGGCTA 8820

RESULT 85
US-11-121-086-45
; Sequence 45, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 45
; LENGTH: 182303
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-45

Query Match 75.8%; Score 14.4; DB 12; Length 182303;
Best Local Similarity 93.8%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTA 16
| | | | | | | | | | | | | | | |
Db 30719 CCCCTGAATGCGGCTA 30734

RESULT 86
US-09-925-065A-84313/c
; Sequence 84313, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO 84313
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84313

Query Match          74.7%; Score 14.2; DB 6; Length 451;
Best Local Similarity 84.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||| ||||| ||||| |||||
Db 313 CACCTGAATGTGCTAGTC 295

RESULT 87
US-09-925-065A-740536
; Sequence 740536, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 740536
; LENGTH: 514
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-740536

Query Match          74.7%; Score 14.2; DB 6; Length 514;
Best Local Similarity 84.2%; Pred. No. 2.8e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||| ||||| ||||| |||||
Db 241 CCCCTGATTACTGCTAATC 259

RESULT 88
US-09-925-065A-84290
; Sequence 84290, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84290
; LENGTH: 451
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84290

; PRIORITY FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84290
; LENGTH: 534
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-84290

Query Match          74.7%; Score 14.2; DB 6; Length 534;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||| ||||| ||||| |||||
Db 265 CCCTTGAATGAGCTATTC 283

RESULT 89
US-09-925-065A-380735
; Sequence 380735, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 380735
; LENGTH: 535
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-380735

Query Match          74.7%; Score 14.2; DB 6; Length 535;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
   ||||| ||||| ||||| |||||
Db 309 CCCTTGAATGAGCTATTC 327

RESULT 90
US-09-925-065A-605576
; Sequence 605576, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 605576
; LENGTH: 536
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-605576
```

; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 605576  
; LENGTH: 535  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-605576

Query Match 74.7%; Score 14.2; DB 6; Length 535;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 27 CCCCTGAATCGGCTAATC 45

## RESULT 91

US-09-925-065A-153402/c  
; Sequence 153402, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 153402  
; LENGTH: 543  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-153402

Query Match 74.7%; Score 14.2; DB 6; Length 543;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 481 CCCAGGAATCGGCTAACC 463

## RESULT 92

US-09-925-065A-430404  
; Sequence 430404, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 430404  
; LENGTH: 548  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-430404

Query Match 74.7%; Score 14.2; DB 6; Length 548;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 31 CCCCTGAATCGGCTAATC 49

## RESULT 93

US-09-925-065A-430405  
; Sequence 430405, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 430405  
; LENGTH: 548  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-430405

Query Match 74.7%; Score 14.2; DB 6; Length 548;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | | |  
Db 31 CCCCTGAATCGGCTAATC 49

## RESULT 94

US-11-096-568A-8418/c  
; Sequence 8418, Application US/11096568A  
; Publication No. US20060048240A1  
; GENERAL INFORMATION:  
; APPLICANT: Alexandrov, Nikolai et al.  
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
; FILE REFERENCE: 2750-1592PUS2  
; CURRENT APPLICATION NUMBER: US/11/096,568A  
; CURRENT FILING DATE: 2005-04-01

```

; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 8418
; LENGTH: 573
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(573)
; OTHER INFORMATION: Ceres S
US-11-096-568A-8418

```

Query Match 74.7%; Score 14.2; DB 9; Length 573;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19  
|||  
Db 405 CCTCTGAATGTGGCTCATC 387

RESULT 95  
US-09-925-065A-442742/c  
; Sequence 442742, Application US/09925065A  
; Publication No. US20040181048A1

```

; CURRENT INVENTION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

```

, CURRENT FILING DATE: 2001-08-08
, PRIOR APPLICATION NUMBER: US 60/243,096
, PRIOR FILING DATE: 2000-10-24
, PRIOR APPLICATION NUMBER: US 60/252,147
, PRIOR FILING DATE: 2000-11-20
, PRIOR APPLICATION NUMBER: US 60/250,092
, PRIOR FILING DATE: 2000-11-30
, PRIOR APPLICATION NUMBER: US 60/261,766
, PRIOR FILING DATE: 2001-01-16
, PRIOR APPLICATION NUMBER: US 60/289,846
, PRIOR FILING DATE: 2001-05-09
, NUMBER OF SEQ ID NOS: 957086
, SOFTWARE: FastSeq for Windows Version 4.0
, SEQ ID NO 442742
, LENGTH: 577

```

```

; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-442742

```

```
Query Match          74.7%; Score 14.2; DB 6; Length 577;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 CCCCTGAATCGGCTAATC 19  
Db 60 CCCCCGTATCGGCTACTC 42

RESULT 96  
US-09-925-065A-740537  
; Sequence 740537, Application US/09925065A  
; Publication No. US20040181048A1

/ INFORMATION:  
 / APPLICANT: Wang, David G.  
 / TITLE OF INVENTION: Identification and Mapping of Single  
 / NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME  
 / FILE REFERENCE: 108827.135  
 / CURRENT APPLICATION NUMBER: US/09/925,065A  
 / CURRENT FILING DATE: 2001-08-08  
 / PRIOR APPLICATION NUMBER: US 60/243,096  
 / PRIOR FILING DATE: 2000-10-24  
 / PRIOR APPLICATION NUMBER: US 60/252,147  
 / PRIOR FILING DATE: 2000-11-20

**; PRIOR FILING DATE: 2000-11-20**

```

; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 740537
; LENGTH: 587
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-740537

```

Query Match 74.7%; Score 14.2; DB 6; Length 587;  
Best Local Similarity 84.2%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 3; Indels

QY 1 CCCCTGAATGCGGCTAATC 19  
|||  
Db 313 CCCCTGATTACTGCTAATC 331

RESULT 97  
US-09-925-065A-123839  
; Sequence 123839, Application US/09925065A  
; Publication No. US20040181048A1

```

; CURRENT INVENTION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A

```

```

, , CURRENT FILING DATE: 2001-08-08
, , PRIOR APPLICATION NUMBER: US 60/243,096
, , PRIOR FILING DATE: 2000-10-24
, , PRIOR APPLICATION NUMBER: US 60/252,147
, , PRIOR FILING DATE: 2000-11-20
, , PRIOR APPLICATION NUMBER: US 60/250,092
, , PRIOR FILING DATE: 2000-11-30
, , PRIOR APPLICATION NUMBER: US 60/261,766
, , PRIOR FILING DATE: 2001-01-16
, , PRIOR APPLICATION NUMBER: US 60/289,846
, , PRIOR FILING DATE: 2001-05-09
, , NUMBER OF SEQ ID NOS: 957086
, , SOFTWARE: FastSEQ for Windows Version 4.0
, , SEQ ID NO 123839
, , LENGTH: 592

```

; LENGTH: 392  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-09-925-065A-123839

```
Query Match      74.7%; Score 14.2; DB 6; Length 592;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 CCCCTGAATGCGGCTAATC 19  
|||  
Db 192 CCCCTGAATCCTGGTAATC 210

RESULT 98  
US-09-925-065A-361613/c  
; Sequence 361613, Application US/09925065A  
; Publication No. US20040181048A1

```

1  / CONTACT:
2  /
3  / APPLICANT: Wang, David G.
4  /
5  / TITLE OF INVENTION: Identification and Mapping of Single
6  /
7  / TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
8  /
9  / FILE REFERENCE: 108827.135
10 /
11 / CURRENT APPLICATION NUMBER: US/09/925,065A
12 /
13 / CURRENT FILING DATE: 2001-08-08
14 /
15 / PRIOR APPLICATION NUMBER: US 60/243,096
16 /

```

; PRIOR APPLICATION NUMBER: US 60/243,096

```
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361613
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361613
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 609;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 221 CCCCTGAATCGACTACTC 203
```

```
RESULT 99
US-09-925-065A-361614/c
; Sequence 361614, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 361614
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-361614
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 609;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 221 CCCCTGAATCGACTACTC 203
```

```
RESULT 100
US-09-925-065A-390368/c
; Sequence 390368, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
```

```
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 390368
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-390368
```

```
Query Match 74.7%; Score 14.2; DB 6; Length 648;
Best Local Similarity 84.2%; Pred. No. 2.9e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 232 CCCAGAAAGCGGTTAATC 214
```

```
Search completed: March 9, 2006, 01:18:52
Job time : 428.942 secs
```

GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:12:30 ; Search time 1492.15 Seconds  
(without alignments)  
595.756 Million cell updates/sec

Title: US-10-829-474-1

Perfect score: 19

Sequence: 1 ccctggaatggcgtaatc 19

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

EST:\*

1: gb\_est1:\*

2: gb\_est2:\*

3: gb\_est3:\*

4: gb\_hic:\*

5: gb\_est4:\*

6: gb\_est5:\*

7: gb\_est6:\*

8: gb\_est7:\*

9: gb\_gss1:\*

10: gb\_gss2:\*

11: gb\_gss3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	18	94.7	543	6	CA083939 SCEPAM205
C 2	18	94.7	613	6	CA138671
C 3	18	94.7	631	6	CA187742
C 4	18	94.7	656	6	CA104389
C 5	18	94.7	904	6	CA085581
C 6	17.4	91.6	589	7	CV608160 L AL-aa0
C 7	17	89.5	320	2	BG933318
C 8	17	89.5	392	6	CF771460
C 9	17	89.5	554	2	BG933077
C 10	17	89.5	590	6	CA104476
C 11	17	89.5	645	6	CD429058
C 12	17	89.5	696	1	AW680038
C 13	16.4	86.3	118	10	C2476191
C 14	16.4	86.3	533	9	BH899915
C 15	16.4	86.3	569	6	CA190230
C 16	16.4	86.3	655	8	CA10223
C 17	16.4	86.3	690	6	CA125729
C 18	16.4	86.3	760	5	EX867956
C 19	16.4	86.3	800	10	AG218963
C 20	16.4	86.3	1104	8	DR126636
C 21	16	84.2	485	9	CC751821
C 22	16	84.2	527	10	CL414924

23	16	84.2	547	9	BZ718658
24	16	84.2	595	8	CX698830
25	16	84.2	596	8	CX683834
26	16	84.2	632	8	CX691884
27	16	84.2	675	8	CX557631
28	16	84.2	676	8	CX692600
C 29	16	84.2	784	9	CC751823
C 30	16	84.2	787	9	CC753964
C 31	16	84.2	809	6	CB945315
C 32	16	84.2	838	10	CG038424
C 33	15.8	83.2	262	2	BE000416
C 34	15.8	83.2	300	1	AU176457
C 35	15.8	83.2	361	2	BE405912
C 36	15.8	83.2	417	3	BJ468982
C 37	15.8	83.2	422	3	BJ473149
C 38	15.8	83.2	431	5	BU971174
C 39	15.8	83.2	443	9	AZ233765
C 40	15.8	83.2	456	8	DN183928
C 41	15.8	83.2	463	1	AV932335
C 42	15.8	83.2	472	6	CA657673
C 43	15.8	83.2	487	1	AV774105
C 44	15.8	83.2	494	9	CC472389
C 45	15.8	83.2	511	8	DN183756
C 46	15.8	83.2	513	1	AW585068
C 47	15.8	83.2	525	6	CB884273
C 48	15.8	83.2	525	6	CD026506
C 49	15.8	83.2	544	3	BJ469271
C 50	15.8	83.2	545	11	FR0012843
C 51	15.8	83.2	546	3	BJ479716
C 52	15.8	83.2	564	7	CF992378
C 53	15.8	83.2	564	7	CK037253
C 54	15.8	83.2	568	1	AU249544
C 55	15.8	83.2	569	10	CE815985
C 56	15.8	83.2	570	6	CB212741
C 57	15.8	83.2	572	2	BE403208
C 58	15.8	83.2	574	2	BG907934
C 59	15.8	83.2	579	8	CK625718
C 60	15.8	83.2	581	7	CF954381
C 61	15.8	83.2	584	6	CA255155
C 62	15.8	83.2	597	6	CD876322
C 63	15.8	83.2	598	3	BM135186
C 64	15.8	83.2	601	6	CB680958
C 65	15.8	83.2	602	8	DN178545
C 66	15.8	83.2	627	1	AV933787
C 67	15.8	83.2	631	10	CB312739
C 68	15.8	83.2	636	3	BJ469064
C 69	15.8	83.2	636	6	CB656521
C 70	15.8	83.2	637	6	CB656403
C 71	15.8	83.2	648	3	BJ472488
C 72	15.8	83.2	654	3	BJ469669
C 73	15.8	83.2	659	1	AJ432460
C 74	15.8	83.2	662	1	AV933115
C 75	15.8	83.2	681	6	CA744325
C 76	15.8	83.2	686	6	CD054348
C 77	15.8	83.2	695	3	BJ471067
C 78	15.8	83.2	698	9	BZ008560
C 79	15.8	83.2	700	8	DN178149
C 80	15.8	83.2	713	9	BH516786
C 81	15.8	83.2	716	6	CA240024
C 82	15.8	83.2	749	6	CB662892
C 83	15.8	83.2	777	7	CO033780
C 84	15.8	83.2	778	6	CB659097
C 85	15.8	83.2	786	6	CB624346
C 86	15.8	83.2	790	6	CB657398
C 87	15.8	83.2	795	6	CB648104
C 88	15.8	83.2	796	6	CB624345
C 89	15.8	83.2	800	10	CL746478
C 90	15.8	83.2	810	6	CB655953
C 91	15.8	83.2	825	6	CB656772
C 92	15.8	83.2	834	6	CB657399
C 93	15.8	83.2	851	6	CB663361
C 94	15.8	83.2	861	7	CK156356
C 95	15.8	83.2	868	6	CF819853

C 96	15.8	83.2	876	6	CB680959	CB680959 OSJNEF06J	169	14.8	77.9	245	11	CR346986	CR346986 mte1-80L1
C 97	15.8	83.2	929	6	CF821836	CF821836 EST699218	C 170	14.8	77.9	254	1	AI868751	AI868751 t193b05.x
C 98	15.8	83.2	941	7	CN512233	CN512233 AGENCOURT	C 171	14.8	77.9	259	2	BB572879	BB572879 BB572879.x
C 99	15.8	83.2	994	7	CO010346	CO010346 EST798681	C 172	14.8	77.9	286	1	AI565236	AI565236 th9e12.x
C 100	15.8	83.2	996	2	BE743432	BE743432 601573680	C 173	14.8	77.9	274	1	AI470419	AI470419 t193e04.x
C 101	15.8	83.2	1001	8	CK114637	CK114637 EI090819	C 174	14.8	77.9	277	11	CR331167	CR331167 mte1-6001
C 102	15.8	83.2	1003	7	CK206868	CK206868 FGAS01847	C 175	14.8	77.9	295	1	AV099619	AV099619 AV099619
C 103	15.8	83.2	1024	7	CK206942	CK206942 FGAS01855	C 176	14.8	77.9	321	10	CG632986	CG632986 OST352167
C 104	15.8	83.2	1034	7	CK207162	CK207162 FGAS01878	C 177	14.8	77.9	325	1	AV524455	AV524455 AV524455
C 105	15.8	83.2	1135	3	BQ063512	BQ063512 AGENCOURT	C 178	14.8	77.9	326	8	CA430229	CA430229 JGI_XG661
C 106	15.8	83.2	1220	10	CL648023	CL648023 CH2113-159	C 179	14.8	77.9	328	1	AW137507	AW137507 UI-H-B11-
C 107	15.8	83.2	1261	6	CD254577	CD254577 AGENCOURT	C 180	14.8	77.9	338	7	CN649096	CN649096 EG_PSPGRB
C 108	15.8	83.2	1336	8	CK114889	CK114889 EI092N07	C 181	14.8	77.9	344	11	CR145136	CR145136 Forward s
C 109	15.4	81.1	58	8	DN955356	DN955356 it86e04.g	C 182	14.8	77.9	346	7	CO278514	CO278514 EK130240.
C 110	15.4	81.1	118	9	AZ089499	AZ089499 RPCI-23-4	C 183	14.8	77.9	351	5	EX552579	EX552579 BX552579
C 111	15.4	81.1	170	10	CW191135	CW191135 104_613.1	C 184	14.8	77.9	352	5	AZ892884	AZ892884 RPCI-24-2
C 112	15.4	81.1	284	2	BE144147	BE144147 MRO-HT016	C 185	14.8	77.9	356	4	AK191345	AK191345 Mus muscu
C 113	15.4	81.1	356	10	CG612471	CG612471 OST298727	C 186	14.8	77.9	366	1	AI127566	AI127566 QC21907.x
C 114	15.4	81.1	403	7	CK936592	CK936592 ZGF100452	C 187	14.8	77.9	369	9	AQ088585	AQ088585 HS_2208.B
C 115	15.4	81.1	430	1	AA219175	AA219175 ZG17f01.s	C 188	14.8	77.9	373	8	QX029433	QX029433 1311329.N
C 116	15.4	81.1	442	2	BF858904	BF858904 RCS-F7019	C 189	14.8	77.9	386	1	AI379965	AI379965 tC81b10.x
C 117	15.4	81.1	443	9	BZ183574	BZ183574 CH230-485	C 190	14.8	77.9	389	9	AQ581636	AQ581636 RPCI-11-4
C 118	15.4	81.1	445	7	CN955933	CN955933 3433_106-	C 191	14.8	77.9	396	8	DN022665	DN022665 JGI_CAA83
C 119	15.4	81.1	450	11	DE056529	DE056529 OryZias 1	C 192	14.8	77.9	405	1	AI900384	AI900384 sc05a05.Y
C 120	15.4	81.1	461	5	BY543692	BY543692	C 193	14.8	77.9	411	10	CG599934	CG599934 OST268024
C 121	15.4	81.1	490	3	BP392262	BP392262	C 194	14.8	77.9	417	11	CR323965	CR323965 mte1-50N1
C 122	15.4	81.1	509	9	CE222506	CE222506 tigr-g88-	C 195	14.8	77.9	421	1	AI951548	AI951548 w36e06.x
C 123	15.4	81.1	568	7	CN124698	CN124698 RHOH1_6.H	C 196	14.8	77.9	421	9	CC763600	CC763600 CH240_4D1
C 124	15.4	81.1	640	8	CF442258	CF442258 EST678603	C 197	14.8	77.9	423	9	BH250888	BH250888 SALK_0106
C 125	15.4	81.1	690	8	DR786856	DR786856 ZM_BF0000	C 198	14.8	77.9	427	7	CO343135	CO343135 EP16153.3
C 126	15.4	81.1	691	7	CK937081	CK937081 CGF100451	C 199	14.8	77.9	431	1	AA808971	AA808971 nv19c02.x
C 127	15.4	81.1	692	1	AI873533	AI873533 wf84e03.x	C 200	14.8	77.9	435	3	BJ636421	BJ636421 BJ636421
C 128	15.4	81.1	717	9	CE174112	CE174112 tigr-g88-	C 201	14.8	77.9	437	7	CK676629	CK676629 ZF101-P00
C 129	15.4	81.1	746	6	CF447698	CF447698	C 202	14.8	77.9	439	5	BU381184	BU381184 B53582009
C 130	15.4	81.1	747	6	CF445823	CF445823 EST682168	C 203	14.8	77.9	439	5	BY188842	BY188842 BY188842
C 131	15.4	81.1	760	10	AG556749	AG556749 Mus muscu	C 204	14.8	77.9	441	1	AW134718	AW134718 UI-H-B11-
C 132	15.4	81.1	761	6	CF342050	CF342050 AGENCOURT	C 205	14.8	77.9	447	1	AU178612	AU178612 AU178612
C 133	15.4	81.1	854	7	CO033897	CO033897 EST812281	C 206	14.8	77.9	452	1	AI128330	AI128330 QC60h02.x
C 134	15.4	81.1	866	5	BQ704899	BQ704899 Bnol_01a2	C 207	14.8	77.9	452	1	AI148787	AI148787 QC59a09.x
C 135	15.4	81.1	872	7	CN171518	CN171518 AGENCOURT	C 208	14.8	77.9	457	5	BU738428	BU738428 UI-E-EU0-
C 136	15.4	81.1	893	6	CF548005	CF548005 AGENCOURT	C 209	14.8	77.9	459	1	AI088714	AI088714 Qa12d02.x
C 137	15.4	81.1	965	11	CNS03KTI	AL248607 Tetradon	C 210	14.8	77.9	461	2	BI135594	BI135594 F055P20Y
C 138	15.4	81.1	1008	3	BQ050772	BQ050772 AGENCOURT	C 211	14.8	77.9	464	5	BX097947	BX097947 BX097947
C 139	15.4	81.1	1022	10	CL036098	CL036098 CH216-400	C 212	14.8	77.9	465	1	AI097552	AI097552 Qa04f09.x
C 140	15.4	81.1	1039	11	CNS039HQ	AL233927 Tetradon	C 213	14.8	77.9	467	9	AQ261983	AQ261983 CITBI-E1-
C 141	15.4	81.1	1068	3	EN479812	EN479812 AGENCOURT	C 214	14.8	77.9	478	1	AI970702	AI970702 w13e02.x
C 142	15.4	81.1	1102	11	CNS038R1	AL232966 Tetradon	C 215	14.8	77.9	478	2	BF461068	BF461068 UI-M-CG0p
C 143	15.4	81.1	1405	2	BE730376	BE730376 601563816	C 216	14.8	77.9	479	9	AQ126088	AQ126088 HS_3036.A
C 144	15.4	81.1	333	9	BZ661537	BZ661537 SALK_0250	C 217	14.8	77.9	482	1	AI779679	AI779679 AL779679
C 145	15.4	81.1	375	7	CK095952	CK095952 UA38BPA09	C 218	14.8	77.9	482	10	CE730627	CE730627 tigr-g88-
C 146	15.4	81.1	410	10	AG970375	AG970375 Drosophila	C 219	14.8	77.9	487	9	AQ927923	AQ927923 RPCI-23-2
C 147	15.4	81.1	420	8	R92106	R92106 YP96d10.s1	C 220	14.8	77.9	488	10	CL682161	CL682161 PRI0133a_
C 148	15.4	81.1	467	6	CE714157	CE714157 AGNNUC:N	C 221	14.8	77.9	490	1	AI740562	AI740562 wgl6g06.x
C 149	15.4	81.1	512	1	AW735958	AW735958 EST336726	C 222	14.8	77.9	492	1	AA494514	AA494514 ne36h05.s
C 150	15.4	81.1	560	1	AJ2808629	AJ2808629	C 223	14.8	77.9	498	2	BI244282	BI244282 EG_PSPGR
C 151	15.4	81.1	593	10	CL739566	CL739566 OR_BBa007	C 224	14.8	77.9	498	7	CN650536	CN650536 EG_PSPGRS
C 152	15.4	81.1	598	3	BQ116146	BQ116146 EST601722	C 225	14.8	77.9	512	10	CE634654	CE634654 tigr-g88-
C 153	15.4	81.1	617	1	AV403771	AV403771	C 226	14.8	77.9	516	6	CA350143	CA350143 C20809 NC
C 154	15.4	81.1	661	3	BI960063	BI960063 HVS03771	C 227	14.8	77.9	526	7	CF834215	CF834215 UCROS02.0
C 155	15.4	81.1	672	1	AJ793847	AJ793847	C 228	14.8	77.9	531	10	AG960099	AG960099 Drosophila
C 156	15.4	81.1	759	6	CB166956	CB166956 BTU602600	C 229	14.8	77.9	533	9	AQ573912	AQ573912 nbx00803C
C 157	15.4	81.1	801	10	CL662642	CL662642 PRI0142a_	C 230	14.8	77.9	536	1	AA778220	AA778220 z19e09.s
C 158	15.4	81.1	824	10	CL662642	CL662642 PRI0158a_	C 231	14.8	77.9	537	1	AI922821	AI922821 woi4d06.x
C 159	15.4	81.1	835	7	CO564696	CO564696 AGENCOURT	C 232	14.8	77.9	537	1	AW202789	AW202789 f122C04.Y
C 160	15.4	81.1	838	7	CO567950	CO567950 AGENCOURT	C 233	14.8	77.9	538	9	AZ409425	AZ409425 IM0181J01
C 161	15.4	81.1	858	10	CZ321096	CZ321096 ZMMBF0023	C 234	14.8	77.9	539	1	AI971512	AI971512 wr05e07.x
C 162	15.4	81.1	902	9	AZ203580	AZ203580 SP_0081.B	C 235	14.8	77.9	542	10	BA242053	BA242053 Danio rer
C 163	15.4	81.1	990	1	AV110510	AV110510	C 236	14.8	77.9	542	11	TX310F02P	TX310F02P
C 164	15.4	81.1	1013	2	BF973291	BF973291 602242213	C 237	14.8	77.9	543	2	BE667658	BE667658 T_brucei
C 165	15.4	81.1	1069	3	BI551860	BI551860 603192766	C 238	14.8	77.9	543	9	AZ258291	AZ258291 RPCI-23-1
C 166	15.4	81.1	1164	3	CC185536	CC185536 CH261-129	C 239	14.8	77.9	544	1	AJ711286	AJ711286
C 167	14.8	77.9	41	9	AZ411946	AZ411946 IM0185009	C 240	14.8	77.9	545	1	AL785793	AL785793
C 168	14.8	77.9	175	9	CC795725	CC795725 SALK_0880	C 241	14.8	77.9	546	10	CE723160	CE723160 tigr-g88-



242	14.8	77.9	547	9	AZ955764	2M0222D04	AZ955764	2M0222D04	14.8	77.9	740	9	BZ278712	CH230-451
243	14.8	77.9	555	7	CN694663	CN694663	CN694663	CN694663	14.8	77.9	741	10	CL795448	OR_CBA000
244	14.8	77.9	556	8	CN988204	IPCGFR1.1	CN988204	IPCGFR1.1	14.8	77.9	742	9	CE029972	tigr-g98-
245	14.8	77.9	563	3	AZ055596	RPCI-23-4	AZ055596	RPCI-23-4	14.8	77.9	747	5	BX700997	KX700997
246	14.8	77.9	565	3	BJ059717	BJ059717	BJ059717	BJ059717	14.8	77.9	747	7	CV512284	KB2a08.Y
247	14.8	77.9	566	3	BJ070137	BJ070137	BJ070137	BJ070137	14.8	77.9	747	8	CV474314	JGI_X2G49
248	14.8	77.9	567	1	A1935287	wp16d12.x	A1935287	wp16d12.x	14.8	77.9	748	8	AQ156029	ndx500021
249	14.8	77.9	572	8	DT006298	VVG032F10	DT006298	VVG032F10	14.8	77.9	748	9	DN023695	JGI_CAAAR4
250	14.8	77.9	580	6	CB110278	K-EST0151	CB110278	K-EST0151	14.8	77.9	749	7	DN597221	AGENCOURT
251	14.8	77.9	582	1	AV599249	AV599249	AV599249	AV599249	14.8	77.9	750	9	CC003285	PUECT95TD
252	14.8	77.9	584	10	AG926251	Drosophil	AG926251	Drosophil	14.8	77.9	752	8	CV411312	JGI_XZT28
253	14.8	77.9	586	10	AG923374	Drosophil	AG923374	Drosophil	14.8	77.9	753	10	CL851044	OR_CBA007
254	14.8	77.9	588	7	CK131326	CH20621.3	CK131326	CH20621.3	14.8	77.9	754	10	AG562056	Mus muscu
255	14.8	77.9	589	8	DT006327	VVG033A04	DT006327	VVG033A04	14.8	77.9	755	10	CL846860	OR_CBA007
256	14.8	77.9	595	7	CN650665	CE535032	CN650665	CE535032	14.8	77.9	760	8	DN023695	JGI_CAAAR4
257	14.8	77.9	598	10	CE535032	tigr-g98-	CE535032	tigr-g98-	14.8	77.9	763	8	DN023694	JGI_CAAAR4
258	14.8	77.9	599	9	AZ291021	RPCI-23-1	AZ291021	RPCI-23-1	14.8	77.9	764	9	BZ372626	ie63h07.b
259	14.8	77.9	600	10	AG924507	Drosophil	AG924507	Drosophil	14.8	77.9	766	9	BZ773948	mcv82h11.
260	14.8	77.9	603	10	CL266204	PHCRC-GT-	CL266204	PHCRC-GT-	14.8	77.9	766	10	AG480043	Mus muscu
261	14.8	77.9	610	8	DT008426	VVG055F04	DT008426	VVG055F04	14.8	77.9	770	8	CV829104	JGI_CAAK6
262	14.8	77.9	617	5	CA012931	HT06004r	CA012931	HT06004r	14.8	77.9	775	5	BX105784	BX105784
263	14.8	77.9	620	9	CT720334	CH240.7J1	CT720334	CH240.7J1	14.8	77.9	778	2	BG916759	BG916759
264	14.8	77.9	621	7	CK968614	4084150.B	CK968614	4084150.B	14.8	77.9	783	1	AT1517505	AT1517505
265	14.8	77.9	622	10	CK968614	4084150.B	CK968614	4084150.B	14.8	77.9	783	5	BM963551	BM963551
266	14.8	77.9	623	6	CB111276	K-EST0152	CB111276	K-EST0152	14.8	77.9	783	9	BM963551	BM963551
267	14.8	77.9	623	10	CL621457	UI-H-ED1-	CL621457	UI-H-ED1-	14.8	77.9	783	9	BM963551	BM963551
268	14.8	77.9	634	1	A1513338	GH26511.5	A1513338	GH26511.5	14.8	77.9	783	9	BM963551	BM963551
269	14.8	77.9	634	3	BQ173414	EG_PSGR.0	BQ173414	EG_PSGR.0	14.8	77.9	783	9	BM963551	BM963551
270	14.8	77.9	639	3	BQ241771	Ta050001A	BQ241771	Ta050001A	14.8	77.9	783	9	BM963551	BM963551
271	14.8	77.9	640	8	CK370623	JGI_XZT55	CK370623	JGI_XZT55	14.8	77.9	783	9	BM963551	BM963551
272	14.8	77.9	641	1	AV274320	AV274320	AV274320	AV274320	14.8	77.9	783	9	BM963551	BM963551
273	14.8	77.9	646	5	BX773414	BX773414	BX773414	BX773414	14.8	77.9	783	9	BM963551	BM963551
274	14.8	77.9	648	1	A1055707	coau0004N	A1055707	coau0004N	14.8	77.9	783	9	BM963551	BM963551
275	14.8	77.9	648	8	CK341808	JGI_XZT46	CK341808	JGI_XZT46	14.8	77.9	783	9	BM963551	BM963551
276	14.8	77.9	649	8	CK345863	JGI_XZT43	CK345863	JGI_XZT43	14.8	77.9	783	9	BM963551	BM963551
277	14.8	77.9	651	5	BU625080	UI-H-FGI-	BU625080	UI-H-FGI-	14.8	77.9	783	9	BM963551	BM963551
278	14.8	77.9	651	9	AZ955752	UI-H-FGI-	AZ955752	UI-H-FGI-	14.8	77.9	783	9	BM963551	BM963551
279	14.8	77.9	651	10	AG047975	Pan trogl	AG047975	Pan trogl	14.8	77.9	783	9	BM963551	BM963551
280	14.8	77.9	652	2	BS35557	BS35557	BS35557	BS35557	14.8	77.9	783	9	BM963551	BM963551
281	14.8	77.9	655	10	CL570964	OB_Ba000	CL570964	OB_Ba000	14.8	77.9	783	9	BM963551	BM963551
282	14.8	77.9	656	3	BM984775	UI-CF-EC1	BM984775	UI-CF-EC1	14.8	77.9	783	9	BM963551	BM963551
283	14.8	77.9	658	6	CA307182	UI-H-F1-	CA307182	UI-H-F1-	14.8	77.9	783	9	BM963551	BM963551
284	14.8	77.9	659	8	CA411311	JGI_XZT28	CA411311	JGI_XZT28	14.8	77.9	783	9	BM963551	BM963551
285	14.8	77.9	661	3	BI604028	BI604028	BI604028	BI604028	14.8	77.9	783	9	BM963551	BM963551
286	14.8	77.9	661	5	BM689223	UI-CF-EC1	BM689223	UI-CF-EC1	14.8	77.9	783	9	BM963551	BM963551
287	14.8	77.9	662	9	AO644975	RPCI93-Dp	AO644975	RPCI93-Dp	14.8	77.9	783	9	BM963551	BM963551
288	14.8	77.9	664	9	BH738406	BOMQ35TR	BH738406	BOMQ35TR	14.8	77.9	783	9	BM963551	BM963551
289	14.8	77.9	677	10	CZ700617	OC_Ba001	CZ700617	OC_Ba001	14.8	77.9	783	9	BM963551	BM963551
290	14.8	77.9	680	6	CA446467	UI-H-ED1-	CA446467	UI-H-ED1-	14.8	77.9	783	9	BM963551	BM963551
291	14.8	77.9	680	10	CE402740	tigr-g98-	CE402740	tigr-g98-	14.8	77.9	783	9	BM963551	BM963551
292	14.8	77.9	682	10	CM158168	104.561.1	CM158168	104.561.1	14.8	77.9	783	9	BM963551	BM963551
293	14.8	77.9	683	10	CE815010	tigr-g98-	CE815010	tigr-g98-	14.8	77.9	783	9	BM963551	BM963551
294	14.8	77.9	692	10	CL596795	OB_Ba005	CL596795	OB_Ba005	14.8	77.9	783	9	BM963551	BM963551
295	14.8	77.9	696	7	CN604421	USDA_FP.1	CN604421	USDA_FP.1	14.8	77.9	783	9	BM963551	BM963551
296	14.8	77.9	696	7	CR580529	CR580529	CR580529	CR580529	14.8	77.9	783	9	BM963551	BM963551
297	14.8	77.9	697	10	AG298311	Mus muscu	AG298311	Mus muscu	14.8	77.9	783	9	BM963551	BM963551
298	14.8	77.9	698	1	A1387486	GHI8030.5	A1387486	GHI8030.5	14.8	77.9	783	9	BM963551	BM963551
299	14.8	77.9	699	9	B2165108	CH230-377	B2165108	CH230-377	14.8	77.9	783	9	BM963551	BM963551
300	14.8	77.9	702	7	CV508738	kc75g01.Y	CV508738	kc75g01.Y	14.8	77.9	783	9	BM963551	BM963551
301	14.8	77.9	702	10	CL852151	OR_CBA008	CL852151	OR_CBA008	14.8	77.9	783	9	BM963551	BM963551
302	14.8	77.9	705	9	BH928557	odi77a01.	BH928557	odi77a01.	14.8	77.9	783	9	BM963551	BM963551
303	14.8	77.9	706	9	BH979064	ode71e06.	BH979064	ode71e06.	14.8	77.9	783	9	BM963551	BM963551
304	14.8	77.9	709	6	CF133289	WHE4356.C	CF133289	WHE4356.C	14.8	77.9	783	9	BM963551	BM963551
305	14.8	77.9	712	7	CK797340	AGENCOURT	CK797340	AGENCOURT	14.8	77.9	783	9	BM963551	BM963551
306	14.8	77.9	715	7	CK714313	ZF201-P00	CK714313	ZF201-P00	14.8	77.9	783	9	BM963551	BM963551
307	14.8	77.9	722	8	CK418682	JGI_XZG65	CK418682	JGI_XZG65	14.8	77.9	783	9	BM963551	BM963551
308	14.8	77.9	725	10	CL909579	OR_ABA000	CL909579	OR_ABA000	14.8	77.9	783	9	BM963551	BM963551
309	14.8	77.9	726	7	CR373915	CR373915	CR373915	CR373915	14.8	77.9	783	9	BM963551	BM963551
310	14.8	77.9	727	9	BH962522	odi48e10.	BH962522	odi48e10.	14.8	77.9	783	9	BM963551	BM963551
311	14.8	77.9	730	8	DN898422	nap33c01.	DN898422	nap33c01.	14.8	77.9	783	9	BM963551	BM963551
312	14.8	77.9	732	10	CL765009	OR_BBa013	CL765009	OR_BBa013	14.8	77.9	783	9	BM963551	BM963551
313	14.8	77.9	737	7	CN055457	Salamande	CN055457	Salamande	14.8	77.9	783	9	BM963551	BM963551
314	14.8	77.9	738	7	CR565974	CR565974	CR565974	CR565974	14.8	77.9	783	9	BM963551	BM963551

388	14.8	77.9	975	5	BU911821	BU911821 AGENCOURT	461	14.4	75.8	539	1	AL925630	AL925630 AL925630
389	14.8	77.9	977	10	AG867779	AG867779 Oryza sat	462	14.4	75.8	541	6	CD569927	CD569927 EESTeg02
390	14.8	77.9	988	10	CZ995518	CZ995518 183868 To	C 463	14.4	75.8	543	3	BJ012157	BJ012157 EEST02157
391	14.8	77.9	1012	10	CL099115	CL099115 ISB1-32E3	C 464	14.4	75.8	547	3	BI999130	BI999130 1031070H0
392	14.8	77.9	1028	9	BH17566	BH17566 BOMV03TR	C 465	14.4	75.8	549	2	BE758836	BE758836 an_3084 A
C 393	14.8	77.9	1050	8	DN783532	DN783532 93003109	C 466	14.4	75.8	550	3	BJ873867	BJ873867 EEST33A02
C 394	14.8	77.9	1055	10	CL285172	CL285172 ZNMVBB062	C 467	14.4	75.8	550	6	CD972535	CD972535 QAE23A02
C 395	14.8	77.9	1061	9	CC307774	CC307774 TAM32-18J	C 468	14.4	75.8	556	6	CA071040	CA071040 SCCAM100
C 396	14.8	77.9	1064	11	CNS048WA	AL279811 Tetradon	C 469	14.4	75.8	560	1	AW967194	AW967194 EEST379268
397	14.8	77.9	1067	10	CNS00AKJ	AL056061 Drosophill	470	14.4	75.8	561	6	CB968362	CB968362 EEST8773
398	14.8	77.9	1078	11	CNS05FRL	AL335370 Tetradon	471	14.4	75.8	561	6	CD974000	CD974000 QAE40011
C 399	14.8	77.9	1101	10	CNS00G56	AL071448 Drosophill	C 472	14.4	75.8	562	10	CL517190	CL517190 PHCRC-GT-
C 400	14.8	77.9	1101	10	CNS014YR	AL104781 Drosophill	C 473	14.4	75.8	567	9	AQ307864	AQ307864 HS_2199_A
401	14.8	77.9	1103	8	DN663574	DN663574 CPW14-F07	C 474	14.4	75.8	567	11	DE046845	DE046845 Oryzias 1
402	14.8	77.9	1156	8	DR046133	DR046133 FP-9 F08.	C 475	14.4	75.8	573	6	CD974157	CD974157 QAE42410
403	14.8	77.9	1171	8	DR046059	DR046059 FP-8 F06.	476	14.4	75.8	575	2	BF895320	BF895320 IL0-WT021
404	14.8	77.9	1203	3	BQ277749	BQ277749 AGENCOURT	477	14.4	75.8	577	3	BI577998	BI577998 RET1785.5
405	14.8	77.9	1226	9	CC200990	CC200990 CH261-134	478	14.4	75.8	586	6	CA172813	CA172813 SCUTS103
406	14.8	77.9	1378	8	DN676524	DN676524 CPW93-A09	479	14.4	75.8	594	6	CF818827	CF818827 EEST69209
407	14.8	77.9	1388	5	BU150187	BU150187 AGENCOURT	480	14.4	75.8	599	9	CC956935	CC956935 BOIFP29TR
408	14.8	77.9	1452	8	DN659817	DN659817 CEC43-B10	481	14.4	75.8	601	7	CO443223	CO443223 MZCCL1006
409	14.8	77.9	1461	4	AK087319	AK087319 Mus muscu	482	14.4	75.8	603	10	CW063436	CW063436 104_309_1
410	14.8	77.9	2075	4	AK009193	AK009193 Mus muscu	483	14.4	75.8	604	10	CW458000	CW458000 EED5001F2
C 411	14.8	77.9	2181	4	AK081300	AK081300 Mus muscu	484	14.4	75.8	605	5	BM441235	BM441235 BM441235
C 412	14.8	77.9	2314	4	AK089301	AK089301 Mus muscu	485	14.4	75.8	605	11	DE049603	DE049603 Oryzias 1
C 413	14.8	77.9	2853	10	CL949051	CL949051 OsIFSB002	486	14.4	75.8	607	6	CB408128	CB408128 IPG001C02
C 414	14.8	77.9	3859	4	AK031340	AK031340 Mus muscu	C 487	14.4	75.8	607	10	CW284148	CW284148 104_760_1
415	14.8	77.9	4347	4	AK019848	AK019848 Mus muscu	488	14.4	75.8	614	6	CD346201	CD346201 EEST8790
416	14.8	77.9	4864	4	CR858274	CR858274 Pongo pyg	489	14.4	75.8	615	8	AX744084	AX744084 JGI_ANNB1
417	14.4	75.8	143	8	DN361287	DN361287 LIB3627-0	C 490	14.4	75.8	616	1	AI757288	AI757288 EESTeal14
C 418	14.4	75.8	154	1	AW849369	AW849369 IL3-CT021	491	14.4	75.8	623	10	CW784399	CW784399 SP_Bb001
C 419	14.4	75.8	185	10	CW100072	CW100072 104_467_1	492	14.4	75.8	627	8	DT012847	DT012847 VWH044F06
C 420	14.4	75.8	284	10	CL229038	CL229038 ZNMVBB014	C 493	14.4	75.8	629	7	CV670071	CV670071 LCPE04EX0
C 421	14.4	75.8	287	6	CD154501	CD154501 MLI-0036T	C 494	14.4	75.8	631	11	DE066977	DE066977 Oryzias 1
C 422	14.4	75.8	302	6	CD140350	CD140350 MGI-0067G	495	14.4	75.8	632	9	AZ246131	AZ246131 RPI1-23-1
423	14.4	75.8	302	6	CD196399	CD196399 MSI-0094G	C 496	14.4	75.8	633	7	CO596495	CO596495 DGB-128j1
C 424	14.4	75.8	306	6	CB636844	CB636844 OSJNEA02M	C 497	14.4	75.8	634	11	CR130872	CR130872 Forward s
C 425	14.4	75.8	325	1	AA786371	AA786371 15a03a1.f	498	14.4	75.8	635	1	AU261149	AU261149 AU261149
C 426	14.4	75.8	335	8	H51561	H51561 yo34a03.a1	499	14.4	75.8	635	6	CA179372	CA179372 SCSGST107
C 427	14.4	75.8	367	1	AA113768	AA113768 zn65906.s	500	14.4	75.8	637	10	CW149115	CW149115 104_548_1
428	14.4	75.8	372	1	AW955727	AW955727 EEST37797							
429	14.4	75.8	396	9	AQ027634	AQ027634 CIT-HSP-2							
430	14.4	75.8	399	1	AU069063	AU069063 AU069063							
431	14.4	75.8	410	6	CB803847	CB803847 AMGNNUC-S							
432	14.4	75.8	418	2	BF588142	BF588142 PMI_38_CO							
C 433	14.4	75.8	423	10	CG955510	CG955510 MBEGK35TR							
434	14.4	75.8	434	9	AQ697140	AQ697140 HS_5528_A							
C 435	14.4	75.8	435	3	BP895692	BP895692 BP895692							
C 436	14.4	75.8	437	1	AA271056	AA271056 va85e09.r							
C 437	14.4	75.8	443	10	CW185416	CW185416 104_503_1							
C 438	14.4	75.8	449	1	AU179238	AU179238 AU179238							
C 439	14.4	75.8	456	3	BU054677	BU054677 BU054677							
C 440	14.4	75.8	458	1	AI327661	AI327661 e0f12a1.f							
441	14.4	75.8	459	5	C82870	C82870 C82870 rabb							
C 442	14.4	75.8	459	5	CB3726	CB3726 C83726 rabb							
C 443	14.4	75.8	463	9	BA1428	BA1428 HS-1053-B1-							
C 444	14.4	75.8	466	1	AA784934	AA784934 g3s04a1.f							
445	14.4	75.8	467	9	BZ177144	BZ177144 CH230-397							
446	14.4	75.8	472	11	CNS03K2R	AL247644 Tetradon							
447	14.4	75.8	475	9	AQ412625	AQ412625 RPI1-11-1							
448	14.4	75.8	478	2	BB700363	BB700363 BB700363							
C 449	14.4	75.8	496	10	AG967565	AG967565 Drosophill							
C 450	14.4	75.8	500	3	BU007823	BU007823 BU007823							
C 451	14.4	75.8	500	9	BZ12180	BZ12180 CH230-461							
C 452	14.4	75.8	515	3	BM481442	BM481442 533681 MA							
C 453	14.4	75.8	519	6	CD077371	CD077371 MA3-0001U							
454	14.4	75.8	519	9	AZ193345	AZ193345 SP_1023_A							
455	14.4	75.8	526	6	CB719879	CB719879 AMGNNUC-U							
C 456	14.4	75.8	533	3	BI672125	BI672125 ft34h02.x							
C 457	14.4	75.8	534	6	CD192055	CD192055 MSI-0074T							
C 458	14.4	75.8	534	6	CD192084	CD192084 MSI-0074T							
459	14.4	75.8	535	8	CX455630	CX455630 JGI_XZG53							
C 460	14.4	75.8	536	5	BQ804135	BQ804135 PTAEST198							

## ALIGNMENTS

RESULT 1	CA083939	543 bp	linear	EST 23-SEP-2003
CA083939/c	SCEPAM2056D03.g	AM2 Saccharum officinarum	cdna clone SCEPAM2056D03	
LOCUS	5', mRNA sequence.			
DEFINITION	CA083939	543 bp	linear	EST 23-SEP-2003
ACCESSION	CA083939	543 bp	linear	EST 23-SEP-2003
VERSION	CA083939.1	GI:34937250		
KEYWORDS	EST.			
SOURCE	Saccharum officinarum			
ORGANISM	Saccharum officinarum			
REFERENCE	1 (bases 1 to 543)			
AUTHORS	Vettore A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.			
TITLE	The libraries that made SUCST			
JOURNAL	Genet. Mol. Biol. 24 (1-4), 1-7 (2001)			
COMMENT	Contact: Arruda P			
	Centro de Biologia Molecular e Engenharia Genetica			
	Universidade Estadual de Campinas			
	Caixa Postal 6010, 13083-970, Campinas SP, Brazil			
	Tel: 55 19 3788 1137			
	Fax: 55 19 3788 1089			
	Email: parruda@unicamp.br			
	Clome distribution: Clome distribution information can be found			
	through the Brazilian Clome Collection Center (BCCC) at			
	http://www.bccccenter.fcav.unesp.br			

Plate: 056 row: D column: 03  
Seq primer: T7 Promoter Primer.

# FEATURES

source  
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/clone="SCBPM2056D03"  
/lab\_host="DH10B"  
/clone\_lib="AM2"

/note="Organ: Apical meristem and tissues surrounding of immature plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Apical meristem and tissues surrounding of immature plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

## ORIGIN

Query Match 94.7%; Score 18; DB 6; Length 543;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

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Db 256 CCCTGAATGCGGCTAATC 239

## RESULT 2

CA138671

LOCUS

DEFINITION SCQR2029D06.g RT2 Saccharum officinarum cDNA clone SCEQR2029D06  
5', mRNA sequence.

ACCESSION CA138671

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 613)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

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Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1. .613

/organism="Saccharum officinarum"

/mol\_type="mRNA"

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/lab\_host="DH10B"

/clone\_lib="RT2"

/note="Organ: Root tips (0.3cm-long) from adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Root

tips (0.3cm-long) from adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Query Match 94.7%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

|||||  
Db 490 CCCTGAATGCGGCTAATC 507

RESULT 3

CA187742/c

LOCUS

DEFINITION SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04  
5', mRNA sequence.

ACCESSION CA187742

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 631)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

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Fax: 55 19 3788 1089

Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1. .631

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

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/lab\_host="DH10B"

/clone\_lib="ST3"

/note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Query Match 94.7%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

|||||  
Db 490 CCCTGAATGCGGCTAATC 507

RESULT 3

CA187742/c

LOCUS

DEFINITION SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04  
5', mRNA sequence.

ACCESSION CA187742

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 631)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1. .631

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/mol\_type="mRNA"

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/lab\_host="DH10B"

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/note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Query Match 94.7%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

|||||  
Db 490 CCCTGAATGCGGCTAATC 507

RESULT 3

CA187742/c

LOCUS

DEFINITION SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04  
5', mRNA sequence.

ACCESSION CA187742

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 631)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

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Fax: 55 19 3788 1089

Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1. .631

/organism="Saccharum officinarum"

/mol\_type="mRNA"

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/clone="SCUTST3130H04"

/lab\_host="DH10B"

/clone\_lib="ST3"

/note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Query Match 94.7%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

|||||  
Db 490 CCCTGAATGCGGCTAATC 507

RESULT 3

CA187742/c

LOCUS

DEFINITION SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04  
5', mRNA sequence.

ACCESSION CA187742

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 631)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

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Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: [parruda@unicamp.br](mailto:parruda@unicamp.br)

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>

Seq primer: T7 Promoter Primer.

Location/Qualifiers

FEATURES

source

1. .631

/organism="Saccharum officinarum"

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/lab\_host="DH10B"

/clone\_lib="ST3"

/note="Organ: Fourth apical stalk internodes of adult plants; Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Fourth apical stalk internodes of adult plants]. cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

Query Match 94.7%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CCCTGAATGCGGCTAATC 19

|||||  
Db 490 CCCTGAATGCGGCTAATC 507

RESULT 3

CA187742/c

LOCUS

DEFINITION SCUTST3130H04.g ST3 Saccharum officinarum cDNA clone SCUTST3130H04  
5', mRNA sequence.

ACCESSION CA187742

VERSION

KEYWORDS

SOURCE

ORGANISM

Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE 1 (bases 1 to 631)

Authors Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Title The libraries that made SUCEST

Journal Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Comment Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade

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QY      2  CCCTGAATGCGGCTAATC 19
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RESULT 4
CA104389/c
LOCUS   CA104389
DEFINITION SCJFHR1033A07.g HR1 Saccharum officinarum cDNA clone SCJFHR1033A07
5', mRNA sequence.
ACCESSION CA104389
VERSION   CA104389.1 GI:34957696
KEYWORDS EST.
SOURCE   Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE   The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 033 row: A column: 07
Seq primer: T7 Promoter Primer.
Location/Qualifiers
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rubrisubalbicans; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspizilum
rubrisubalbicans]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 94.7%; Score 18; DB 6; Length 656;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CCCTGAATGCGGCTAATC 19
Db      525 CCCTGAATGCGGCTAATC 542

RESULT 6
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LOCUS   CV608160
DEFINITION L_AL-aaa07f02.b1 Hc6AS_M Ajellomyces capsulatus cDNA 3', mRNA
sequence.
ACCESSION CV608160
VERSION   CV608160.1 GI:54595742
KEYWORDS EST.
SOURCE   Ajellomyces capsulatus
ORGANISM Ajellomyces capsulatus

REFERENCE
AUTHORS Rukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE   Onygenales; Ajellomycetaceae; Ajellomyces.
JOURNAL 1 (bases 1 to 589)
COMMENT Magrini,V., Sil,A., Goldman,W. and Mardis,R.
Genomic Resources for Histoplasma Sequencing Mardis/WashU
Histoplasma capsulatum Sequencing Project
Unpublished (2004)
Contact: Vincent Magrini
Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
Washington University School of Medicine

QY      2  CCCTGAATGCGGCTAATC 19
Db      269 CCCTGAATGCGGCTAATC 252

RESULT 5
CA085581
LOCUS   CA085581
DEFINITION SCULAM2093D05.b AM2 Saccharum officinarum cDNA clone SCULAM2093D05
3', mRNA sequence.
ACCESSION CA085581
VERSION   CA085581.1 GI:34938888

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KEYWORDS EST.
SOURCE   Saccharum officinarum
ORGANISM Saccharum officinarum

REFERENCE
1 (bases 1 to 904)
Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 093 row: D column: 05
Seq primer: SP6 Promoter primer.
Location/Qualifiers
FEATURES
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1. 904
/organism="Saccharum officinarum"
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/clone="SCJLAM2093D05"
/lab_host="DH10B"
/clone_lib="AM2"
/note="Organ: Apical meristem and tissues surrounding of
immature plants; Vector: pSport1; Site_1: SalI; Site_2:
NotI; An unidirectional cDNA library generated from
[Apical meristem and tissues surrounding of immature
plants]. cDNA was prepared from polyA+ mRNA using
SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match 94.7%; Score 18; DB 6; Length 904;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2  CCCTGAATGCGGCTAATC 19
Db      525 CCCTGAATGCGGCTAATC 542

RESULT 6
CV608160
LOCUS   CV608160
DEFINITION L_AL-aaa07f02.b1 Hc6AS_M Ajellomyces capsulatus cDNA 3', mRNA
sequence.
ACCESSION CV608160
VERSION   CV608160.1 GI:54595742
KEYWORDS EST.
SOURCE   Ajellomyces capsulatus
ORGANISM Ajellomyces capsulatus

REFERENCE
AUTHORS Rukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
TITLE   Onygenales; Ajellomycetaceae; Ajellomyces.
JOURNAL 1 (bases 1 to 589)
COMMENT Magrini,V., Sil,A., Goldman,W. and Mardis,R.
Genomic Resources for Histoplasma Sequencing Mardis/WashU
Histoplasma capsulatum Sequencing Project
Unpublished (2004)
Contact: Vincent Magrini
Mardis/Goldman/Sil Genomic Resources for Histoplasma Sequencing
Washington University School of Medicine

```

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: vmagrini@watson.wustl.edu  
 Contact Vincent Magrini (vmagrini@watson.wustl.edu) for further  
 information relating to organism, libraries, or clone availability.  
 Seq primer: M13 reverse.

## FEATURES

source

Location/Qualifiers

1. .589  
 /organism="Ajellomyces capsulatus"  
 /mol\_type="mRNA"

/strain="G186A-S"

/db\_xref="taxon:5037"

/dev\_stage="Mycelia"

/lab\_host="GC10"

/clone\_lib="Hc6AS M"

/note="Vector: PCR4-TOPO; Site 1: EcoRI flanks TA cloning  
 site; Site 2: EcoRI flanks TA cloning site; polyA mRNA was  
 captured with oligo d(T) magnetic beads and eluted.  
 AAGCAGTGTACACGACGAGTACTTTTTTTTTTTTNN was used for  
 priming reverse transcription in the presence of  
 SuperScript II RTase. The 5' primer (5',  
 GCGCGCGCTAATACGACTACTATAGG) annealed to cytosine  
 nucleosides added by terminal transferase to the 5' end of  
 the transcript. Amplification during the PCR used primers  
 5' AAGCAGTGTACACGACGAGA and 5' GCGCGCTAATACGACTACTATAGG  
 and Clone-TECH TAC DNA polymerase. PCR products between  
 500 and 2,000 bp were size-fractionated from 0.7% LE/TAE  
 agarose and cloned into the Topo TA site of Invitrogen  
 plasmid vector PCR4-TOPO."

## ORIGIN

Query Match 91.6%; Score 17.4; DB 7; Length 589;  
 Best Local Similarity 94.7%; Pred. No. 2.1e+02;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19

Db 273 CCCCTGAGTGGGCTAATC 291

## RESULT 7

BG933318

LOCUS

DEFINITION WS1\_3\_H09\_b2\_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA  
 linear EST 07-JUN-2001

ACCESSION BG933318

VERSION BG933318.1 GI:14328450

KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 320)

AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and  
 Pratt, L.H.

TITLE An EST database from Sorghum: water-stressed plants

JOURNAL

COMMENT Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.

Seq primer: JEN REV

High quality sequence stop: 308

POLYA=No.

## FEATURES

Location/Qualifiers

source

1. .320

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/db\_xref="taxon:4558"

/clone\_lib="Water-stressed 1 (WS1)"

/note="Organ: Mix of 5-week old plants on days 7 & 8 after  
 water was withheld; Vector: Lambda Zap; Site 1: XhoI;  
 Site 2: EcoRI; The library was made from poly-A RNA in the  
 cloning vector lambda ZAP II. Clones to be sequenced were  
 prepared by mass excision."

## ORIGIN

Query Match 89.5%; Score 17; DB 2; Length 320;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18

Db 287 CCCTGAATGCGGCTAAT 303

## RESULT 8

CF771460

LOCUS

DEFINITION CF771460 392 bp mRNA linear EST 20-OCT-2003  
 bicolor cDNA clone DSBF1\_19\_G07\_A010 3', mRNA sequence.

ACCESSION CF771460

VERSION CF771460.1 GI:37756870

KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 392)

AUTHORS Cordonnier-Pratt, M.-M., Zhang, D., McCartor, K., Nguyen, H.T. and  
 Pratt, L.H.

TITLE An EST Database from Sorghum: Subtracted pre-flowering drought  
 stressed leaf tissues

JOURNAL Unpublished (2003)

COMMENT Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 583 0210

Email: mmpratt@uga.edu

Library constructed at Texas Tech University by Deshui Zhang in the  
 Laboratory of Dr. Henry Nguyen. Sequencing was done in the  
 Laboratory for Genomics and Bioinformatics, University of Georgia.  
 Sequence ends have been trimmed to exclude vector and regions below  
 Phred quality 16. Three-prime sequences are presented as their  
 reverse complement and have been trimmed to exclude polyA.

Seq primer: T7 (TAATAGACTCACTATAGG)

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1. .392

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="Tx7000"

/db\_xref="taxon:4558"

/clone="DSBF1\_19\_G07\_A010"

/dev\_stage="Pre-flowering"

/lab\_host="ElectroMax DH10B (BRL)"

/clone\_lib="Drought-stressed before flowering"

/note="Organ: Leaf; Vector: pBluescriptSK-; Site 1: XhoI;  
 Site 2: EcoRI; The library was prepared from polyA+ RNA  
 from leaves harvested from pre-flowering, drought-stressed  
 Sorghum bicolor, cv. TX7000. Double-stranded cDNA was  
 cloned unidirectionally using the Unizap system from  
 Stratagene. After amplification, the library was  
 subtracted by re-association hybridization. Inserts can be  
 excised with XhoI and EcoRI."

```

ORIGIN
Query Match      89.5%; Score 17; DB 6; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
|||||
Db 167 CCCTGAATGCGGCTAAT 183
|||||

RESULT 9
BG933077      554 bp mRNA linear EST 07-JUN-2001
LOCUS
DEFINITION WSI_3_H09.b1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA
sequence.
VERSION BG933077.1 GI:14328209
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 554)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and
Pratt,L.H.
An EST database from Sorghum: water-stressed plants
Unpublished (2000)
CONTACT: Cordonnier-Pratt MM
Laboratory for Genomics and Bioinformatics
The University of Georgia, Department of Plant Biology
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 583 0210
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence start: 13
High quality sequence stop: 543
POLYA=No.

FEATURES
source Location/Qualifiers
1..554
/mol_type="mRNA"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site1: XhoI;
Site2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."

ORIGIN
Query Match      89.5%; Score 17; DB 2; Length 554;
Best Local Similarity 100.0%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAAT 18
|||||
Db 282 CCCTGAATGCGGCTAAT 298
|||||

RESULT 10
CA104476      590 bp mRNA linear EST 23-SEP-2003
LOCUS
DEFINITION SCUFHR1033A07.b HR1 Saccharum officinarum cDNA clone SCUFHR1033A07
3', mRNA sequence.
ACCESSION CA104476
VERSION CA104476.1 GI:34957783
KEYWORDS EST.

Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
REFERENCE 1 (bases 1 to 590)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
The libraries that made SUCSST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
JOURNAL
COMMENT Contact: Arruda P
Centro de Biologia Molecular e Engenhariaia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bccceniter.fcav.unesp.br
Plate: 033 row: A column: 07
Seq primer: SP6 Promoter primer.
Location/Qualifiers
1..590
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCUFHR1033A07"
/lab_host="DH10B"
/clone_lib="HR1"
/note="Organ: seedlings inoculated with Herbaspirillum
rubrisubalbicans; Vector: pSPORT1; Site 1: SalI; Site 2:
NotI; An unidirectional cDNA library generated from
[seedlings inoculated with Herbaspirillum
rubrisubalbicans]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CU-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN
Query Match      89.5%; Score 17; DB 6; Length 590;
Best Local Similarity 94.4%; Pred. No. 3.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATGCGGCTAATC 19
|||||
Db 525 CCCTGAATGCGGCTAATC 542
|||||

RESULT 11
CD429058      645 bp mRNA linear EST 03-JUN-2003
LOCUS
DEFINITION ETH1_2_B02.b1_A002 Ethylene-treated seedlings Sorghum bicolor cDNA
clone ETH1_2_B02_A002 3', mRNA sequence.
ACCESSION CD429058
VERSION CD429058.1 GI:31344701
KEYWORDS EST.
SOURCE Sorghum bicolor (sorghum)
ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 645)
AUTHORS Cordonnier-Pratt,M.-M., Wentzel,V., Suzuki,Y., Sugano,S.,
Klein,R.R., Liang,C., Sun,F., Sullivan,R., Shah,M., Salzman,R.,
Chua Tan,N., Gonzalez,M., Lane,S., Miller,V., Nanda,P.,
Olaseinde,O., Eastman,A. and Pratt,L.H.
An EST database from Sorghum: 1-aminocyclopropane-1-carboxylic acid
(ACC)-treated seedlings
Unpublished (2003)
JOURNAL

```

## COMMENT

Other ESTs: ETH1\_2\_B02\_g1\_A002  
 Contact: Cordonnier-Pratt MM  
 Laboratory for Genomics and Bioinformatics  
 The University of Georgia, Department of Plant Biology  
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA  
 Tel: 706 542 1860  
 Fax: 706 583 0210  
 Email: mmpratt@uga.edu  
 Library constructed by Dr. Yutaka Suzuki and Dr. Sumio Sugano in  
 the Human Genome Center, University of Tokyo Institute of Medical  
 Science; plant material and RNA prepared at Texas A & M University;  
 sequencing done in the Laboratory for Genomics and Bioinformatics,  
 University of Georgia. Sequence ends have been trimmed to exclude  
 vector and regions below Phred quality 16. Three-prime sequences  
 are presented as their reverse complement and have been trimmed to  
 exclude polyA.  
 Seq primer: Sug3 (CGACCTGCAGCTCGAGCACA)  
 POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..645

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/cultivar="BTx623"

/db\_xref="taxon:4558"

/clones="ETH1\_2\_B02\_A002"

/lab\_host="DH10B-TI phage-resistant E. coli"

/clone\_lib="Ethylene-treated seedlings"

/note="Vector: pME18S-FL3; Site 1: XhoI; Site 2: XhoI; The

library was prepared from polyA+ RNA from seedlings grown

in hydroponic culture. At 8 days of age, medium was

supplemented with 0.5 mM 1-aminocyclopropane-1-carboxylic

acid (ACC) to induce endogenous ethylene (ETH) production.

Roots and shoots were harvested after 27 and 72 hr and

material from both time points was combined prior to RNA

isolation. Double-stranded cDNA was cloned

unidirectionally into different DraIII sites of the

pME18S-FL3 vector (5'-prime DraIII site is CACTGTGTG,

3'-prime DraIII site is CACCATGTG). XhoI excises the cDNA

insert."

## ORIGIN

Query Match 89.5%; Score 17; DB 6; Length 645;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18

|||||

Db 372 CCCTGAATGGCGCTAAT 388

## RESULT 12

AW680038

LOCUS

DEFINITION WS1\_3\_H09\_g1\_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA

sequence.

ACCESSION AW680038

VERSION AW680038.1 GI:7553818

KEYWORDS EST.

SOURCE Sorghum bicolor (sorghum)

ORGANISM Sorghum bicolor

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 696)

Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and

Pratt, L.H.

An EST database from Sorghum: water-stressed plants

Unpublished (2000)

Contact: Cordonnier-Pratt MM

Laboratory for Genomics and Bioinformatics

The University of Georgia, Department of Plant Biology

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

## FEATURES

source

Location/Qualifiers

1..118

Fax: 706 583 0210

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions  
 below Phred quality 16. The threshold for highest quality sequence  
 is 20.

Seq primer: T7

High quality sequence start: 71

High quality sequence stop: 696

POLYA=Yes.

## FEATURES

source

Location/Qualifiers

1..696

/organism="Sorghum bicolor"

/mol\_type="mRNA"

/db\_xref="taxon:4558"

/clone\_lib="Water-stressed 1 (WS1)"

/note="Organ: Mix of 5-week old plants on days 7 &amp; 8 after

water was withheld; Vector: Lambda Zap; Site 1: XhoI;

Site 2: EcoRI; The library was made from polyA+ RNA in the

cloning vector lambda Zap II. Clones to be sequenced were

prepared by mass excision."

## ORIGIN

Query Match 89.5%; Score 17; DB 1; Length 696;

Best Local Similarity 100.0%; Pred. No. 3.6e+02;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCCTGAATGGCGCTAAT 18

|||||

Db 269 CCCTGAATGGCGCTAAT 285

## RESULT 13

CZ476191/c

LOCUS

DEFINITION d08347-5prime Exelixis P element XP insertions Drosophila

melanogaster genomic Sequence recovered from 5' end of P element,

genomic survey sequence.

ACCESSION CZ476191

VERSION CZ476191.1 GI:62970314

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 118)

Thibault, S.T., Singer, M.A., Miyazaki, W.Y., Milash, B., Dompe, N.A.,

Singh, C.M., Buchholz, R., Demsky, M., Fawcett, R., Francis-Lang, H.L.,

Ryner, L., Cheung, L.M., Chong, A., Erickson, C., Fisher, W.W.,

Greer, K., Hartouni, S.R., Howie, E., Jakkula, L., Joo, D., Killpack, K.,

Laufer, A., Mazzotta, J., Smith, R.D., Stevens, L.M., Stuber, C.,

Tan, L.R., Ventura, R., Woo, A., Zakrajsek, I., Zhao, L., Chen, F.,

Swimmer, C., Koczynski, C., Duyk, G., Winberg, M.L. and Margolis, J.

A complementary transposon tool kit for Drosophila melanogaster

using P and piggyBac

Nat. Genet. 36 (3), 283-287 (2004)

14981521

Contact: Roger A Hoskins

Berkeley Drosophila Genome Project

Lawrence Berkeley National Laboratory

Mailstop 64-121, One Cyclotron Road, Berkeley, CA 94720, USA

Tel: 510 486 4015

Fax: 510 486 6798

Email: Rhoskins@lbl.gov

Sequence recovery method was inverse PCR.

Sequence orientation is forward strand relative to 5' end of P

element.

The P element insertion position is 111 in the 118 bases. This

insertion position refers to the first base of the 8 base target

recognition sequence.

Class: transposon insertion site.

Location/Qualifiers

1..118

/organism="Drosophila melanogaster"  
/mol\_type="genomic DNA"  
/strain="isogenic w- strain"  
/db\_xref="taxon:7227"  
/clone\_lib="Exelixis P element XP insertions"  
/note="Vector: P element XP (GenBank accession number AY1515149); An isogenic w- Drosophila melanogaster strain was mutagenized by remobilization of transposable elements. For the P element XP, we selected an easily mobilized ammunition element among inserts hopped onto the Binsinsky balancer. New insertions were collected in vias from dysgenic females using the standard chromosomal source of transposase, delta2-3. All lines were mapped to a chromosome by standard genetic methods, examined for homozygous viability and used for recovery of flanking genomic sequence by inverse PCR."

# ORIGIN

Query Match 86.3%; Score 16.4; DB 10; Length 118;  
Best Local Similarity 94.4%; Pred. No. 6.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGGCTAAT 18  
| | | | | | | | | | | | | | | | | | | |  
Db 103 CCCTGAATCGGCTAAT 86

RESULT 14  
BH899915  
LOCUS  
DEFINITION  
Ota00982 Ostreococcus tauri genomic shotgun library Ostreococcus tauri genomic clone ota04c08.g 5', genomic survey sequence.

ACCESSION  
BH899915  
VERSION  
BH899915.1 GI:22551410  
KEYWORDS  
GSS.  
SOURCE  
Ostreococcus tauri

ORGANISM  
Ostreococcus tauri  
Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae; Mamiellales; Mamiellaceae; Ostreococcus.

REFERENCE  
1 (bases 1 to 533)  
Dereille, E., Ferraz, C., Lagoda, P., Eychenie, S., Cooke, R., Regad, F., Sabau, X., Courties, C., Delseny, M., Demaille, J., Picard, A. and Moreau, H.

TITLE  
DNA libraries for sequencing the genome of Ostreococcus tauri (Chlorophytae, Prasinophyceae): the smallest free-living eukaryotic cell

J. Phycol. 38 (6), 1150-1156 (2002)  
Contact: Moreau H  
Laboratoire Arago  
CNRS UMR 7628  
BP 44, Avenue Fontaule, 66651 Banyuls sur mer, France

Tel: (33)468887309  
Fax: (33)468887398  
Email: h.moreau@obs-banyuls.fr  
Seq primer: reverse  
Class: shotgun.

## FEATURES

Location/Qualifiers  
1..533  
/organism="Ostreococcus tauri"  
/mol\_type="genomic DNA"  
/strain="OTTH0595"  
/db\_xref="taxon:70448"  
/clone="ota04c08.g"  
/clone\_lib="Ostreococcus tauri genomic shotgun library"  
/note="Vector: Bluescript; Site 1: EcoRV; Site 2: EcoRV; Shotgun library prepared after sonication of the genomic DNA. Blunt ligation in EcoRV site of Bluescript. Size selection of the inserts after agarose electrophoresis between 1 and 3 Kb."

# ORIGIN

Query Match 86.3%; Score 16.4; DB 9; Length 533;  
Best Local Similarity 94.4%; Pred. No. 7.5e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 CCCTGAATCGGCTAAT 18  
| | | | | | | | | | | | | | | | | | | |  
Db 500 CCCTGAATCGGCTACT 517

RESULT 15  
CA190230/c  
LOCUS  
DEFINITION  
SCCCLR1C10E02.g LRI Saccharum officinarum cDNA clone SCCCLR1C10E02 5', mRNA sequence.

ACCESSION  
CA190230  
VERSION  
CA190230.1 GI:35134178  
KEYWORDS  
EST.  
SOURCE  
Saccharum officinarum

ORGANISM  
Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum complex.

REFERENCE  
1 (bases 1 to 569)  
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.  
The libraries that made SUCEST  
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found through the Brazilian Clone Collection Center (BCCC) at <http://www.bcccenter.fcav.unesp.br>  
Plate: C10 row: E column: 02  
Seq primer: T7 Promoter Primer.

## FEATURES

Location/Qualifiers  
1..569  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCCCLR1C10E02"  
/lab\_host="DH108"  
/clone\_lib="LRI"  
/notes="Organ: Leaf roll from field grown adult plants (large insert library); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from leaf roll from field grown adult plants (large insert library). cDNA was prepared from polyA+ mRNA using SuperScript Plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 Kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at <http://sucest.lad.ic.unicamp.br/public>"

# ORIGIN

Query Match 86.3%; Score 16.4; DB 6; Length 569;  
Best Local Similarity 94.4%; Pred. No. 7.6e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATCGGCTAATC 19  
| | | | | | | | | | | | | | | | | | | |  
Db 299 CCCTGAATGTGGCTAATC 282

RESULT 16  
CX410223  
LOCUS  
DEFINITION  
JGI\_XZT32869.rev NIH XGC tropTad5 Xenopus tropicalis cDNA clone IMAGE:7609044 3', mRNA sequence.  
ACCESSION  
CX410223



```

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
CX410223.1 GI:57190925
Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
1 (bases 1 to 655)
Richardson, P., Lucas, S., Rokhe, D., Dettler, J.C., Ng, D.C.,
Brookstein, P., and Lindquist, E.A.
DOE Joint Genome Institute Xenopus tropicalis EST project
Unpublished (2004)
Other ESTs: JGI.XZT32869.fwd
Contact: Lindquist, E.A., Richardson, P.
DOE Joint Genome Institute
2800 Mitchell Drive, Walnut Creek, CA 94598, USA
Tel: 925 296 5600
Fax: 925 296 5710
Email: cdna@jgi-psf.org
Tissue Procurement: Richard M. Harland Laboratory, University of
California, Berkeley: http://tropicalis.berkeley.edu/home
cDNA Library Preparation: Richard M. Harland Laboratory, University
of California, Berkeley
DNA Sequencing: DOE Joint Genome Institute: http://www.jgi.doe.gov
Clone Distribution: I.M.A.G.E. Consortium/LLNL:
http://image.llnl.gov
Naming Conventions: EST name is generated by the concatenation of
the JGI Clone Id and the direction of sequencing. The suffix '.rev'
indicates a reverse sequencing read of the insert. It does not
necessarily reflect the orientation of the insert.
Poly-A: Based upon the presence of a run of 14 or more T residues
at the beginning of the sequence, this clone was polyadenylated.
The resulting Poly-T sequence has been removed.
Plate: XZT 0341 row: i column: 10
High quality sequence stop: 503
POLYA=Yes.
FEATURES
source
Location/Qualifiers
1..655
/organism="Xenopus tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="IMAGE.7609044"
/tissue_type="whole embryo"
/dev_stage="Tadpole (st. 36-41)"
/lab_host="E. coli XL1-Blue derivative, Stratagene
Electrofen-Blue"
/clone_lib="NIH XGC tropTads"
/notes="Vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole
library constructed by Russell B. Fletcher in R. Harland's
lab using poly A RNA and oligo dt primers (Invitrogen
SuperScript Plasmid System for cDNA Synthesis and
Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted
into vector PCS108
(http://mcb.berkeley.edu/labs/harland/pages/plasmids.html)"
ORIGIN
Query Match 86.3%; Score 16.4; DB 8; Length 655;
Best Local Similarity 94.4%; Pred. No. 7.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 CCCCTGAATGGCGCTAAT 18
|||||
Db 325 CCCCTGAATGGCGCTAAT 342
|||||
RESULT 17
CA125729/c
LOCUS
DEFINITION
5' mRNA sequence.
ACCESSION
CA125729
VERSION
CA125729.1 GI:35003921
EST.
Saccharum officinarum
Saccharum officinarum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum
complex.
1 (bases 1 to 690)
Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.
The libraries that made SUCEST
Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
Contact: Arruda, P.
Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 110 row: E column: 08
Seq primer: T7 Promoter Primer.
Location/Qualifiers
1..690
/organism="Saccharum officinarum"
/mol_type="mRNA"
/db_xref="taxon:4547"
/clone="SCRLR1110E08"
/lab_host="DH10B"
/clone_lib="LRI"
/notes="Organ: Leaf roll from field grown adult plants
(large insert library); Vector: pSport1; Site 1: SalI;
Site 2: NotI; An unidirectional cDNA library generated
from [Leaf roll from field grown adult plants (large
insert library)]. cDNA was prepared from polyA+ mRNA
using SuperScript Plasmid System Kit (Invitrogen). The
double-strand cDNAs were fractionated in a sepharose
CL-2B 40cm-columns and fragments sizing between 0.8 and
1.5 Kb were directionally cloned into the vector. Details
of each source of RNA and library construction can be
obtained at http://sucest.lad.ic.unicamp.br/public"
ORIGIN
Query Match 86.3%; Score 16.4; DB 6; Length 690;
Best Local Similarity 94.4%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 CCCTGAATGGCGCTAATC 19
|||||
Db 299 CCCTGAATGGCGCTAATC 282
|||||
RESULT 18
BX867956/c
LOCUS
DEFINITION
BX867956 tcba Oncorhynchus mykiss cDNA clone tcba0023c.o.02 5prim,
mRNA sequence.
ACCESSION
BX867956
VERSION
BX867956.1 GI:39991469
KEYWORDS
EST.
ORGANISM
Oncorhynchus mykiss (rainbow trout)
Oncorhynchus mykiss
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
1 (bases 1 to 760)
Govoroun, M., Guiguen, Y. and Le Gac, P.
Construction and primary characterization of normalized cDNA
libraries in rainbow trout, Oncorhynchus mykiss
Unpublished (2003)
Contact: Guiguen Y
INRA - SCRIBE

```

Campus de beaulieu, RENNES cedex, 35042, France  
 Tel: 02.23.48.50.09  
 Fax: 02.23.48.50.20  
 Email: Yann.Guiguen@beaulieu.rennes.inra.fr  
 Sequence cleaned of vector, adaptor and repetitions. Contact us  
 at signenasupport@jouy.inra.fr to obtain the chromatogram of this  
 sequence.  
 Plate: 0023 row: o column: 2  
 Seq primer: M13R.

## FEATURES

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source
1..760
/organism="Oncorhynchus mykiss"
/mol_type="mRNA"
/db_xref="taxon:8022"
/clone="tcba0023c.o.02"
/tissue_type="multi-tissues"
/dev_stage="from embryos to adults"
/lab_host="DH10B"
/clone_lib="tcba"
/notes="vector: pT7T3D-pac; Rainbow trout multi-tissues -
normalized + 1 subtraction; Clone distribution : AGENAE
Resource centre. Francois PIUMI,
Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et
Etude du genome (LREG), Domaine de Vilvert, 78352,
Jouy-en-Josas cedex, FRANCE, +33 (0) 1.34.65.28.02, +33
(0) 1.34.65.22.73"

ORIGIN
Query Match      86.3%; Score 16.4; DB 5; Length 760;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCCTGAATCGCGCTAATC 19
Db 510 CCCTGAATCGCGTTAATC 493
|||||

```

## RESULT 19

```

AG218963/c
LOCUS
DEFINITION
AG218963
AG218963.1 GI:22766383
GSS.
Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 Hayashi, S., Ito, K., Sado, Y., Taniguchi, M., Akimoto, A., Takeuchi, H.,
Aigaki, T., Matsuzaki, F., Nakagoshi, H., Tanimura, T., Ueda, R.,
Uemura, T., Yoshihara, M. and Goto, S.
GENDB, a database compiling expression patterns and molecular
locations of a collection of Gal4 enhancer traps
Genesis (2002) In press
REFERENCE
2 (bases 1 to 800)
Hayashi, S.
Direct Submission
Submitted (27-AUG-2002) Shigeo Hayashi, RIKEN Center for
Developmental Biology, Laboratory for Morphogenetic Signaling;
Chuo-ku, Minatojima-minamimachi 2-2-3, Kobe, Hyogo 650-0047, Japan
(E-mail: shayashi@cdb.riken.go.jp, Tel: 81-78-301-3184,
Fax: 81-78-301-3183)
This clone was isolated from genomic DNA flanking an insertion of
the P element vector P[GawB] of a Drosophila strain.

FEATURES
source
1..800
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/strain="NP5046"
/db_xref="taxon:7227"

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/chromosome="1"
/map="5C4"
/clone="NP5046-3-1"
/notes="flanking P[GawB] transposon insertion"

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ORIGIN
Query Match      86.3%; Score 16.4; DB 10; Length 800;
Best Local Similarity 94.4%; Pred. No. 7.9e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGCGCTAAT 18
Db 186 CCCTGAATCGCGCAAT 169
|||||

```

## RESULT 20

```

DRL126636
LOCUS
DEFINITION
DRL126636
DRL126636.1 GI:67843334
EST.
Drosophila pseudoobscura
Drosophila pseudoobscura
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 1104)
Richards, S., Liu, Y., Bettencourt, B.R., Hradecky, P., Letovsky, S.,
Nielsen, R., Thornton, K., Hubisz, M.J., Chen, R., Meisel, R.P.,
Couronne, O., Hua, S., Smith, M.A., Zhang, P., Liu, J., Bussemaker, H.J.,
van Batenburg, M.F., Howells, S.L., Scherer, S.E., Sodergren, E.,
Matthews, B.B., Crosby, M.A., Schroeder, A.J., Ortiz-Barrientos, D.,
Rives, C.M., Metzker, M.L., Muzny, D.M., Scott, G., Steffen, D.,
Wheeler, D.A., Worley, K.C., Havlak, P., Durbin, K.J., Egan, A.,
Gill, R., Hume, J., Morgan, M.B., Miner, G., Hamilton, C., Huang, Y.,
Waldron, L., Verduzco, D., Clerc-Blankenburg, K.P., Dubchak, I.,
Noor, M.A., Anderson, W., White, K.P., Clark, A.G., Schaeffer, S.W.,
Geibart, W., Weinstein, G.M. and Gibbs, R.A.
Comparative genome sequencing of Drosophila pseudoobscura:
chromosomal, gene, and cis-element evolution
Genome Res. 15 (1), 1-18 (2005)
15632085
Contact: Stephen Richards
Human Genome Sequencing Center
Baylor College of Medicine
One Baylor Plaza, Houston, TX 77030, USA
Tel: 713-798-6667
Email: stephen@bcm.tmc.edu
NCBI Trace Archive: 226715407
Insert length: 1750 Std Error: 0.25.

FEATURES
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1..1104
/organism="Drosophila pseudoobscura"
/mol_type="mRNA"
/db_xref="taxon:7237"
/clone="A19"
/dev_stage="0-18h embryos"
/clone_lib="Drosophila pseudoobscura embryonic cDNA
library"
/notes="vector: pOTB7; Site 1: EcoRI; Site 2: XhoI; oligo
dt priming from poly A+ RNA, directionally cloned"

ORIGIN
Query Match      86.3%; Score 16.4; DB 8; Length 1104;
Best Local Similarity 94.4%; Pred. No. 8.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CCCTGAATCGCGCTAAT 18
Db 740 CCCTGAATCGCGCTAAT 757
|||||

```

```

RESULT 21
CC751821/c
LOCUS
DEFINITION ZMMBB0133A01.r ZMMBBB Zea mays genomic clone ZMMBB0133A01 3',
genomic survey sequence.
ACCESSION CC751821
VERSION CC751821
KEYWORDS GSS.
SOURCE CC751821.1 GI:32211287
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 485)
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
and Wing,R.
TITLE Sequencing of the maize genome
JOURNAL Unpublished (2003)
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0133 row: A column: 01
Seq primer: M13r
Class: BAC ends.
FEATURES
source
location/Qualifiers
1..485
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0133A01"
/lab_host="DH10B"
/clone_lib="ZMMBB"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. esp. mays"
ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 485;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CCTGAATCGCGCTAAT 18
Db 199 CCTGAATCGCGCTAAT 184

RESULT 22
CL414924/c
LOCUS
DEFINITION ZMMBB0422D13r ZMMBBB (HindIII) Zea mays genomic clone
ZMMBB0422D13 3', genomic survey sequence.
ACCESSION CL414924
VERSION CL414924
KEYWORDS GSS.
SOURCE CL414924.1 GI:45273060
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 527)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
Sequencing of the maize genome at PGIR (2003c)
TITLE
JOURNAL Unpublished (2003)

Contact: Bharti,A.K.
Dr. Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Freelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: SP6
Class: BAC ends
High quality sequence start: 94.
FEATURES
source
location/Qualifiers
1..527
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMMBB0422D13"
/lab_host="E. coli DH10B"
/clone_lib="ZMMBB"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
ORIGIN
Query Match 84.2%; Score 16; DB 10; Length 527;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 3 CCTGAATCGCGCTAAT 18
Db 273 CCTGAATCGCGCTAAT 258

RESULT 23
BZ718658
LOCUS
DEFINITION PUCEY99TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMBTa13K17,
genomic survey sequence.
ACCESSION BZ718658
VERSION BZ718658
KEYWORDS GSS.
SOURCE BZ718658.1 GI:28505644
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 547)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reinick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
Maize Genomics Consortium
Unpublished (2003)
TITLE
JOURNAL Unpublished (2003)
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP
Class: sheared ends.
FEATURES
source
location/Qualifiers
1..547
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTa13K17"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"
ORIGIN
Query Match 84.2%; Score 16; DB 9; Length 547;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;

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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18
    |||||
Db 408 CCTGAATGCGGCTAAT 423

RESULT 24
CX698830 595 bp mRNA linear EST 19-JAN-2005
LOCUS ydb82909.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydb82909 5' similar to TR:Q94532 Q94532 PUTATIVE TYPE III
ALCOHOL DEHYDROGENASE. [1] ; mRNA sequence.
ACCESSION CX698830
VERSION CX698830.1 GI:57961723
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 595)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RppOT
High quality sequence stop: 595.
FEATURES
source
1..595
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd56d01"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"
/notes="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
Site 2: SmaI; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN
Query Match 84.2%; Score 16; DB 8; Length 595;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17
    |||||
Db 376 CCTGAATGCGGCTAA 391

RESULT 26
CX691884 632 bp mRNA linear EST 19-JAN-2005
LOCUS ydd36h05.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydd36h05 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
; mRNA sequence.
ACCESSION CX691884
VERSION CX691884.1 GI:57953941
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center

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Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 596)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center
Seq primer: -28RppOT
High quality sequence stop: 596.
FEATURES
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1..596
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="ydd56d01"
/lab_host="DH10B"
/clone_lib="Sea urchin EST Lib1"
/notes="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;
Site 2: SmaI; Arrayed normalized library of full-length
cDNAs representing blastula stage transcriptome of the sea
urchin Strongylocentrotus purpuratus, cloned into the
vector pCMVSPORT6.1 (Invitrogen)"

ORIGIN
Query Match 84.2%; Score 16; DB 8; Length 596;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17
    |||||
Db 376 CCTGAATGCGGCTAA 391

RESULT 26
CX691884 632 bp mRNA linear EST 19-JAN-2005
LOCUS ydd36h05.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA
DEFINITION clone ydd36h05 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]
; mRNA sequence.
ACCESSION CX691884
VERSION CX691884.1 GI:57953941
KEYWORDS EST.
SOURCE Strongylocentrotus purpuratus
ORGANISM Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida;
Strongylocentrotidae; Strongylocentrotus.
REFERENCE 1 (bases 1 to 632)
AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,
Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,
Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and
Wilson,R.
TITLE WashU Sea Urchin EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Dr. James A. Coffman
WashU Sea Urchin EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
DNA sequencing by: Washington University Genome Sequencing Center

```

Seq primer: -28RppOT  
 High quality sequence stop: 591.  
 Location/Qualifiers  
 1..632  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="ydd36h05"  
 /lab\_host="DH10B"  
 /clone\_lib="Sea urchin EST Lib1"  
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;  
 Site 2: SmaI; Arrayed normalized library of full-length  
 cDNAs representing blastula stage transcriptome of the sea  
 urchin Strongylocentrotus purpuratus, cloned into the  
 vector pCMVSPORT6.1 (Invitrogen)"

## ORIGIN

Query Match 84.2%; Score 16; DB 8; Length 632;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 2 CCTGAATGCGGCTAA 17  
 |||||  
 Db 364 CCTGAATGCGGCTAA 379

RESULT 27  
 CX557631 675 bp mRNA linear EST 12-JAN-2005  
 LOCUS yda39d02.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA  
 DEFINITION clone yda39d02 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]  
 ;, mRNA sequence.

ACCESSION CX557631  
 VERSION CX557631.1 GI:57584660  
 KEYWORDS EST.  
 SOURCE Strongylocentrotus purpuratus  
 ORGANISM Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidea; Euechinoidea; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 675)  
 AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,  
 Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,  
 Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and  
 Wilson,R.

TITLE WashU Sea Urchin EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Dr. James A. Coffman  
 WashU Sea Urchin EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Seq primer: -28RppOT  
 High quality sequence stop: 519.  
 Location/Qualifiers

## FEATURES

source 1..675  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="ydd39d02"  
 /lab\_host="DH10B"

/clone\_lib="Sea urchin EST Lib1"  
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;  
 Site 2: SmaI; Arrayed normalized library of full-length  
 cDNAs representing blastula stage transcriptome of the sea  
 urchin Strongylocentrotus purpuratus, cloned into the  
 vector pCMVSPORT6.1 (Invitrogen)"

## ORIGIN

Query Match 84.2%; Score 16; DB 8; Length 675;

Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17  
 |||||  
 Db 113 CCTGAATGCGGCTAA 128

RESULT 28  
 CX692600 676 bp mRNA linear EST 19-JAN-2005  
 LOCUS yde83d07.y2 Sea urchin EST Lib1 Strongylocentrotus purpuratus cDNA  
 DEFINITION clone yde83d07 5' similar to TR:Q9U2M4 Q9U2M4 Y38F1A.6 PROTEIN. [1]  
 ;, mRNA sequence.

ACCESSION CX692600  
 VERSION CX692600.1 GI:57954747  
 KEYWORDS EST.  
 SOURCE Strongylocentrotus purpuratus  
 ORGANISM Strongylocentrotus purpuratus  
 Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
 Echinoidea; Euechinoidea; Echinacea; Echinoida;  
 Strongylocentrotidae; Strongylocentrotus.

REFERENCE 1 (bases 1 to 676)  
 AUTHORS Coffman,J.A., Robertson,A.J., Clifton,S., Pape,D., Hillier,L.,  
 Martin,J., Wylie,T., Dante,M., Meyer,R., Theising,B., Bowers,Y.,  
 Gibbons,M., Ronko,I., Tsagareishvili,R., Ritter,E., Kennedy,S. and  
 Wilson,R.

TITLE WashU Sea Urchin EST Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Dr. James A. Coffman  
 WashU Sea Urchin EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 DNA sequencing by: Washington University Genome Sequencing Center  
 Seq primer: -28RppOT  
 High quality sequence stop: 578.  
 Location/Qualifiers

## FEATURES

source 1..676  
 /organism="Strongylocentrotus purpuratus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7668"  
 /clone="yde83d07"  
 /lab\_host="DH10B"  
 /clone\_lib="Sea urchin EST Lib1"  
 /note="Vector: pCMVSPORT6.1 (Invitrogen); Site 1: NotI;  
 Site 2: SmaI; Arrayed normalized library of full-length  
 cDNAs representing blastula stage transcriptome of the sea  
 urchin Strongylocentrotus purpuratus, cloned into the  
 vector pCMVSPORT6.1 (Invitrogen)"

## ORIGIN

Query Match 84.2%; Score 16; DB 8; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCTGAATGCGGCTAA 17  
 |||||  
 Db 363 CCTGAATGCGGCTAA 378

RESULT 29  
 CC751823/c 784 bp DNA linear GSS 25-JUN-2003  
 LOCUS ZMMBBb0133A03.r ZMMBBb Zea mays genomic clone ZMMBBb0133A03 3',  
 DEFINITION genomic survey sequence.

ACCESSION CC751823  
 VERSION CC751823.1 GI:32211291  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.

TITLE Sequencing of the maize genome

JOURNAL Unpublished (2003)

COMMENT Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: T7

BACKWARD: M13r

Plate: 0133 row: A column: 03

Seq primer: M13r

Class: BAC ends.

FEATURES

source

1. 784  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0133A03"  
/lab\_host="DH10B"  
/clone\_lib="ZMMBBb"  
/notes="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 784;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18

|||||

Db 293 CCTGAATGCGGCTAAT 278

RESULT 30

CC753964/c

LOCUS

DEFINITION ZMMBB0137J07.r ZMMBBb Zea mays genomic clone ZMMBBb0137J07 3', 787 bp DNA linear GSS 25-JUN-2003

ACCESSION CC753964

VERSION CC753964.1

KEYWORDS GSS.

SOURCE

ORGANISM

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J. and Wing,R.

TITLE Sequencing of the maize genome

JOURNAL Unpublished (2003)

COMMENT Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 440A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: T7

BACKWARD: M13r

Plate: 0137 row: J column: 07  
Seq primer: M13r  
Class: BAC ends.

FEATURES

source

1. 787  
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/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0137J07"  
/lab\_host="DH10B"  
/clone\_lib="ZMMBBb"  
/notes="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 84.2%; Score 16; DB 9; Length 787;  
Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18

|||||

Db 295 CCTGAATGCGGCTAAT 280

RESULT 31

CB945315

LOCUS

DEFINITION AGENCOURT 13841963 NICHD\_XGC\_Tad2 Xenopus laevis cDNA clone IMAGE:6933220 5', mRNA sequence. 809 bp mRNA linear EST 29-APR-2003

ACCESSION CB945315

VERSION CB945315.1

KEYWORDS EST.

SOURCE

ORGANISM

Xenopus laevis

Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 809)

AUTHORS NCI-CGAP

TITLE http://www.ncbi.nlm.nih.gov/ncicgap.

COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapsb@mail.nih.gov

Tissue Procurement: Drs. Donald Brown and Liqun Cai

cDNA Library Preparation: CLONTECH

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLCM3248 row: b column: 03

High quality sequence stop: 447.

FEATURES

source

1. 809  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:6933220"  
/dev\_stage="metamorphosis stage 62"  
/clone\_lib="NICHD\_XGC\_Tad2"

/notes="Organ: Developing tadpole; Vector: pDNR-LIB; Site 1: SfiI; Site 2: SfiI; 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGCGCGGCGGCATG-TT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.7 kb (range 0.8-3.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."

ORIGIN

Query Match 84.2%; Score 16; DB 6; Length 809;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCCTGAATGCGGCTA 16  
 |||||  
 Db 454 CCCTGAATGCGGCTA 469

RESULT 32  
 CG038424/c  
 LOCUS  
 DEFINITION PUFKT95TD\_ZM\_0.6\_1.0\_KB\_Zea\_mays\_genomic\_clone\_ZMBT0672P22,  
 genomic survey sequence.

ACCESSION CG038424  
 VERSION CG038424.1 GI:33910580  
 KEYWORDS GSS.

SOURCE Zea mays  
 ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 838)  
 AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and  
 Bennetzen,J.

TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Other GSSs: PUFKT95TB  
 Contact: Cathy Whitelaw

TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TF  
 Class: sheared ends.

FEATURES  
 source  
 1..838  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMBT0672P22"  
 /clone\_lib="ZM\_0.6\_1.0\_KB"  
 /note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high  
 Cot selected genomic DNA library"

## ORIGIN

Query Match 84.2%; Score 16; DB 10; Length 838;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+03;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CCTGAATGCGGCTAAT 18  
 |||||  
 Db 317 CCTGAATGCGGCTAAT 302

RESULT 33  
 BE000416  
 LOCUS  
 DEFINITION MRO-BN0070-120500-021-a06\_1 BN0070 Homo sapiens cDNA, mRNA  
 sequence.

ACCESSION BE000416  
 VERSION BE000416.1 GI:8260636  
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.

REFERENCE 1 (bases 1 to 262)  
 AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

## TITLE

JOURNAL  
 PUBMED  
 COMMENT

Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.P.,  
 Goldman,G.H., Carvalho,A.F., Matsumura,A., Baia,G.S., Simpson,D.H.,  
 Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,  
 O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
 Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed  
 sequence tags  
 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
 10737800

Contact: Simpson A.J.G.

Laboratory of Cancer Genetics  
 Ludwig Institute for Cancer Research  
 Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
 Brazil

Tel: +55-11-2704922  
 Fax: +55-11-2707001

Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome  
 Project. This entry can be seen in the following URL  
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2=MR0-BN0070-120  
 500-021-a06\_1&t3=2000-05-12&t4=1)

Seq primer: puc 18 forward

High quality sequence stop: 262.

FEATURES  
 source

Location/Qualifiers  
 1..262

/organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /dev\_stage="Adult"  
 /clone\_lib="EN0070"

/note="Organ: breast normal; Vector: puc18; Site 1: SmaI;  
 Site 2: SmaI; A mini-library was made by cloning products  
 derived from ORESTES PCR (U.S. Letters Patent application  
 No. 196,716 - Ludwig Institute for Cancer Research)  
 profiles into the pUC 18 vector. Reverse transcription of  
 tissue mRNA and cDNA amplification were performed under  
 low stringency conditions."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 2; Length 262;  
 Best Local Similarity 89.5%; Pred. No. 1.5e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
 |||||  
 Db 11 CCCCTCAATGCGGCTGATC 29

RESULT 34  
 AUI176457

LOCUS

DEFINITION AUI176457 Rice panicle at flowering stage Oryza sativa (japonica  
 cultivar-group) cDNA clone E3017, mRNA sequence.

ACCESSION AUI176457

VERSION AUI176457.1 GI:13422398

KEYWORDS EST.

SOURCE

ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 300)

Sasaki,T. and Yamamoto,K.

Rice cDNA from panicle at flowering stage (2001)

Unpublished (2001)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

305-8602, Japan

Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/

PROJECT = 'RGP'

```

FEATURES
source
  Location/Qualifiers
  1. 300
    /organism="Oryza sativa (japonica cultivar-group)"
    /mol_type="mRNA"
    /db_xref="taxon:39947"
    /clone="E3017"
    /dev_stage="flowering stage"
    /clone_lib="Rice panicle at flowering stage"
    /note="Organ: Panicle; Rice cDNA from panicle at flowering
stage"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 300;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 261 CCCCTGAGTCGAGCTAATC 279

RESULT 35
BE405912
LOCUS
DEFINITION
  BE405912 361 bp mRNA linear EST 21-JUL-2000
  WHE0401_g02_g022B Wheat etiolated seedling root cDNA library
  Triticum aestivum cDNA clone WHE0401_g02_g02, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Triticum aestivum (bread wheat)
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Triticum.
REFERENCE
  1 (bases 1 to 361)
  Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rauech, C.J.,
  Seaton, C.L. and Tong, J.C.
  The structure and function of the expressed portion of the wheat
  genomes
  Unpublished (2000)
  Contact: Olin Anderson
  US Department of Agriculture, Agriculture Research Service, Pacific
  West Area, Western Regional Research Center
  800 Buchanan Street, Albany, CA 94710, USA
  Tel: 510595773
  Email: andersn@pw.usda.gov
  Fax: 510595818
  Sequence have been trimmed to remove vector sequence and low
  quality sequence with phred score less than 20
  Seq primer: Strategene pBluescript SK reverse primer.
  Location/Qualifiers
  1. 361
    /organism="Triticum aestivum"
    /mol_type="mRNA"
    /cultivar="Chinese Spring"
    /db_xref="taxon:4565"
    /clone="WHE0401_g02_g02"
    /tissue_type="Root"
    /dev_stage="Five day old etiolated seedling"
    /lab_host="E. coli SOLR"
    /clone_lib="Wheat etiolated seedling root cDNA library"
    /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
  Site 1: EcoRI; Site 2: XhoI; Seeds were
  surface-sterilized, germinated and grown aseptically in
  the dark at room temperature on filter paper with water,
  nystatin and cefotaxime in covered crystallization
  dishes. Roots were harvested. The tissue, total RNA, and
  poly(A) RNA were prepared, a cDNA library was made, and
  the cDNA clones were in vivo excised to give phagescript
  phagemids in the TJ Close lab (Choi, Close, Fenton) at the
  University of California, Riverside. Plasmid DNA

```

```

preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

ORIGIN
Query Match      83.2%; Score 15.8; DB 2; Length 361;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 323 CCCCTGAGTCGAGCTAATC 341

RESULT 36
BJ468982
LOCUS
DEFINITION
  BJ468982 417 bp mRNA linear EST 23-MAY-2002
  BJ468982 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal12e23 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
  Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Hordeum.
REFERENCE
  1 (bases 1 to 417)
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tehini@genes.nig.ac.jp.
  Location/Qualifiers
  1. 417
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Haruna Nijo"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baal12e23"
    /tissue_type="top three leaves"
    /dev_stage="adult, heading stage"
    /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
  Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 417;
Best Local Similarity 89.5%; Pred. No. 1.5e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 232 CCCCTGAGTCGAGCTAATC 250

RESULT 37
BJ473149
LOCUS
DEFINITION
  BJ473149 422 bp mRNA linear EST 23-MAY-2002
  BJ473149 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal38103 5', mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```



Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Hordeum.

## REFERENCE

AUTHORS Sato, K., Saisho, D. and Takeda, K.  
TITLE Barley EST sequencing project in NIG and Okayama Univ  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadao Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

## FEATURES

source

1. .422

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Haruna Nijo"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="baal38103"

/tissue\_type="top three leaves"

/dev\_stage="adult, heading stage"

/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna Nijo adult, heading stage top three leaves"

## ORIGIN

Query Match

Best Local Similarity 83.2%; Score 15.8; DB 3; Length 422;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

||||| ||| |||||

Db 254 CCCCTGAGTCGAGCTAATC 272

## RESULT 38

BU971174

LOCUS

DEFINITION HB16N07: BC Hordeum vulgare subsp. vulgare cDNA clone HB16N07

5-PRIME, mRNA sequence.

BU971174

BU971174.1 GI:24221967

EST.

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

1 (bases 1 to 431)

Radchuk, V., Zhang, H., Weschke, W., Potokina, E. and Wobus, U.

Barley ESTs from developing seeds

Unpublished (2002)

Contact: Stein Nils

Molecular Markers Group, Department Genbank

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466, Gatersleben, Germany

Tel: 039482-5522

Fax: 039482-5595

Email: stein@ipk-gatersleben.de

Insert Length: 431 Std Error: 0.00

Plate: 16 row: N column: 7

Seq primer: M13rev.

Location/Qualifiers

1. 431

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Barke"

/sub\_species="vulgare"

/db\_xref="GABI:236006"

/db\_xref="taxon:112509"

/clone="HB16N07"

/tissue\_type="developing caryopsis"

/dev\_stage="8-15 DAP (days after pollination)"

/clone\_lib="XLI0-Gold"

/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of

cDNA); Site 2: XhoI (3'-end of cDNA); developing

caryopsis; 8-15 DAP(days after pollination) Due to a

cloning artefact caused by the kit, in most cases the

EcoRI site is NOT present, as well as the EcoRI adapter

used for cloning. To excise the insert, restriction sites

upstream EcoRI should be used (e.g. BamHI, SalI, PstI).

NOTE: Also due to the cloning system used Blue/white

selection for recombinants is not 100% reliable."

## ORIGIN

Query Match

Best Local Similarity 83.2%; Score 15.8; DB 5; Length 431;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

||||| ||| |||||

Db 249 CCCCTGAGTCGAGCTAATC 267

## RESULT 39

AZ233765

LOCUS

DEFINITION

RPCI-23-99L13.TJ RPCI-23

genomic survey sequence.

ACCESSION

AZ233765

VERSION

AZ233765.1

KEYWORDS

GSS.

SOURCE

ORGANISM

Mus musculus

(house mouse)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridea; Muridae; Murinae; Mus.

1 (bases 1 to 443)

Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,

Akinret, B., Levins, M., Moggan, S., Teegave, G., Geer, K., Krol, M., de

Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-99L13.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

http://www.tigr.org/tdb/bac ends/mouse/bac\_end\_intro.html

Plate: 99 row: L column: 13

Seq primer: SP6

Class: BAC ends.

Location/Qualifiers

1. .443

/organism="Mus musculus"

/mol\_type="genomic DNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="RPCI-23-99L13"

/sex="Female"

/lab\_host="DH10B"

/clone\_lib="RPCI-23"

/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1:

EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or

brain genomic DNA was isolated and partially digested

with a combination of EcoRI and EcoRI Methylase. Size

selected DNA was cloned into the pBACE3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

## ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 443;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
||||| ||||| ||||| |||||  
Db 345 CCCCTAAATGCTGCTAATC 363

RESULT 40  
DN183928  
LOCUS  
DEFINITION DN183928 456 bp mRNA linear EST 24-FEB-2005  
H016114S HO Hordeum vulgare cDNA clone H016114 5-PRIME, mRNA  
sequence.

ACCESSION DN183928  
VERSION DN183928.1 GI:60279185  
KEYWORDS EST.  
SOURCE Hordeum vulgare  
ORGANISM Hordeum vulgare

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
JOURNAL Pooideae; Triticeae; Hordeum.  
COMMENT 1 (bases 1 to 456)

REFERENCE  
AUTHORS Zierold, U. and Schweizer, P.  
TITLE Transcriptome analysis of mlo-mediated resistance in the epidermis  
JOURNAL of barley  
COMMENT Mol. Plant Pathol. (2005) In press

CONTACT: Patrick Schweizer  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, D-06466 Gatersleben, Germany  
Tel: 0049 (0)39482-5660  
Fax: 0049 (0)39482-5595  
Email: schweiz@ipk-gatersleben.de  
Insert Length: 456 Std Error: 0.00  
Plate: 16 row: I column: 14  
Seq primer: SK.

## FEATURES

Location/Qualifiers  
1..456  
/organism="Hordeum vulgare"  
/mol\_type="mRNA"  
/cultivar="Ingrid BC mlo-5"  
/db\_xref="GABI:1094605"  
/db\_xref="taxon:4513"  
/clone="H016114"  
/tissue\_type="leaf epidermis, 6 h and 24 h post  
inoculation with Blumeria graminis"  
/dev\_stage="7 d after germination"  
/lab\_host="XL10-Gold"  
/clone\_lib="HO"

/note="vector: pBlueScript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis hordei and tritici, respectively. Due to a cloning artefact present by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1.2 kb"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 8; Length 456;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 227 CCCCTGAGTCAGCTAATC 245  
||||| ||||| ||||| |||||

## RESULT 41

AV932335  
LOCUS

DEFINITION AV932335 463 bp mRNA linear EST 18-JAN-2002  
K. Sato unpublished cDNA library, cv. Haruna Nijo adult,  
heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA  
clone baal3d09 5', mRNA sequence.

ACCESSION AV932335  
VERSION AV932335.1 GI:18228132  
KEYWORDS EST.  
SOURCE Hordeum vulgare subsp. vulgare  
ORGANISM Hordeum vulgare subsp. vulgare

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
JOURNAL Pooideae; Triticeae; Hordeum.  
COMMENT 1 (bases 1 to 463)

REFERENCE  
AUTHORS Sato, K., Saisho, D. and Takeda, K.  
TITLE Barley EST sequencing project in NIG and Okayama Univ  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: teshini@genes.nig.ac.jp.

## FEATURES

Location/Qualifiers  
1..463  
/organism="Hordeum vulgare subsp. vulgare"  
/mol\_type="mRNA"  
/cultivar="Haruna Nijo"  
/sub\_species="vulgare"  
/db\_xref="taxon:112509"  
/clone="baal3d09"  
/tissue\_type="top three leaves"  
/dev\_stage="adult, heading stage"  
/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna  
Nijo adult, heading stage top three leaves"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 463;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
||||| ||||| ||||| |||||  
Db 236 CCCCTGAGTCAGCTAATC 254

## RESULT 42

CA657673  
LOCUS

DEFINITION CA657673 472 bp mRNA linear EST 24-NOV-2002  
wlm0.pk038.i13 wlm0 Triticum aestivum cDNA clone wlm0.pk038.i13 5'  
end, mRNA sequence.

ACCESSION CA657673  
VERSION CA657673.1 GI:25236198  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

REFERENCE  
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
TITLE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
JOURNAL Pooideae; Triticeae; Triticum.  
COMMENT 1 (bases 1 to 472)

REFERENCE  
AUTHORS Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
Miao, G., Caraher, N., and Hanafey, M.K.  
TITLE DuPont Wheat cDNA Sequence  
JOURNAL Unpublished (2002)  
COMMENT Contact: Scott V. Tingey  
Crop Genetics  
E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602  
 Fax: 302-631-2607  
 Email: Scott.V.Tingey@USA.dupont.com  
 Seq primer: M13.

# FEATURES

source  
 1. 472  
 Location/Qualifiers  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /cultivar="Stephens"  
 /db\_xref="taxon:4565"  
 /clone="wlm0.pk038.il3"  
 /tissue\_type="leaf"  
 /clone\_lib="wlm0"  
 /note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2: XhoI; Wheat (Triticum aestivum L.) seedlings 0 hr after inoculation with Erysiphe graminis f. sp. tritici"

# ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 472;  
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

Db 65 CCCCTGAATGGCGCTAATC 83

# RESULT 43

LOCUS AV774105/c  
 DEFINITION AV774105 Lotus japonicus Pods (20-30 mm in length) Lotus coniculatus var. japonicus cDNA clone MPD061h04\_f 3', mRNA  
 sequence.

ACCESSION AV774105.1 GI:45397780

# VERSION

# KEYWORDS

# SOURCE

ORGANISM Lotus corniculatus var. japonicus (Lotus japonicus)

LOCUS AV774105/c  
 DEFINITION AV774105 Lotus japonicus Pods (20-30 mm in length) Lotus coniculatus var. japonicus cDNA clone MPD061h04\_f 3', mRNA  
 sequence.

Qy 1 (bases 1 to 487)

Db 65 CCCCTGAATGGCGCTAATC 83

# REFERENCE

Ashimizu, E., Nakamura, Y., Sato, S. and Tabata, S.  
 Characteristics of the Lotus japonicus gene repertoire deduced from large-scale expressed sequence tag (EST) analysis  
 Plant Mol. Biol. 54 (3), 405-414 (2004)

# JOURNAL

# PUBMED

# COMMENT

Contact: Erika Asamizu  
 The First Laboratory for Plant Gene Research  
 Kazusa DNA Research Institute  
 Yana 1532-3, Kisarazu, Chiba 292-0812, Japan  
 Email: asamizu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.  
 Location/Qualifiers  
 1. 487  
 /organism="Lotus corniculatus var. japonicus"  
 /mol\_type="mRNA"  
 /isolate="Wiyakojima MG-20"  
 /db\_xref="taxon:34305"  
 /clone="MPD061h04\_f"  
 /tissue\_type="Pods (20-30 mm in length)"  
 /clone\_lib="Lotus japonicus Pods (20-30 mm in length)"  
 /note="Vector: pBluescriptII SK-; Site\_1: EcoRI; Site\_2: XhoI"

# ORIGIN

Query Match 83.2%; Score 15.8; DB 1; Length 487;  
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19

|||||

Db 448 CCCCTGAATGGCTAAAC 430

# RESULT 44

# LOCUS

# DEFINITION

# ACCESSION

# VERSION

# KEYWORDS

# SOURCE

# ORGANISM

# Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

# Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

# Pecora; Bovidae; Bovinae; Bos.

# REFERENCE

# AUTHORS

# 1 (bases 1 to 494)

# Holt, R., Stott, J., Yang, G., Barber, S., Smailus, D., Prabhu, A.-L.,

# Tsai, W., Cloutier, A., Lee, D., Gilm, N., Olson, T., Mayo, M.,

# Butterfield, Y., Kirkpatrick, R., Liu, J., Guin, R., Chan, A., Chiu, R.,

# Mathewson, C., Wye, N., Masson, A., Brown-John, M., Jones, S.,

# Schein, J., Marra, M., de Jong, P., McWilliam, S., Barris, W.,

# Dalrymple, B. P. and Tellam, R.

# Bovine BAC End Sequences from Library CHORI-240, PLATES 294 to 398

# Unpublished (2003)

# Other GSSs: CH240\_296A12.T7

# Contact: Rob Holt

# Sequencing

# The British Columbia Cancer Agency Genome Science Centre

# 600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6

# Tel: 604-877-6085

# Fax: 604-877-6276

# Email: rholt@bccsc.ca

# Clones are derived from the bovine BAC library CHORI-240

# (http://www.chori.org/bacpac/bovine240.htm). For BAC library

# availability, please contact Pieter de Jong (pdejong@chc.cho.org).

# Clones may be purchased from BACPAC Resources

# (http://www.chori.org/bacpac/ordering/information.htm). This work

# was undertaken as part of the International Bovine BAC Mapping

# Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the

# British Columbia Genome Sciences Centre, Canada.

# Plate: 296 row: A column: 12

# Seq primer: SP6

# Class: BAC ends.

# Location/Qualifiers

# 1. 494

# /organism="Bos taurus"

# /mol\_type="genomic DNA"

# /strain="breed: Hereford"

# /db\_xref="taxon:9913"

# /clones="CH240\_296A12"

# /sex="Male"

# /cell\_type="Blood"

# /clone\_lib="CHORI-240"

# /note="vector: pTARBAC1.3; Site\_1: MboI; Site\_2: MboI;

# Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC

# library (Male) produced by Pieter de Jong"

# ORIGIN

# Query Match 83.2%; Score 15.8; DB 9; Length 494;

# Best Local Similarity 89.5%; Pred. No. 1.6e+03;

# Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

# Qy 1 CCCCTGAATGGCGCTAATC 19

# |||||

# Db 468 CCCCTGAATTCGCTAATC 450

# RESULT 45

# LOCUS

# DEFINITION

# DN183756

# HO Hordeum vulgare cDNA clone HO16J13 5-PRIME, mRNA

# sequence.

# 1 (bases 1 to 511)

# DN183756

# HO Hordeum vulgare cDNA clone HO16J13 5-PRIME, mRNA

# sequence.

**ACCESSION** DNI183756  
**VERSION** DNI183756.1 GI:60279013  
**KEYWORDS** EST.  
**SOURCE** Hordeum vulgare  
**ORGANISM** Hordeum vulgare  
**REFERENCE** Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.  
**AUTHORS** 1 (bases 1 to 511)  
**TITLE** Zierold, U. and Schweizer, P.  
**JOURNAL** Transcriptionome analysis of mlo-mediated resistance in the epidermis of barley  
**COMMENT** Mol. Plant Pathol. (2005) In press  
 Contact: Patrick Schweizer  
 Transcriptionome Analysis, Cytogenetics Department  
 Institute of Plant Genetics and Crop Plant Research (IPK)  
 Corrensstr. 3, D-06466 Gatersleben, Germany  
 Tel: 0049 (0)39482-5660  
 Fax: 0049 (0)39482-5595  
 Email: schweiz@ipk-gatersleben.de  
 Insert Length: 511 Std Error: 0.00  
 Plate: 16 row: j column: 13  
 Seq primer: SK.  
**FEATURES** Location/Qualifiers  
 source 1..511  
 /organism="Hordeum vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Ingrid BC mlo-5"  
 /db\_xref="GABI:1094623"  
 /db\_xref="taxon:4513"  
 /clone="H016U13"  
 /tissue\_type="leaf epidermis, 6 h and 24 h post inoculation with Blumeria graminis"  
 /dev\_stage="7 d after germination"  
 /lab\_host="XL10-Gold"  
 /clone\_lib="HO"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis hordai and tritici, respectively. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1.2 kb"  
**ORIGIN**  
 Query Match 83.2%; Score 15.8; DB 8; Length 511;  
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGCGCTAATC 19  
 ||||| ||||| |||||  
 Db 227 CCCCTGAGTCGAGCTAATC 245  
**RESULT 46**  
**LOCUS** AW585068  
**DEFINITION** N211264e MHAM Medicago truncatula/Glomus versiforme mixed EST  
**ACCESSION** AW585068  
**VERSION** AW585068.1 GI:7262122  
**KEYWORDS** EST.  
**SOURCE** Medicago truncatula/Glomus versiforme mixed EST library  
**ORGANISM** Eukaryota; mixed EST libraries.  
**REFERENCE** 1 (bases 1 to 513)  
**AUTHORS** Harrison, M.J., Liu, J., Peng, H., Gonzales, M., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Fraser, C.M.  
**TITLE** ESTs from roots of Medicago truncatula after colonization with

**JOURNAL** COMMENT  
 Glomus versiforme  
 Unpublished (2000)  
 Contact: Harrison M.J.  
 Plant Biology Division  
 The Samuel Roberts Noble Foundation  
 2510 Sam Noble Parkway, Ardmore, OK 73401  
 Tel: 580-223-5810  
 Fax: 580-221-7380  
 Email: mjharrison@noble.org  
 Other name: MHAM-23b-B04; Date: 3/14/00; Updated to the Database of Expressed Sequence Tags (dbEST) on 04/27/00; More information is available at: <http://chrysie.tamu.edu/medicago/>.  
 Seq primer: T3.  
**FEATURES** Location/Qualifiers  
 source 1..513  
 /organism="Medicago truncatula/Glomus versiforme mixed EST library"  
 /mol\_type="mRNA"  
 /cultivar="Medicago truncatula genotype A17"  
 /db\_xref="taxon:119092"  
 /clone="MHAM-23C8"  
 /tissue\_type="roots colonized with Glomus versiforme"  
 /dev\_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."  
 /lab\_host="E. coli strain XL0LR"  
 /clone\_lib="MHAM"  
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propagated in XL0LR cells."  
**ORIGIN**  
 Query Match 83.2%; Score 15.8; DB 1; Length 513;  
 Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
 Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CCCCTGAATCGCGCTAATC 19  
 ||||| ||||| |||||  
 Db 254 CCCCTAATCGGCTAATC 272  
**RESULT 47**  
**LOCUS** CB884273/c  
**DEFINITION** EST00104 Oryza minuta 101144 subtracted cDNA library Oryza minuta cDNA clone omwi-146 similar to cysteine protease, mRNA sequence.  
**ACCESSION** CB884273  
**VERSION** CB884273.1 GI:46931502  
**KEYWORDS** EST.  
**SOURCE** Oryza minuta  
**ORGANISM** Oryza minuta  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoidae; Oryzae; Oryza.  
**REFERENCE** 1 (bases 1 to 525)  
**AUTHORS** Cho, S.K., Jeung, J.U., Shim, K.S., Jung, K.W., Kang, K.H., Chung, Y.S., Ok, S.H., Choi, H.C. and Shin, J.S.  
**TITLE** Oryza minuta 101144 subtracted cDNA library  
**JOURNAL** Unpublished (2003)  
**COMMENT** Contact: Sung Ki Cho, Ji Ung Jeung, Kyu Suk Shim, Kwang Wook Jung, Kyung Ho Kang, Young Soo Chung, Sung Han Ok, Hae Chune Choi and Jeong Sheop Shin  
 Plant Molecular Genetics  
 School of Life Science and Biotechnology, Korea University  
 5 Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701, Republic of Korea  
 Tel: 82 2 3290 3430  
 Fax: 82 2 927 9028

Email: jshin@korea.ac.kr

Seq primer: M13R.

Location/Qualifiers  
1. 525

/organism="Oryza minuta"  
/mol\_type="mRNA"  
/strain="101144"  
/db\_xref="taxon:63629"  
/clone="omwi-146"  
/tissue\_type="leaf"  
/dev\_stage="Wound treatment & vegetative stage"  
/clone\_lib="Oryza minuta 101144 subtracted cDNA library"  
/note="Vector: PCR2.1(Invitrogen); After the suppression  
subtractive hybridization and MOS (Nucleic Acids Research,  
Vol 28, No 20, e90), cDNA fragments induced by wound  
treatment were cloned by TA cloning method, and screened  
by microarray."

FEATURES  
source

## ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 525;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
|||||  
Db 488 CCCCTGAGTGCAGCTAATC 470

## RESULT 48

## LOCUS

CD026506 525 bp mRNA linear EST 01-MAY-2004  
DEFINITION EST00444 Oryza minuta 101144 subtracted cDNA library Oryza minuta  
cDNA clone omi-855, mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehrhartoideae; Oryzaceae; Oryza.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

1 (bases 1 to 525)  
Cho, S.K., Jeung, J.U., Shim, K.S., Jung, K.W., Kang, K.H., Chung, Y.S.,  
Ok, S.H., Choi, H.C. and Shin, J.S.  
Oryza minuta 101144 subtracted cDNA library  
Unpublished (2003)  
Contact: Sung Ki Cho, Ji Ung Jeung, Kyu Suk Shim, Kwang Wook Jung,  
Kyung Ho Kang, Young Soo Chung, Sung Han Ok, Hae Chune Choi and  
Jeong Sheop Shin

Plant Molecular Genetics

School of Life Science and Biotechnology, Korea University

5 Ga, Anam-Dong, Sungbuk-Gu, Seoul, 136-701, Republic of Korea

Tel: 82 2 3290 3430

Fax: 82 2 927 9028

Email: jshin@korea.ac.kr

Seq primer: M13R.

Location/Qualifiers  
1. 525

FEATURES  
source

/organism="Oryza minuta"  
/mol\_type="mRNA"  
/strain="101144"  
/db\_xref="taxon:63629"  
/clone="omi-855"  
/tissue\_type="leaf"  
/dev\_stage="Wound treatment & vegetative stage"  
/clone\_lib="Oryza minuta 101144 subtracted cDNA library"  
/note="Vector: PCR2.1(Invitrogen); After the suppression  
subtractive hybridization and MOS (Nucleic Acids Research,  
Vol 28, No 20, e90), cDNA fragments induced by wound  
treatment were cloned by TA cloning method, and screened  
by microarray."

## ORIGIN

## Query Match

83.2%; Score 15.8; DB 6; Length 525;

Best Local Similarity 89.5%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

|||||

Db 488 CCCCTGAGTGCAGCTAATC 470

## RESULT 49

## LOCUS

BJ469271

DEFINITION

BJ469271 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baall13p10 5', mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Pooidae; Triticeae; Hordeum.

1 (bases 1 to 544)

Sato, K., Saisho, D. and Takeda, K.

Barley EST sequencing project in NIG and Okayama Univ

Unpublished (2002)

Contact: Tadasu Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

1. 544

source

/organism="Hordeum vulgare subsp. vulgare"

/mol\_type="mRNA"

/cultivar="Haruna Nijo"

/sub\_species="vulgare"

/db\_xref="taxon:112509"

/clone="baall13p10"

/tissue\_type="top three leaves"

/dev\_stage="adult, heading stage"

/clone\_lib="K. Sato unpublished cDNA library, cv. Haruna

Nijo adult, heading stage top three leaves"

ORIGIN

Query Match 83.2%; Score 15.8; DB 3; Length 544;

Best Local Similarity 89.5%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

|||||

Db 328 CCCCTGAGTGCAGCTAATC 346

## RESULT 50

## LOCUS

FR0012843

DEFINITION

F.rubripes GSS sequence, clone 096E20aa7, genomic survey sequence.

ACCESSION

AL004093

VERSION

KEYWORDS

SOURCE

ORGANISM

Takifugu rubripes (Fugu rubripes)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;

Tetraodontoidea; Tetraodontidae; Takifugu.

1

REFERENCE

AUTHORS

Elgar, G., Clark, M.S., Meek, S., Smith, S., Warner, S., Edwards, Y.J.,

Bouchire, N., Cottage, A., Yeo, G.S., Umrana, Y., Williams, G. and



```

KEYWORDS EST.
SOURCE Oryza sativa
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.

REFERENCE
AUTHORS Yu,J., Wang,J., Lin,W., Li,S., Li,H., Zhou,J., Ni,P., Dong,W.,
Hu,S., Zeng,C., Zhang,J., Zhang,Y., Li,R., Xu,Z., Li,S., Li,X.,
Zheng,H., Cong,L., Lin,L., Yin,J., Geng,J., Li,G., Shi,J., Liu,J.,
Lv,H., Li,J., Wang,J., Deng,Y., Ran,L., Shi,X., Wang,X., Wu,Q.,
Li,C., Ren,X., Wang,X., Wang,X., Li,D., Liu,D., Zhang,X., Ji,Z.,
Zhao,W., Sun,Y., Zhang,Z., Bao,J., Han,Y., Dong,L., Ji,J., Chen,P.,
Wu,S. and Liu,J.
TITLE The Genomes of Oryza sativa: A History of Duplications
JOURNAL PLOS Biol. 3 (2), e38. (2005)
PUBLISHED 15685292
COMMENT Contact: Yan Zhou
Bioinformatics Department
Hangzhou Genomics Institute
No.51 Zhijiang Road, Hangzhou 310008, China
Tel: 86-571-56805886
Fax: 86-571-56805884
Email: zhoyuan@genomics.org.cn
Seq primer: M3 Forward
High quality sequence stop: 564
POLYA=No.

FEATURES
source Location/Qualifiers
1..564
/organism="Oryza sativa"
/mol_type="mRNA"
/cultivar="93-11"
/db_xref="taxon:4530"
/tissue_type="whole plant"
/dev_stage="tillering"
/clone_lib="Oryza sativa cv. 93-11 tillering whole plant
cDNA library"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 564;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 521 CCCCTGAGTGCGAGCTAATC 539

RESULT 54
AU249544 568 bp mRNA linear EST 14-MAR-2005
LOCUS AU249544 LE Lolium multiflorum cDNA clone LE009H09-5, mRNA
DEFINITION AU249544
ACCESSION AU249544
VERSION AU249544.1 GI:46506813
KEYWORDS EST.
SOURCE Lolium multiflorum (Italian ryegrass)
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Pooidae; Poaceae; Lolium.
REFERENCE 1 (bases 1 to 568)
AUTHORS Ikeda,S.
TITLE Lolium multiflorum EST Project
JOURNAL Unpublished (2004)
COMMENT Contact: Seiji Yazaki
Japan Grassland Agriculture and Forage Seed Association
Forage Crop Research Institute (FCRI)
Higashiakada 388-5, Nishinasuno, Tochigi 329-2742, Japan
Tel: 81-287-37-6755
Fax: 81-287-37-6757
Email: yazakis@frcs.or.jp
contact:Tadaaki Takamizo (takamizo@affrc.go.jp)

```

```

National Institute of Livestock and Grassland Science, Nishinasuno
Resistance gene analog.
Location/Qualifiers
1..568
/organism="Lolium multiflorum"
/mol_type="mRNA"
/db_xref="taxon:4521"
/clone_lib="LE009H09-5"
/tissue_type="leaf"
/clone_lib="LE"

ORIGIN
Query Match 83.2%; Score 15.8; DB 1; Length 568;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 533 CCCCTGAGTGCGAGCTAATC 551

RESULT 55
CE815985 569 bp DNA linear GSS 30-SEP-2003
LOCUS tigr-gss-dog-17000318393613 Dog Library Canis familiaris genomic,
DEFINITION CE815985
ACCESSION CE815985
VERSION CE815985.1 GI:37157005
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
REFERENCE 1 (bases 1 to 569)
AUTHORS Kirkness,B.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
PUBLISHED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.

FEATURES
source Location/Qualifiers
1..569
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BatXI; Libraries were prepared from
peripheral blood"

ORIGIN
Query Match 83.2%; Score 15.8; DB 10; Length 569;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATGGCGCTAATC 19
|||||
Db 261 CCCCTGAGTGCGAGCTAATC 279

RESULT 56
CB212741 570 bp mRNA linear EST 05-FEB-2003
LOCUS CB212741
DEFINITION OML03021 Oryza minuta HybridZAP-2.1 XR library Oryza minuta cDNA 5',

```

```

mRNA sequence.
ACCESSION CB212741
VERSION CB212741.1 GI:28258832
KEYWORDS EST.
SOURCE Oryza minuta
ORGANISM Oryza minuta
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Erihartoideae; Oryzeae; Oryza.
1 (bases 1 to 570)
REFERENCE
AUTHORS Shin,J.S.
TITLE Oryza minuta HybriZAP-2.1 XR library
JOURNAL Unpublished (2003)
COMMENT Contact: Jeong Sheop Shin
Plant Molecular Genetics
Graduate School of Biotechnology, University of Korea
136-701 Anam-dong 5/1 Seoul, Korea
Tel: 00 82 2 3290 3430
Fax: 00 82 2 927 9028
Email: jshin@kucn.ac.kr.
FEATURES
source
1..570
Location/Qualifiers
/organism="Oryza minuta"
/mol_type="mRNA"
/db_xref="taxon:63629"
/dev_stage="4-weeks after germination"
/clone_lib="Oryza minuta HybriZAP-2.1 XR library"
/note="Organ: immature leaf"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 570;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGCTAATC 19
||||| |||||
Db 144 CCCCTGAGTCGAGCTAATC 162

RESULT 57
BE403208
LOCUS BE403208 572 bp mRNA linear EST 21-JUL-2000
DEFINITION WHE0426 F08 K162S Wheat etiolated seedling root cDNA library
Triticum aestivum cDNA clone WHE0426_F08_K16, mRNA sequence.
ACCESSION BE403208
VERSION BE403208.1 GI:9362676
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 572)
REFERENCE
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D.,
Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,
Seaton,C.I. and Tong,J.C.
TITLE The structure and function of the expressed portion of the wheat
genomes
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanderson@w.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Strategene SK primer.
FEATURES
source
1..572
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"

/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0426_F08_K16"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the T3 Close lab (Choi, Close, Fenton) at the
University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
```



race BBB carrying the avirulence gene Avr1."

## ORIGIN

Query Match 83.2%; Score 15.8; DB 2; Length 574;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAAATC 19  
|||||

Db 519 CCCCTGAATCGCGTAAATC 537  
|||||

## RESULT 59

LOCUS CX625718/c  
DEFINITION CX625718 GAN Hordeum vulgare cDNA clone GAN006111 3-PRIME, mRNA  
sequence.

ACCESSION CX625718.1 GI:57824505

VERSION CX625718

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

REFERENCE 1 (bases 1 to 579)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
pooideae; Triticeae; Hordeum.

## AUTHORS

Biemelt, S., Jansen, C., Schaefer, P., Hueckelhoven, R., Felk, A.,  
Schaefer, W., Scholz, U., Sonnenschein, U. and Kogel, K.H.

TITLE Batley ESTs from different tissues challenged with fungal pathogens  
JOURNAL Unpublished (2004)

COMMENT Contact: Sophia Biemelt

Molecular Developmental Physiology, Department Molecular Cell

Biology

Institute of Plant Genetics and Crop Plant Research (IPK)

Corrensstr. 3, 06466 Gatersleben, Germany

Tel: +49 (0)39482-5476

Fax: +49 (0)39482-5515

Email: biemelt@ipk-gatersleben.de

Insert Length: 579 Std Error: 0.00

Plate: 6 row: 1 column: 11

Seq primer: M13uni.

## FEATURES

source

Location/Qualifiers

1..579

/organism="Hordeum vulgare"

/mol\_type="mRNA"

/cultivar="Ingred WT"

/db\_xref="GABI:861142"

/db\_xref="taxon:4513"

/clones="GAN006111"

/tissue\_type="leaf epidermis"

/lab\_host="XLI-Blue"

/clone\_lib="GAN"

/note="Vector: PCR blunt (Invitrogen); Site 1: NotI;  
Site 2: NotI; seedlings were grown at 18 degr. C, 60 %  
rel. humidity, and a photoperiod of 16 h (100 micromol s-1  
\* m-2). A. 8 days, seedl. were treated with ASM (syn. BTH;  
20 ppm soil drench). Leaf epid. was harv. 8, 24, 48, 72  
hpt). PolyA-RNA was isolated from leaf epidermis and used  
to create a cDNA-library using the Time Saver  
cDNA-Synthesis Kit (Amersham). Normalisation was performed  
essentially as described by Ko (1990, Nucl. Acid Res. 16,  
9877) with some modification of Kohchi et al. (1995, Plant  
J. 8, 771-776). Normalised cDNAs were digested with NotI  
and cloned into NotI digested pCRblunt vector.  
(GABI-Agrotech Project)"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 8; Length 579;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAAATC 19  
|||||

Db 200 CCCCTGAATCGCGTAAATC 182

## RESULT 60

LOCUS CF954381

DEFINITION CF954381

ACCESSION CF954381

VERSION CF954381

KEYWORDS EST.

SOURCE Oryza sativa (indica cultivar-group)

ORGANISM Oryza sativa (indica cultivar-group)

REFERENCE 1 (bases 1 to 581)

AUTHORS

Yu, J., Wang, J., Lin, W., Li, S., Li, H., Zhou, J., Ni, P., Dong, W.,  
Hu, S., Zeng, C., Zhang, J., Zhang, Y., Li, R., Xu, Z., Li, S., Li, X.,  
Zheng, H., Cong, L., Lin, L., Yin, J., Geng, J., Li, G., Shi, J., Liu, J.,  
Lv, H., Li, J., Wang, J., Deng, Y., Ran, L., Shi, X., Wang, X., Wu, Q.,  
Li, C., Ren, X., Wang, J., Wang, X., Li, D., Liu, D., Zhang, X., Ji, Z.,  
Zhao, W., Sun, Y., Zhang, Z., Bao, J., Han, Y., Dong, L., Ji, J., Chen, P.,  
Wu, S. and Liu, J.

TITLE The Genomes of Oryza sativa: A History of Duplications

JOURNAL PLOS Biol. 3 (2), e38 (2005)

PUBMED 15685292

COMMENT Contact: Yan Zhou

Bioinformatics Department

Hangzhou Genomics Institute

No. 51 Zhijiang Road, Hangzhou 310008, China

Tel: 86-571-56805886

Fax: 86-571-56805884

Email: zhouyan@genomics.org.cn

Seq primer: M13 Forward

High quality sequence stop: 581

POLYA=No.

Location/Qualifiers

1..581

/organism="Oryza sativa (indica cultivar-group)"

/mol\_type="mRNA"

/cultivar="PA64s"

/db\_xref="taxon:39946"

/tissue\_type="leaf"

/dev stage="trefoil"

/clone\_lib="Oryza sativa cv. PA64s leaf cDNA library"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 7; Length 581;

Best Local Similarity 89.5%; Pred. No. 1.6e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGCGTAAATC 19  
|||||

Db 526 CCCCTGAATCGCGTAAATC 544  
|||||

## RESULT 61

LOCUS CA255155

DEFINITION CA255155

ACCESSION CA255155

VERSION CA255155

KEYWORDS EST.

SOURCE Saccharum officinarum

ORGANISM Saccharum officinarum

REFERENCE 1 (bases 1 to 594)

AUTHORS

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

TITLE The libraries that made SUCEST  
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
COMMENT Contact: Arruda P  
Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
<http://www.bcccenter.fcav.unesp.br>  
Plate: 176 row: B column: 07  
Seq primer: T7 Promoter Primer.  
Location/Qualifiers  
1. .594  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCEPFL4176B07"  
/lab\_host="DH10B"  
/clone\_lib="FL4"  
/note="Organ: Developed inflorescence and rachis  
(20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI;  
An unidirectional cDNA library generated from [Developed  
inflorescence and rachis (20cm-long)]. cDNA was prepared  
from polyA+ mRNA using Superscript Plasmid System Kit  
(Invitrogen). The double-strand cDNAs were fractionated  
in a sapharose CL-2B 40cm-columns and fragments sizing  
between 0.8 and 1.5 Kb were directionally cloned into the  
vector. Details of each source of RNA and library  
construction can be obtained at  
<http://sucest.lad.ic.unicamp.br/public>"

ORIGIN  
Query Match 83.2%; Score 15.8; DB 6; Length 594;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
||||| ||||| ||||| |||||  
Db 2 CCCCTGGATGCAGCTAATC 20

RESULT 62  
CD876322 597 bp mRNA linear EST 11-JUL-2003  
LOCUS AZ03.109F19F011010 AZ03 Triticum aestivum cDNA clone AZ03109F19,  
DEFINITION mRNA sequence.  
ACCESSION CD876322 GI:32560138  
VERSION CD876322  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 597)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).  
Location/Qualifiers  
1. .597  
/organism="Triticum aestivum"  
/mol\_type="mRNA"

FEATURES  
source  
/cultivar="recital"  
/db\_xref="taxon:4565"  
/clone="AZ03109F19"  
/tissue\_type="leaf"  
/clone\_lib="AZ03"

ORIGIN  
Query Match 83.2%; Score 15.8; DB 6; Length 597;  
Best Local Similarity 89.5%; Pred. No. 1.6e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19  
||||| ||||| ||||| |||||  
Db 216 CCCCTGATGCAGCTAATC 234

RESULT 63  
BM135186 598 bp mRNA linear EST 28-NOV-2001  
LOCUS WHE0454\_H12\_H12S Wheat Fusarium graminearum infected spike cDNA  
DEFINITION library\_Triticum aestivum cDNA clone WHE0454\_H12\_H12, mRNA  
sequence.  
ACCESSION BM135186 GI:17143456  
VERSION BM135186  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 598)  
AUTHORS Anderson, O.D., Chao, S., Han, P.S., Heinen, S., Hsia, C.C., Kang, Y.,  
Kruger, W.M., Iazog, G.R., Miller, S., Muehlbauer, G.J., Miller, R.,  
Pritsch, C., Rausch, C.J., Seaton, C.L., Tong, J.C., Vance, C. and  
Wilson, C.F.  
The structure and function of the expressed portion of the wheat  
genes - Fusarium graminearum infected spike cDNA library  
Unpublished (2001)  
Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific  
West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: anders@pw.usda.gov  
Sequences have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20. No effort was taken  
to identify ESTs of fungal origin from this library, thus this EST  
could be of wheat or fungal origin.  
Seq primer: Stratagene SK primer.  
Location/Qualifiers  
1. .598  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Sumai3"  
/db\_xref="taxon:4565"  
/clone="WHE0454\_H12\_H12"  
/tissue\_type="Spike"  
/dev\_stage="Adult plant"  
/lab\_host="E. coli SOLR"  
/clone\_lib="Wheat Fusarium graminearum infected spike cDNA  
library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid  
pBluescript SK; Site\_1: EcoRI; Site\_2: XhoI; Plants were  
grown in the greenhouse. Spikes were sprayed at anthesis  
with Fusarium graminearum. Total RNA, and poly(A) RNA were  
prepared and pooled from infected spike at 0, 6, 12, 24,  
36 and 48 hours after inoculation, a cDNA library was  
made, and the cDNA clones were in vivo excised to give  
pBluescript phagemids in G. Muehlbauer lab at the  
University of Minnesota (Kruger, W.M., Muehlbauer, G.J.,  
Pritsch, C., Vance, C.). The cDNA library should contain  
genes of both wheat and fungal pathogen origin. Plasmid

DNA preparations and DNA sequencing were performed in the  
OD Anderson lab (all other authors)."

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ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 598;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||| ||| |||||
Db 578 CCCCTGAGTCGAGCTAATC 596

RESULT 64
CB680958
LOCUS
DEFINITION OSJNEF06J19.f OSJNEF Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEF06J19 5', mRNA sequence.
ACCESSION CB680958
VERSION CB680958
KEYWORDS EST.
SOURCE CB680958.1 GI:29684683
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Eriatolidae; Oryzaeae; Oryza.
1 (bases 1 to 601)
Jantassuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 06 row: J column: 19
Seq primer: gta aaa cga cgg cca gtg.
FEATURES
Location/Qualifiers
1..601
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEF06J19"
/tissue_type="leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEF"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 601;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||| ||| |||||
Db 495 CCCCTGAGTCGAGCTAATC 513

RESULT 65
DN178545
LOCUS
DEFINITION HO33C05S HO Hordeum vulgare cDNA clone HO33C05 5-PRIME, mRNA
sequence.
ACCESSION DN178545
VERSION DN178545.1 GI:60273802
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
1 (bases 1 to 602)
Zierold,U. and Schweizer,P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
of barley
Mol. Plant Pathol. (2005) In press
Contact: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert Length: 602 Std Error: 0.00
Plate: 33 row: C column: 5
Seq primer: SK.
FEATURES
Location/Qualifiers
1..602
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:1099872"
/db_xref="taxon:4513"
/clone="HO33C05"
/tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Approximately 5 % of
the clones correspond to cDNA from the fungi B. graminis
hordei and tritici, respectively. Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
1.2 kb"

ORIGIN
Query Match      83.2%; Score 15.8; DB 8; Length 602;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19
||||| ||| |||||
Db 212 CCCCTGAGTCGAGCTAATC 230

RESULT 66
AV933787
LOCUS
DEFINITION AV933787 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
clone baal8p11 5', mRNA sequence.
ACCESSION AV933787
VERSION AV933787.1 GI:18229584
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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1. .631
/organism="Sorghum bicolor"
/mol type="genomic DNA"
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DEFINITION OSJNEC10P06.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB5656403
VERSION CB5656403.1 GI:29660246
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 636)
AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15888683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: p column: 06
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1..636
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10P06"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/organism="Oryza sativa (japonica cultivar-group)"
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 636;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 494 CCCCTGAGTCGAGCTAATC 512

RESULT 70
CB5656403
LOCUS OSJNEC10L13.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
DEFINITION OSJNEC10L13.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION CB5656403
VERSION CB5656403.1 GI:29660128
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 637)
AUTHORS Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in

```

```

rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 15888683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 10 row: l column: 13
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1..637
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC10L13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/organism="Oryza sativa (japonica cultivar-group)"
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 637;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 495 CCCCTGAGTCGAGCTAATC 513

RESULT 71
CB472488
LOCUS BJ472488 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
ACCESSION BJ472488
VERSION BJ472488.1 GI:21150991
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 648)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..648
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal34n08"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 637;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 495 CCCCTGAGTCGAGCTAATC 513

RESULT 71
CB472488
LOCUS BJ472488 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,
DEFINITION heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
ACCESSION BJ472488
VERSION BJ472488.1 GI:21150991
KEYWORDS EST.
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 648)
AUTHORS Sato,K., Saisho,D. and Takeda,K.
TITLE Barley EST sequencing project in NIG and Okayama Univ
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center for Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..648
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal34n08"

FEATURES
source

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/tissue type="top three leaves"
/dev stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 648;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 255 CCCCTGAGTCAGCTAATC 273

RESULT 72
BJ469669
LOCUS
DEFINITION
  BJ469669 K. Sato unpublished cDNA library, linear EST 23-MAY-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal27n10 5', mRNA sequence.
ACCESSION
BJ469669
VERSION
BJ469669.1 GI:21148172
KEYWORDS
EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 654)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  source
    1..654
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Haruna Nijo"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baal27n10"
    /tissue type="top three leaves"
    /dev stage="adult, heading stage"
    /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
    Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 3; Length 654;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 256 CCCCTGAGTCAGCTAATC 274

RESULT 73
AJ432460
LOCUS
DEFINITION
  AJ432460 S00007 Hordeum vulgare cDNA clone S0000700037F06P1, mRNA
  sequence.
ACCESSION
AJ432460
VERSION
AJ432460.1 GI:19520912
KEYWORDS
EST.
SOURCE
  Hordeum vulgare
  Hordeum vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 659)
REFERENCE
  Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
  Barley EST's
  Unpublished (2002)
  Contact: Schulman AH
  Institute of Biotechnology
  University of Helsinki
  P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
  Finland.
FEATURES
  source
    1..659
    /organism="Hordeum vulgare"
    /mol_type="mRNA"
    /db_xref="taxon:4513"
    /clone="S0000700037F06P1"
    /dev stage="Shoot"
    /clone_lib="S00007"
    /note="2,3-,4-days after germination"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 659;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 161 CCCCTGAGTCAGCTAATC 179

RESULT 74
AV933115
LOCUS
DEFINITION
  AV933115 K. Sato unpublished cDNA library, linear EST 18-JAN-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal59l8 5', mRNA sequence.
ACCESSION
AV933115
VERSION
AV933115.1 GI:18228912
KEYWORDS
EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 662)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  source
    1..662
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Haruna Nijo"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baal59l8"
    /tissue type="top three leaves"
    /dev stage="adult, heading stage"
    /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
    Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 662;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 659)
REFERENCE
  Saren, A.-M., Tanskanen, J., Paulin, L. and Schulman, A.H.
  Barley EST's
  Unpublished (2002)
  Contact: Schulman AH
  Institute of Biotechnology
  University of Helsinki
  P.O.Box 56 (Viikinkaari 6A), University of Helsinki FIN-00014,
  Finland.
FEATURES
  source
    1..659
    /organism="Hordeum vulgare"
    /mol_type="mRNA"
    /db_xref="taxon:4513"
    /clone="S0000700037F06P1"
    /dev stage="Shoot"
    /clone_lib="S00007"
    /note="2,3-,4-days after germination"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 659;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
    ||||| ||| |||||
Db 161 CCCCTGAGTCAGCTAATC 179

RESULT 74
AV933115
LOCUS
DEFINITION
  AV933115 K. Sato unpublished cDNA library, linear EST 18-JAN-2002
  heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA
  clone baal59l8 5', mRNA sequence.
ACCESSION
AV933115
VERSION
AV933115.1 GI:18228912
KEYWORDS
EST.
SOURCE
  Hordeum vulgare subsp. vulgare
  Hordeum vulgare subsp. vulgare
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
  Pooideae; Triticeae; Hordeum.
  1 (bases 1 to 662)
REFERENCE
  Sato, K., Saisho, D. and Takeda, K.
  Barley EST sequencing project in NIG and Okayama Univ
  Unpublished (2002)
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
FEATURES
  source
    1..662
    /organism="Hordeum vulgare subsp. vulgare"
    /mol_type="mRNA"
    /cultivar="Haruna Nijo"
    /sub_species="vulgare"
    /db_xref="taxon:112509"
    /clone="baal59l8"
    /tissue type="top three leaves"
    /dev stage="adult, heading stage"
    /clone_lib="K. Sato unpublished cDNA library, cv. Haruna
    Nijo adult, heading stage top three leaves"

ORIGIN
Query Match      83.2%; Score 15.8; DB 1; Length 662;
Best Local Similarity 89.5%; Pred. No. 1.6e+03;

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
||||| ||| |||||  
Db 256 CCCCTGAGTGCAGCTAATC 274

## RESULT 75

CA744325 681 bp mRNA linear EST 26-NOV-2002  
LOCUS wrils.pk007.018 wrils Triticum aestivum cDNA clone wrils.pk007.018  
DEFINITION 5' end, mRNA sequence.

ACCESSION CA744325 GI:25560148

VERSION CA744325.1

KEYWORDS EST.

SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 681)

AUTHORS Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,

Miao, G., Caraher, N. and Hanafey, M.K.

TITLE DuPont Wheat cDNA Sequence

JOURNAL Unpublished (2002)

COMMENT Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: T7.

## FEATURES

source

1. 681  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4565"  
/clone="wrils.pk007.018"  
/tissue\_type="leaf"  
/lab\_host="DH10B"  
/clone\_lib="wrils"  
/note="Vector: pGEM-T Easy; Site 1: SmaI; Riband (susceptible) wheat leaves infected with Septoria tritici strain A, 24 hours after infection, subtracted w/ comparable uninfected leaves"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 681;

Best Local Similarity 89.5%; Pred. NO. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
||||| ||| |||||

Db 253 CCCCTGAGTGCAGCTAATC 271  
||||| ||| |||||

## RESULT 76

CD054348 686 bp mRNA linear EST 05-JUN-2003  
LOCUS HO01L09r HO Hordeum vulgare cDNA clone HO01L09 5-PRIME, mRNA  
DEFINITION sequence.

ACCESSION CD054348

VERSION CD054348.1

KEYWORDS EST.

SOURCE Hordeum vulgare

ORGANISM Hordeum vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 686)

AUTHORS Zierold, U. and Schweizer, P.

TITLE Transcriptome analysis of mlo-mediated resistance in the epidermis

## JOURNAL

## COMMENT

of barley  
Mol. Plant Pathol. (2005) In press  
Contact: Patrick Schweizer  
Transcriptome Analysis, Cytogenetics Department  
Institute of Plant Genetics and Crop Plant Research (IPK)  
Corrensstr. 3, D-06466 Gatersleben, Germany  
Tel: 0049 (0)39482-5660  
Fax: 0049 (0)39482-5595

Email: schweiz@ipk-gatersleben.de

Insert Length: 686 Std Error: 0.00

Plate: 1 row: L column: 9

Seq primer: M13rev.

Location/Qualifiers

## FEATURES

source

1. 686  
/organism="Hordeum vulgare"

/mol\_type="mRNA"

/cultivar="Ingrid BC mlo-5"

/db\_xref="GABI:703932"

/db\_xref="taxon:4513"

/clone="HO01L09"

/tissue\_type="leaf epidermis, 6 h and 24 h post

inoculation with Blumeria graminis"

/dev\_stage="7 d after germination"

/lab\_host="XL10-Gold"

/clone\_lib="HO"

/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of the clones correspond to cDNA from the fungi B. graminis hordei and tritici, respectively. Due to a cloning artefact caused by the kit, in most cases the EcoRI site is NOT present, as well as the EcoRI adapter used for cloning. To excise the insert, restriction sites upstream EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also due to the cloning system used Blue/white selection for recombinants is not 100% reliable. Average insert size is 1.2 kb"

## ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 686;

Best Local Similarity 89.5%; Pred. No. 1.7e+03;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19  
||||| ||| |||||

Db 80 CCCCTGAGTGCAGCTAATC 98  
||||| ||| |||||

## RESULT 77

BJ471067

LOCUS

DEFINITION

695 bp mRNA linear EST 23-MAY-2002

BJ471067 K. Sato unpublished cDNA library, cv. Haruna Nijo adult,

heading stage top three leaves Hordeum vulgare subsp. vulgare cDNA

clone baal30j04 5', mRNA sequence.

ACCESSION BJ471067

VERSION BJ471067.1

KEYWORDS EST.

SOURCE Hordeum vulgare subsp. vulgare

ORGANISM Hordeum vulgare subsp. vulgare

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Hordeum.

REFERENCE 1 (bases 1 to 695)

AUTHORS Sato, K., Saisho, D. and Takeda, K.

TITLE Barley EST sequencing project in NIG and Okayama Univ

JOURNAL Unpublished (2002)

COMMENT Contact: Tadashi Shin-i

Center For Genetic Resource Information

National Institute of Genetics

1111 Yata, Mishima, Shizuoka 411-8540, Japan

Tel: 81-559-81-6856

Fax: 81-559-81-6855

Email: tshini@genes.nig.ac.jp.

Location/Qualifiers

```

source
1. .695
/organism="Hordeum vulgare subsp. vulgare"
/mol_type="mRNA"
/cultivar="Haruna Nijo"
/sub_species="vulgare"
/db_xref="taxon:112509"
/clone="baal30j04"
/tissue_type="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, cv. Haruna
Nijo adult, heading stage top three leaves"

ORIGIN
Query Match 83.2%; Score 15.8; DB 3; Length 695;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 265 CCCCTGAGTCAGCTAATC 283

RESULT 78
BZ008560
LOCUS
DEFINITION osf04h07.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
sequence.
ACCESSION BZ008560
VERSION BZ008560.1 GI:23556906
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE 1 (bases 1 to 698)
Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T.,
Nash,W., Rabinowicz,P.D. and Wilson,R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
CONTACT: Richard K. Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Plate: oef04 row: h column: 07
Seq primer: -21UPPOT forward
Class: shotgun
High quality sequence start: 17
High quality sequence stop: 543.
FEATURES
Location/Qualifiers
source
1. .698
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pOTW13; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear
prep using Brassica oleracea T01000DH3 buds provided by
Thomas Osborn at the University of Wisconsin. Genomic
DNA was provided by Pablo Rabinowicz (CSHL) and the
shotgun library prepared at Washington University Genome
Sequencing Center."

ORIGIN
Query Match 83.2%; Score 15.8; DB 9; Length 698;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 177 CCCCTGACGCGGCTAATC 195

```

```

RESULT 79
DN178149
LOCUS
DEFINITION HO34C21S HO Hordeum vulgare cDNA clone HO34C21 5-PRIME, mRNA
sequence.
ACCESSION DN178149
VERSION DN178149.1 GI:60273406
KEYWORDS EST.
SOURCE Hordeum vulgare
ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 700)
Zierold,U. and Schweizer,P.
Transcriptome analysis of mlo-mediated resistance in the epidermis
of barley
Mol. Plant Pathol. (2005) In press
CONTACT: Patrick Schweizer
Transcriptome Analysis, Cytogenetics Department
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, D-06466 Gatersleben, Germany
Tel: 0049 (0)39482-5660
Fax: 0049 (0)39482-5595
Email: schweiz@ipk-gatersleben.de
Insert Length: 700 Std Error: 0.00
Plate: 34 row: C column: 21
Seq primer: SK.
FEATURES
Location/Qualifiers
source
1. .700
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Ingrid BC mlo-5"
/db_xref="GABI:1100216"
/db_xref="taxon:4513"
/clone="HO34C21"
/tissue_type="leaf epidermis, 6 h and 24 h post
inoculation with Blumeria graminis"
/dev_stage="7 d after germination"
/lab_host="XL10-Gold"
/clone_lib="HO"
/note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
cDNA); Site 2: XhoI (3'-end of cDNA); Approximately 5 % of
the clones correspond to cDNA from the fungi B. graminis
hordel and tritici, respectively. Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is
1.2 kb"

ORIGIN
Query Match 83.2%; Score 15.8; DB 8; Length 700;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
||||| ||| |||||
Db 83 CCCCTGAGTCAGCTAATC 101

RESULT 80
BH516786/c
LOCUS
DEFINITION BOHGR66TR BOHG Brassica oleracea genomic clone BOHGR66, genomic
survey sequence.
ACCESSION BH516786
VERSION BH516786.1 GI:17724876
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea

```



Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

# REFERENCE AUTHORS

1 (bases 1 to 713)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis Genome Res. 15 (4), 487-495 (2005)

# JOURNAL PUBMED

15805490

Other\_GSSs: BOHGR66TF

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TR

Class: sheared ends.

# FEATURES source

Location/Qualifiers

1..713

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TOL000DH3"

/db\_xref="taxon:3712"

/clones="BOHGR66"

/clone\_lib="BOHG"

/note="Vector: pHOSt1; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOSt1 using BstXI linkers"

# ORIGIN

Query Match 83.2%; Score 15.8; DB 9; Length 713;  
Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 348 CCCCTGGACGGCTAATC 330

RESULT 81  
CA240024 716 bp mRNA linear EST 25-SEP-2003  
LOCUS SCSBFL4063E11.9 FLA Saccharum officinarum cDNA clone SCSBFL4063E11  
DEFINITION 5', mRNA sequence.

CA240024

CA240024.1 GI:35313215

EST.

KEYWORDS

SOURCE

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade: Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum

complex.

1 (bases 1 to 716)

Vettore, A.L., da Silva, F.R., Kemper, E.L. and Arruda, P.

The libraries that made SUCEST

Genet. Mol. Biol. 24 (1-4), 1-7 (2001)

Contact: Arruda P

Centro de Biologia Molecular e Engenharia Genetica

Universidade Estadual de Campinas

Caixa Postal 6010, 13083-970, Campinas SP, Brazil

Tel: 55 19 3788 1137

Fax: 55 19 3788 1089

Email: parruda@unicamp.br

Clone distribution: clone distribution information can be found

through the Brazilian Clone Collection Center (BCCC) at

http://www.bcccenter.fcav.unesp.br

Plate: 063 row: E column: 11

Seq primer: T7 Promoter Primer.

Location/Qualifiers

1..716

/organism="Saccharum officinarum"

/mol\_type="mRNA"

/db\_xref="taxon:4547"

/clones="SCSBFL4063E11"

/lab\_host="DH10B"

/clone\_lib="FLA"

/note="Organ: Developed inflorescence and rachis (20cm-long); Vector: pSport1; Site 1: SalI; Site 2: NotI; An unidirectional cDNA library generated from [Developed inflorescence and rachis (20cm-long)]. cDNA was prepared from polyA+ mRNA using SuperScript plasmid System Kit (Invitrogen). The double-strand cDNAs were fractionated in a sepharose CL-2B 40cm-columns and fragments sizing between 0.8 and 1.5 kb were directionally cloned into the vector. Details of each source of RNA and library construction can be obtained at http://sucest.lad.ic.unicamp.br/public"

# ORIGIN

Query Match 83.2%; Score 15.8; DB 6; Length 716;  
Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19

Db 684 CCCCTGGATCGAGCTAATC 702

# RESULT 82

CB662892

LOCUS

DEFINITION

OSJNBD07F03.f OSJNBD Oryza sativa (japonica cultivar-group) cDNA

clone OSJNBD07F03 5', mRNA sequence.

ACCESSION

CB662892

VERSION

CB662892.1 GI:29666617

KEYWORDS

EST.

SOURCE

Oryza sativa (japonica cultivar-group)

Eukaryota; Viridiplantae; Streptophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzaceae; Oryza.

1 (bases 1 to 749)

Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,

Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,

Soderlund, C. and Wang, G.L.

Large-scale identification of expressed sequence tags involved in

rice and rice blast fungus interaction

Plant Physiol. 138 (1), 105-115 (2005)

15888683

COMMENT

Contact: Rod Wing

Arizona Genomics Institute

University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 626 3967

Fax: 520 621 9288

Email: rwing@genome.arizona.edu

PCR Primers

FORWARD: gta aac cga cgg cca gtc

BACKWARD: gga aac agc tat gac cat g

Plate: 07 row: F column: 03

Seq primer: gta aac cga cgg cca gtc.

Location/Qualifiers

1..749

/organism="Oryza sativa (japonica cultivar-group)"

/mol\_type="mRNA"

/cultivar="Nipponbare"

/db\_xref="taxon:39947"

/clones="OSJNBD07F03"

/tissue\_type="Leaf"

/dev\_stage="3 week"

/lab\_host="DH10B"

/clone\_lib="OSJNBD"

/note="vector: pBluescript II KS +; Site 1: EcoRI; Site 2: XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

```

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 749;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGCGCTAATC 19
    ||||| ||||| ||||| |||||
Db 501 CCCCTGAGTCGAGCTAATC 519

RESULT 83
CO033780/c
LOCUS
DEFINITION
EST812164 Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb Coccidioides posadasii cDNA clone C1FBP43 3' end, mRNA sequence.
CO033780
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 777)
AUTHORS
Gardner, M.J. and Cole, G.T.
TITLE
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
JOURNAL
Unpublished (2003)
COMMENT
Other ESTs: EST812165
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.

FEATURES
source
Location/Qualifiers
1..777
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="C1FBP43"
/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii spherule cDNA library,
0.5 to 5.3 kb"
/note="vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.5 to 5.3
kb"

ORIGIN
Query Match      83.2%; Score 15.8; DB 7; Length 777;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGCGCTAATC 19
    ||||| ||||| ||||| |||||
Db 343 CCCCTGATTCGGGCTAATC 325

RESULT 84
CB659097
LOCUS
DEFINITION
OSJNEC15M06.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNEC15M06 5', mRNA sequence.
CB659097
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

/
note="vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"

REFERENCE
1 (bases 1 to 778)
AUTHORS
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C., and Wang, G.L.
TITLE
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL
Plant Physiol. 138 (1), 105-115 (2005)
PUBMED
15888683
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 15 row: M column: 06
Seq primer: gta aaa cga cgg cca gtc.
Location/Qualifiers
1..778
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC15M06"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 778;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGCGCTAATC 19
    ||||| ||||| ||||| |||||
Db 518 CCCCTGAGTCGAGCTAATC 536

RESULT 85
CB624346/c
LOCUS
DEFINITION
OSIIEal2N18.r OSIIEa Oryza sativa (indica cultivar-group) cDNA
clone OSIIEal2N18 3', mRNA sequence.
CB624346
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzae; Oryza.
1 (bases 1 to 786)
Jantasuriyarat, C., Gowda, M., Haller, K., Hatfield, J., Lu, G.,
Stahlberg, E., Zhou, B., Li, H., Kim, H., Yu, Y., Dean, R.A., Wing, R.A.,
Soderlund, C., and Wang, G.L.
TITLE
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL
Plant Physiol. 138 (1), 105-115 (2005)
PUBMED
15888683
COMMENT
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA

```

```

Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: N column: 18
Seq primer: gga aac agc tat gac cat g.
Location/Qualifiers
1. .786
/organism="Oryza sativa (indica cultivar-group)"
/mol_type="mRNA"
/db_xref="taxon:39946"
/clone="OSJNE12K24"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNE"
/notes="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Lesion Mimic SPL II"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 786;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 782 CCCCTGAGTGCGAGCTAATC 764

RESULT 86
CB657398
LOCUS
DEFINITION
OSJNE12K24.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNE12K24 5', mRNA sequence.
ACCESSION
CB657398
VERSION
CB657398
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 790)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
1. .790
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNE12K24"

FEATURES
source
Query Match 83.2%; Score 15.8; DB 6; Length 786;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 782 CCCCTGAGTGCGAGCTAATC 764

RESULT 86
CB657398
LOCUS
DEFINITION
OSJNE12K24.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
clone OSJNE12K24 5', mRNA sequence.
ACCESSION
CB657398
VERSION
CB657398
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 790)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 12 row: K column: 24
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="OSJNE12K24"

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Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 503 CCCCTGAGTGCGAGCTAATC 521

RESULT 87
CB648104
LOCUS
DEFINITION
OSJNE11F13.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNE11F13 5', mRNA sequence.
ACCESSION
CB648104
VERSION
CB648104
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 795)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 13
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/db_xref="taxon:39947"
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/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
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XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||

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/lab_host="DH10B"
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XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
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Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||
Db 503 CCCCTGAGTGCGAGCTAATC 521

RESULT 87
CB648104
LOCUS
DEFINITION
OSJNE11F13.f OSJNEB Oryza sativa (japonica cultivar-group) cDNA
clone OSJNE11F13 5', mRNA sequence.
ACCESSION
CB648104
VERSION
CB648104
KEYWORDS
EST.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 795)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 11 row: F column: 13
Seq primer: gta aac cga cgg cca gtc.
Location/Qualifiers
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/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
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/db_xref="taxon:39947"
/clone="OSJNE11F13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEB"
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XhoI; 24 hrs after inoculation with Rice Blast (Che
86061)"

ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 795;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGCGGCTAATC 19
||||| ||| |||||

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Db 497 CCCTGAGTGCAGCTAATC 515

RESULT 88  
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LOCUS  
DEFINITION  
OSIIEa12N18.f OSIIEa Oryza sativa (indica cultivar-group) cDNA  
clone OSIIEa12N18 5', mRNA sequence.

ACCESSION  
CB624345

VERSION  
CB624345.1 GI:29619333

KEYWORDS  
EST.

SOURCE  
Oryza sativa (indica cultivar-group)

ORGANISM  
Oryza sativa (indica cultivar-group)

REFERENCE  
AUTHORS  
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,  
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,  
Soderlund,C. and Wang,G.L.

TITLE  
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85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 12 row: N column: 18  
Seq primer: gta aaa cga cgg cca gtc.

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGAGTGCAGCTAATC 19  
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Db 629 CCCTGAGTGCAGCTAATC 647

RESULT 89  
CL746478/c

LOCUS  
DEFINITION  
OR\_BBa0083P09.r OR\_BBa Oryza sativa genomic clone OR\_BBa0083P09 3',  
genomic survey sequence.

ACCESSION  
CL746478

VERSION  
CL746478.1 GI:50688734

KEYWORDS  
GSS.

SOURCE  
Oryza sativa

ORGANISM  
Oryza sativa

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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85721-0088, USA  
Tel: 520 626 3967  
Fax: 520 621 9288  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 12 row: N column: 18  
Seq primer: gta aaa cga cgg cca gtc.

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/clone\_lib="OR\_BBa"  
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGAGTGCAGCTAATC 19  
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Db 644 CCCTGAGTGCAGCTAATC 626

RESULT 90  
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LOCUS  
DEFINITION  
CB655953  
clone OSJNEC09M13 5', mRNA sequence.

ACCESSION  
CB655953

VERSION  
CB655953.1 GI:29659678

KEYWORDS  
EST.

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Oryza sativa (japonica cultivar-group)

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

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Fax: 520 621 9288  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
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Plate: 12 row: N column: 18  
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/lab\_host="DH10B-T1 phage resistant"  
/clone\_lib="OR\_BBa"  
/note="Vector: pGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

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Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGAGTGCAGCTAATC 19  
|||||  
644 CCCTGAGTGCAGCTAATC 626

Db 644 CCCTGAGTGCAGCTAATC 626

RESULT 90  
CB655953

LOCUS  
DEFINITION  
CB655953  
clone OSJNEC09M13 5', mRNA sequence.

ACCESSION  
CB655953

VERSION  
CB655953.1 GI:29659678

KEYWORDS  
EST.

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Oryza sativa (japonica cultivar-group)

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE  
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Fax: 520 621 9288  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGAGTGCAGCTAATC 19  
|||||  
644 CCCTGAGTGCAGCTAATC 626

Db 644 CCCTGAGTGCAGCTAATC 626

RESULT 90  
CB655953

LOCUS  
DEFINITION  
CB655953  
clone OSJNEC09M13 5', mRNA sequence.

ACCESSION  
CB655953

VERSION  
CB655953.1 GI:29659678

KEYWORDS  
EST.

SOURCE  
Oryza sativa (japonica cultivar-group)

ORGANISM  
Oryza sativa (japonica cultivar-group)

REFERENCE  
AUTHORS  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

TITLE  
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Fax: 520 621 9288  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: gta aaa cga cgg cca gtc  
BACKWARD: gga aac agc tat gac cat g  
Plate: 12 row: N column: 18  
Seq primer: gta aaa cga cgg cca gtc.

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Query Match 83.2%; Score 15.8; DB 10; Length 800;  
Best Local Similarity 89.5%; Pred. No. 1.7e+03;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCTGAGTGCAGCTAATC 19  
|||||  
644 CCCTGAGTGCAGCTAATC 626

Db 644 CCCTGAGTGCAGCTAATC 626

RESULT 90  
CB655953

LOCUS  
DEFINITION  
CB655953  
clone OSJNEC09M13 5', mRNA sequence.

ACCESSION  
CB655953

VERSION  
CB655953.1 GI:29659678

KEYWORDS  
EST.

S

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/clone="OSJNEC09M13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 810;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
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Db 501 CCCCTGAGTGCAGCTAATC 519

RESULT 91
CB656772
LOCUS      825 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEC11H22.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION  CB656772
VERSION     1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 825)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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COMMENT     Contact: Rod Wing
            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtcg
            BACKWARD: gga aac agc tat gac cat g
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            /cultivar="Nipponbare"
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            /tissue_type="Leaf"
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            /lab_host="DH10B"
            /clone_lib="OSJNEC"
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FEATURES
source
Plate: 09 row: M column: 13
Seq primer: gta aaa cga cgg cca gtcg.
Location/Qualifiers
1. .810
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNEC09M13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNEC"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 810;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
    ||||| ||| |||||
Db 501 CCCCTGAGTGCAGCTAATC 519

RESULT 91
CB656772
LOCUS      825 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEC11H22.f OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION  CB656772
VERSION     1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 825)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtcg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 11 row: H column: 22
            Seq primer: gta aaa cga cgg cca gtcg.
            Location/Qualifiers
            1. .825
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /clone="OSJNEC11H22"
            /tissue_type="Leaf"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /clone_lib="OSJNEC"
            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
            XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source

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ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 825;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
    ||||| ||| |||||
Db 658 CCCCTGAGTGCAGCTAATC 676

RESULT 92
CB657399/c
LOCUS      834 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEC12K24.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA
ACCESSION  CB657399
VERSION     1
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
ORGANISM    Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 834)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
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rice and rice blast fungus interaction
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            Arizona Genomics Institute
            University of Arizona
            Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
            85721-0088, USA
            Tel: 520 626 3967
            Fax: 520 621 9288
            Email: rwing@genome.arizona.edu
            PCR Primers
            FORWARD: gta aaa cga cgg cca gtcg
            BACKWARD: gga aac agc tat gac cat g
            Plate: 12 row: K column: 24
            Seq primer: gga aac agc tat gac cat g.
            Location/Qualifiers
            1. .834
            /organism="Oryza sativa (japonica cultivar-group)"
            /mol_type="mRNA"
            /cultivar="Nipponbare"
            /db_xref="taxon:39947"
            /clone="OSJNEC12K24"
            /tissue_type="Leaf"
            /dev_stage="3 week"
            /lab_host="DH10B"
            /clone_lib="OSJNEC"
            /note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
            XhoI; 6 hrs after inoculation with Rice Blast (C9240-1)"

FEATURES
source
Query Match      83.2%; Score 15.8; DB 6; Length 834;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGGCTAATC 19
    ||||| ||| |||||
Db 777 CCCCTGAGTGCAGCTAATC 759

RESULT 93
CB663361/c
LOCUS      851 bp mRNA linear EST 09-APR-2003
DEFINITION OSJNEC08D13.r OSJNEC Oryza sativa (japonica cultivar-group) cDNA

```

```

clone OSJNE08D13 3', mRNA sequence.
ACCESSION CB663361
VERSION CB663361.1 GI:29667086
KEYWORDS EST.
SOURCE Oryza sativa (japonica cultivar-group)
ORGANISM Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehartoideae; Oryzeae; Oryza.
1 (bases 1 to 851)
REFERENCE Jantaauriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
AUTHORS Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
TITLE Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
JOURNAL Plant Physiol. 138 (1), 105-115 (2005)
PUBMED 1588683
COMMENT Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aaa cga cgg cca gtc
BACKWARD: gga aac agc tat gac cat g
Plate: 08 row: D column: 13
Seq primer: gga aac agc tat gac cat g.
FEATURES
source
Location/Qualifiers
1..851
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="mRNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/clone="OSJNE08D13"
/tissue_type="Leaf"
/dev_stage="3 week"
/lab_host="DH10B"
/clone_lib="OSJNE"
/note="Vector: pBluescript II KS +; Site 1: EcoRI; Site 2:
XhoI; 24 hrs after inoculation with Rice Blast (C9240-1)"
ORIGIN
Query Match 83.2%; Score 15.8; DB 6; Length 851;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 764 CCCCTGAGTCGAGCTAATC 746

RESULT 94
CK156356 861 bp mRNA linear EST 05-DEC-2003
LOCUS FGAS037309 Triticum aestivum FGAS: TaLT4 Triticum aestivum cDNA,
DEFINITION mRNA sequence.
ACCESSION CK156356
VERSION CK156356.1 GI:38979376
KEYWORDS EST.
SOURCE Triticum aestivum (bread wheat)
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.
1 (bases 1 to 861)
REFERENCE Allard,F., Crosby,W.L., Danyluk,J., Eudes,F., Frick,M., Gaudet,D.,
AUTHORS Genswein,B., Grat,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Penniket,C., Roach,J.L. and Sarhan,F.
TITLE Functional Genomics of Abiotic Stress In Wheat and Canola Crops

clone OSJNE08D13 3', mRNA sequence.
JOURNAL COMMENT
Unpublished (2003)
Contact: Wm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada
Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_esta@cs.usask.ca
This sequence is the direct result of the Base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [122,733].
Plate: TaLT411, row: K column: 10.
FEATURES
source
Location/Qualifiers
1..861
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wheat line PI 178383"
/db_xref="taxon:4565"
/lab_host="DH5 alpha"
/clone_lib="Triticum aestivum FGAS: TaLT4"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
PI178383 cold hardened at 2 C for 1 day (24 H)(tester) and
subtracted against genotype Norstar cold hardened at 2 C
for 21 days and 49 days (equal amount of cDNA pooled
together before subtraction, driver). Modified Smart cDNA
(Clontech) priming and non-directional cloning."
ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 861;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 CCCCTGAATCGGCTAATC 19
Db 346 CCCCTGAGTCGAGCTAATC 364

RESULT 95
CF819853/c 868 bp mRNA linear EST 01-APR-2004
LOCUS CF819853
DEFINITION CF819853 Coccidioides posadasii saprobic phase cDNA library, 2 to
4 kb Coccidioides posadasii cDNA clone CIDA109 5' end, mRNA
sequence.
ACCESSION CF819853
VERSION CF819853.1 GI:45925894
KEYWORDS EST.
SOURCE Coccidioides posadasii
ORGANISM Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; Mitosporic Onygenales; Coccidioides.
1 (bases 1 to 868)
REFERENCE Gardner,M.J. and Cole,G.T.
AUTHORS Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
TITLE Unpublished (2003)
JOURNAL Other ESTs: EST697234
COMMENT Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org
Seq primer: M13 Reverse.
FEATURES
source
Location/Qualifiers
1..868
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"

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/clone="CIDA109"
/dev_stage="saprobic phase (mycelia)"
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library, 2 to 4 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 868;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19
||||| ||||| ||||| |||||
75 CCCCTGAATCGGCTAATC 57

RESULT 96
CB680959/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 876)
Jantasuriyarat,C., Gowda,M., Haller,K., Hatfield,J., Lu,G.,
Stahlberg,E., Zhou,B., Li,H., Kim,H., Yu,Y., Dean,R.A., Wing,R.A.,
Soderlund,C. and Wang,G.L.
Large-scale identification of expressed sequence tags involved in
rice and rice blast fungus interaction
Plant Physiol. 138 (1), 105-115 (2005)
15888683
Contact: Rod Wing
Arizona Genomics Institute
University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
Tel: 520 626 3967
Fax: 520 621 9288
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: gta aac cga cgg cca gtg
BACKWARD: gga aac agc tat gac cat g
Plate: 06 row: J column: 19
Seq primer: gga aac agc tat gac cat g.

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Location/Qualifiers
1..876
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/clone_lib="OSJNEf"
/note="Vector: pBluescript II KS +; Site_1: EcoRI; Site_2:
XhoI; Uninfected Control"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 876;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19

```

```

||||| ||||| ||||| |||||
797 CCCCTGAATCGGCTAATC 779

RESULT 97
CF821836/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Orygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 929)
Gardner,M.J. and Cole,G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST699219
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@igr.org
Location/Qualifiers
1..929
/organism="Coccidioides posadasii"
/mol_type="mRNA"
/strain="C735"
/db_xref="taxon:199306"
/clone="CIDAC39"
/dev_stage="saprobic phase (mycelia)"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_lib="Coccidioides posadasii saprobic phase cDNA
library, 2 to 4 kb"
/note="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii saprobic phase cDNA library, size
fractionated cDNA 2 to 4 kb"

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 929;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19
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343 CCCCTGAATCGGCTAATC 325

RESULT 98
CN512233
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE
1 (bases 1 to 941)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

ORIGIN
Query Match      83.2%; Score 15.8; DB 6; Length 941;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCCCTGAATCGGCTAATC 19
||||| ||||| ||||| |||||
343 CCCCTGAATCGGCTAATC 325

```

```

National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chi-Bin Chien
cDNA Library Preparation: Dr. Sumio Sugano
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM1523 row: d column: 11
High quality sequence start: 28
High quality sequence stop: 313.

FEATURES
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/db_xref="taxon:7955"
/clones="IMAGE:7270525"
/tissue_type="neural retina, retinal pigment epithelium,
lens and overlying skin, pooled embryos"
/lab_host="DH10B Tona"
/clone_libs="NIH_ZGC_9"
/notes="Organ: eye; Vector: pME18S-FL3; Site 1: DraIII;
Site 2: DraIII; 1st strand cDNA was primed with an
oligo(dT) primer
[GGCGCTGAGACGGCTATGTGGCTTTTCTTTTCTTTT];
double-stranded cDNA was ligated to a DraIII adaptor
[GGCCUACUGG], digested and directionally cloned into
distinct DraIII sites of the pME18S-FL3. Library was size
selected for 1.0 kb, with a average insert size of ~1.2kb,
and is not amplified. Library constructed by Yutaka Suzuki
(University of Tokyo Institute of Medical Science). Custom
primers recommended for sequencing: 5' end primer
5'-GGATGTGCTTACTTACTTA-3' and 3' end primer
5'-CGACCTGAGCTCGACACA-3'. Note: This is a Zebrafish Gene
Collection (ZGC) library"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 941;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 449 CCATGAGGCGGCTAATC 467

RESULT 99
CO010346/c
LOCUS
DEFINITION
EST798681 Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb Coccidioides posadasii cDNA clone CIEBH07 3' end, mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Coccidioides posadasii
Coccidioides posadasii
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Onygenales; mitosporic Onygenales; Coccidioides.
REFERENCE
1 (bases 1 to 994)
Gardner, M.J. and Cole, G.T.
Analysis of gene expression in Coccidioides posadasii mycelia and
spherules via expressed sequence tags
Unpublished (2003)
Other ESTs: EST798682
Contact: Gardner MJ
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301 838 3519
Fax: 301 838 0208
Email: gardner@tigr.org.
Location/Qualifiers

FEATURES
Source
1..994
/organism="Coccidioides posadasii"
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/strain="C735"
/db_xref="taxon:199306"
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/dev_stage="spherules"
/lab_host="E. coli DH10B, T1 phage resistant"
/clone_libs="Coccidioides posadasii spherule cDNA library,
0.4 to 2.3 kb"
/notes="Vector: pExpress 1; Site 1: Not I; Site 2: Eco RV;
Coccidioides posadasii spherule cDNA library, 0.4 to 2.3
kb"

ORIGIN
Query Match 83.2%; Score 15.8; DB 7; Length 994;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATCGGCTAATC 19
|||||
Db 136 CCCTGATCCGCTAATC 118

RESULT 100
BE743432
LOCUS
DEFINITION
601573680F1 NIH_MGC_9 Homo sapiens CDNA clone IMAGE:3834883 5',
mRNA sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE
1 (bases 1 to 996)
NIH-MGC http://mgi.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTF
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: L1CM515 row: p column: 20
High quality sequence start: 4
High quality sequence stop: 467.
Location/Qualifiers

FEATURES
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1..996
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3834883"
/lab_host="DH10B (phage-resistant)"
/clone_libs="NIH_MGC_9"
/notes="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 83.2%; Score 15.8; DB 2; Length 996;
Best Local Similarity 89.5%; Pred. No. 1.7e+03;

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Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCCCTGAATGGCGCTAATC 19  
Db 438 CCCCTGAATGGCGCTAATC 456

Search completed: March 9, 2006, 02:45:10  
Job time : 1531.15 secs

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GenCore version 5.1.7

Copyright (C) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:09:45 ; Search time 844.272 Seconds  
(without alignments)  
1346.567 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacacccaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_in.\*

3: gb\_env.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pr.\*

9: gb\_ro.\*

10: gb\_sts.\*

11: gb\_sv.\*

12: gb\_un.\*

13: gb\_vi.\*

14: gb\_htg.\*

15: gb\_pl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	73	13 AY189930	AY189930 Human ent
C 2	20	100.0	73	13 AY189933	AY189933 Human ent
C 3	20	100.0	103	13 ESU55869	US55869 Enterovirus
C 4	20	100.0	109	13 AY049767	AY049767 Enterovir
C 5	20	100.0	109	13 EU000872	U000872 Enterovirus
C 6	20	100.0	112	13 AY189929	AY189929 Human ent
C 7	20	100.0	115	13 AY189177	AY189177 Human pol
C 8	20	100.0	115	13 AY189178	AY189178 Human pol
C 9	20	100.0	115	13 AY189210	AY189210 Human ent
C 10	20	100.0	115	13 AY189213	AY189213 Human ent
C 11	20	100.0	115	13 FEN295168	AJ295168 Porcine e
C 12	20	100.0	116	13 AY189158	AY189158 Human ent
C 13	20	100.0	116	13 AY189160	AY189160 Human ent
C 14	20	100.0	116	13 AY189161	AY189161 Human ent
C 15	20	100.0	116	13 AY189162	AY189162 Human ent
C 16	20	100.0	116	13 AY189163	AY189163 Human ent
C 17	20	100.0	116	13 AY189164	AY189164 Human ent
C 18	20	100.0	116	13 AY189165	AY189165 Human ent

C 19	20	100.0	116	13 AY189166	AY189166 Human ent
C 20	20	100.0	116	13 AY189170	AY189170 Human ent
C 21	20	100.0	116	13 AY189171	AY189171 Human ent
C 22	20	100.0	116	13 AY189172	AY189172 Human ent
C 23	20	100.0	116	13 AY189173	AY189173 Human ent
C 24	20	100.0	116	13 AY189175	AY189175 Human ent
C 25	20	100.0	116	13 AY189176	AY189176 Human ent
C 26	20	100.0	116	13 AY189180	AY189180 Human ent
C 27	20	100.0	116	13 AY189181	AY189181 Human ent
C 28	20	100.0	116	13 AY189182	AY189182 Human ent
C 29	20	100.0	116	13 AY189183	AY189183 Human ent
C 30	20	100.0	116	13 AY189184	AY189184 Human ent
C 31	20	100.0	116	13 AY189186	AY189186 Human ent
C 32	20	100.0	116	13 AY189187	AY189187 Human ent
C 33	20	100.0	116	13 AY189188	AY189188 Human ent
C 34	20	100.0	116	13 AY189189	AY189189 Human ent
C 35	20	100.0	116	13 AY189190	AY189190 Human ent
C 36	20	100.0	116	13 AY189192	AY189192 Human ent
C 37	20	100.0	116	13 AY189194	AY189194 Human ent
C 38	20	100.0	116	13 AY189195	AY189195 Human ent
C 39	20	100.0	116	13 AY189196	AY189196 Human ent
C 40	20	100.0	116	13 AY189197	AY189197 Human ent
C 41	20	100.0	116	13 AY189198	AY189198 Human ent
C 42	20	100.0	116	13 AY189199	AY189199 Human ent
C 43	20	100.0	116	13 AY189200	AY189200 Human ent
C 44	20	100.0	116	13 AY189202	AY189202 Human ent
C 45	20	100.0	116	13 AY189203	AY189203 Human ent
C 46	20	100.0	116	13 AY189204	AY189204 Human ent
C 47	20	100.0	116	13 AY189206	AY189206 Human ent
C 48	20	100.0	116	13 AY189208	AY189208 Human ent
C 49	20	100.0	116	13 AY189211	AY189211 Human ent
C 50	20	100.0	116	13 AY189214	AY189214 Human ent
C 51	20	100.0	116	13 AY189215	AY189215 Human ent
C 52	20	100.0	116	13 AY189216	AY189216 Human ent
C 53	20	100.0	117	13 AB133003	AB133003 Human ent
C 54	20	100.0	119	13 S66302S1	S66302 VP1/2A [5'
C 55	20	100.0	128	13 AJ783777	AJ783777 Human pol
C 56	20	100.0	145	13 HEN312090	AJ312090 Human cox
C 57	20	100.0	145	13 HEN312091	AJ312091 Human cox
C 58	20	100.0	147	13 AF314006	AF314006 Enterovir
C 59	20	100.0	147	13 AF316322	AF316322 Enterovir
C 60	20	100.0	153	13 AF314004	AF314004 Enterovir
C 61	20	100.0	154	13 AF314003	AF314003 Enterovir
C 62	20	100.0	154	13 AF314005	AF314005 Enterovir
C 63	20	100.0	154	13 AF314007	AF314007 Enterovir
C 64	20	100.0	154	13 AY027864	AY027864 Enterovir
C 65	20	100.0	154	13 AY027865	AY027865 Enterovir
C 66	20	100.0	155	13 HEN312089	AJ312089 Human cox
C 67	20	100.0	171	13 HCO295181	AJ295181 Human cox
C 68	20	100.0	172	13 HEN312088	AJ312088 Human ent
C 69	20	100.0	177	13 ESP295207	AJ295207 Echovirus
C 70	20	100.0	184	13 AF521491	AF521491 Human ech
C 71	20	100.0	185	13 AF521433	AF521433 Human ech
C 72	20	100.0	185	13 AF521434	AF521434 Human cox
C 73	20	100.0	185	13 AF521435	AF521435 Human cox
C 74	20	100.0	185	13 AF521436	AF521436 Human ech
C 75	20	100.0	185	13 AF521440	AF521440 Human ech
C 76	20	100.0	185	13 AF521444	AF521444 Human ech
C 77	20	100.0	185	13 AF521445	AF521445 Human ech
C 78	20	100.0	185	13 AF521446	AF521446 Human ech
C 79	20	100.0	185	13 AF521447	AF521447 Human ech
C 80	20	100.0	185	13 AF521448	AF521448 Human cox
C 81	20	100.0	185	13 AF521449	AF521449 Human ech
C 82	20	100.0	185	13 AF521450	AF521450 Human ech
C 83	20	100.0	185	13 AF521451	AF521451 Human ech
C 84	20	100.0	185	13 AF521458	AF521458 Human ech
C 85	20	100.0	185	13 AF521461	AF521461 Human ech
C 86	20	100.0	185	13 AF521464	AF521464 Human ech
C 87	20	100.0	185	13 AF521471	AF521471 Human cox
C 88	20	100.0	185	13 AF521473	AF521473 Human cox
C 89	20	100.0	185	13 AF521474	AF521474 Human cox
C 90	20	100.0	185	13 AF521475	AF521475 Human ech
C 91	20	100.0	185	13 AF521476	AF521476 Human ech

C	92	20	100.0	185	13	AF521477	Human	ech	AF521477	Human	ech	AY342841	188	13	AY342841	20	100.0	C	165
C	93	20	100.0	185	13	AF521478	Human	ech	AF521478	Human	ech	AY342842	188	13	AY342842	20	100.0	C	166
C	94	20	100.0	185	13	AF521480	Human	cox	AF521480	Human	cox	AY342843	188	13	AY342843	20	100.0	C	167
C	95	20	100.0	185	13	AF521481	Human	ech	AF521481	Human	ech	AY342844	188	13	AY342844	20	100.0	C	168
C	96	20	100.0	185	13	AF521482	Human	ech	AF521482	Human	ech	AY342845	188	13	AY342845	20	100.0	C	169
C	97	20	100.0	185	13	AF521483	Human	ech	AF521483	Human	ech	AY342847	188	13	AY342847	20	100.0	C	170
C	98	20	100.0	185	13	AF521484	Human	ech	AF521484	Human	ech	AY342848	188	13	AY342848	20	100.0	C	171
C	99	20	100.0	185	13	AF521485	Human	ech	AF521485	Human	ech	AY342849	188	13	AY342849	20	100.0	C	172
C	100	20	100.0	185	13	AF521486	Human	ech	AF521486	Human	ech	AY342850	188	13	AY342850	20	100.0	C	173
C	101	20	100.0	185	13	AF521487	Human	ech	AF521487	Human	ech	AY342853	188	13	AY342853	20	100.0	C	174
C	102	20	100.0	185	13	AF521488	Human	ech	AF521488	Human	ech	AY342854	188	13	AY342854	20	100.0	C	175
C	103	20	100.0	185	13	AF521492	Human	ech	AF521492	Human	ech	AY342856	188	13	AY342856	20	100.0	C	176
C	104	20	100.0	185	13	AF521493	Human	cox	AF521493	Human	cox	AY342857	188	13	AY342857	20	100.0	C	177
C	110	20	100.0	185	13	AF521494	Human	cox	AF521494	Human	cox	AY342858	188	13	AY342858	20	100.0	C	178
C	106	20	100.0	185	13	AF521495	Human	ech	AF521495	Human	ech	AY342859	188	13	AY342859	20	100.0	C	179
C	107	20	100.0	185	13	AF521496	Human	ech	AF521496	Human	ech	AY342860	188	13	AY342860	20	100.0	C	180
C	108	20	100.0	185	13	AF521497	Human	ech	AF521497	Human	ech	AY342862	188	13	AY342862	20	100.0	C	181
C	109	20	100.0	185	13	AF521501	Human	ech	AF521501	Human	ech	AY342864	188	13	AY342864	20	100.0	C	182
C	111	20	100.0	185	13	AF521502	Human	ech	AF521502	Human	ech	AY342865	188	13	AY342865	20	100.0	C	183
C	112	20	100.0	185	13	AF521503	Human	ech	AF521503	Human	ech	AY342866	188	13	AY342866	20	100.0	C	184
C	113	20	100.0	185	13	AF521504	Human	ech	AF521504	Human	ech	AY342868	188	13	AY342868	20	100.0	C	185
C	114	20	100.0	185	13	AF521505	Human	ech	AF521505	Human	ech	AY342869	188	13	AY342869	20	100.0	C	186
C	125	20	100.0	185	13	AF521507	Human	ech	AF521507	Human	ech	AY342870	188	13	AY342870	20	100.0	C	187
C	115	20	100.0	185	13	AF521508	Human	ech	AF521508	Human	ech	AY342871	188	13	AY342871	20	100.0	C	188
C	116	20	100.0	185	13	AF521509	Human	ech	AF521509	Human	ech	AY342872	188	13	AY342872	20	100.0	C	189
C	117	20	100.0	185	13	AF521511	Human	ech	AF521511	Human	ech	AY342873	188	13	AY342873	20	100.0	C	190
C	118	20	100.0	185	13	AF521512	Human	ech	AF521512	Human	ech	AY342874	188	13	AY342874	20	100.0	C	191
C	119	20	100.0	185	13	AF521513	Human	ech	AF521513	Human	ech	AY342876	188	13	AY342876	20	100.0	C	192
C	120	20	100.0	185	13	AF521514	Human	ech	AF521514	Human	ech	AY342878	188	13	AY342878	20	100.0	C	193
C	121	20	100.0	185	13	AF521515	Human	ech	AF521515	Human	ech	AY342879	188	13	AY342879	20	100.0	C	194
C	122	20	100.0	185	13	AF521516	Human	ech	AF521516	Human	ech	AY342880	188	13	AY342880	20	100.0	C	195
C	123	20	100.0	185	13	AF521517	Human	ech	AF521517	Human	ech	AY342883	188	13	AY342883	20	100.0	C	196
C	124	20	100.0	185	13	AF521518	Human	ech	AF521518	Human	ech	AY342884	188	13	AY342884	20	100.0	C	197
C	125	20	100.0	185	13	AF521519	Human	ech	AF521519	Human	ech	AY342885	188	13	AY342885	20	100.0	C	198
C	126	20	100.0	185	13	AF521520	Human	ech	AF521520	Human	ech	AY342886	188	13	AY342886	20	100.0	C	199
C	127	20	100.0	185	13	AF521521	Human	ech	AF521521	Human	ech	AY342887	188	13	AY342887	20	100.0	C	200
C	128	20	100.0	185	13	AF521522	Human	cox	AF521522	Human	cox	AY342888	188	13	AY342888	20	100.0	C	201
C	129	20	100.0	185	13	AF521523	Human	ech	AF521523	Human	ech	AY342889	188	13	AY342889	20	100.0	C	202
C	130	20	100.0	185	13	AF521525	Human	ech	AF521525	Human	ech	AY342891	188	13	AY342891	20	100.0	C	203
C	131	20	100.0	185	13	AF521526	Human	ech	AF521526	Human	ech	AY342892	188	13	AY342892	20	100.0	C	204
C	132	20	100.0	185	13	AF521527	Human	ech	AF521527	Human	ech	AY342893	188	13	AY342893	20	100.0	C	205
C	133	20	100.0	185	13	AF521528	Human	ech	AF521528	Human	ech	AY342894	188	13	AY342894	20	100.0	C	206
C	134	20	100.0	185	13	AF521529	Human	ech	AF521529	Human	ech	AY342895	188	13	AY342895	20	100.0	C	207
C	135	20	100.0	185	13	AF521530	Human	ech	AF521530	Human	ech	AY342896	188	13	AY342896	20	100.0	C	208
C	136	20	100.0	185	13	AF521533	Human	ech	AF521533	Human	ech	AY342897	188	13	AY342897	20	100.0	C	209
C	137	20	100.0	185	13	AF521534	Human	ech	AF521534	Human	ech	AY342898	188	13	AY342898	20	100.0	C	210
C	138	20	100.0	185	13	AF521535	Human	ech	AF521535	Human	ech	AY342899	188	13	AY342899	20	100.0	C	211
C	139	20	100.0	185	13	AF521537	Human	ech	AF521537	Human	ech	AY342901	188	13	AY342901	20	100.0	C	212
C	140	20	100.0	185	13	AF521539	Human	ech	AF521539	Human	ech	AY342902	188	13	AY342902	20	100.0	C	213
C	141	20	100.0	185	13	AF521541	Human	ech	AF521541	Human	ech	AY342903	188	13	AY342903	20	100.0	C	214
C	142	20	100.0	185	13	AF521542	Human	ech	AF521542	Human	ech	AY342904	188	13	AY342904	20	100.0	C	215
C	143	20	100.0	185	13	AF521543	Human	ech	AF521543	Human	ech	AY342905	188	13	AY342905	20	100.0	C	216
C	144	20	100.0	185	13	AF521546	Human	ech	AF521546	Human	ech	AY342906	188	13	AY342906	20	100.0	C	217
C	145	20	100.0	185	13	AF521547	Human	ech	AF521547	Human	ech	AY342907	188	13	AY342907	20	100.0	C	218
C	146	20	100.0	185	13	AF521548	Human	cox	AF521548	Human	cox	AY342908	188	13	AY342908	20	100.0	C	219
C	147	20	100.0	185	13	AF521549	Human	ech	AF521549	Human	ech	AY342909	188	13	AY342909	20	100.0	C	220
C	148	20	100.0	185	13	AF521550	Human	ech	AF521550	Human	ech	AY342910	188	13	AY342910	20	100.0	C	221
C	149	20	100.0	185	13	AF521551	Human	ech	AF521551	Human	ech	AY342911	188	13	AY342911	20	100.0	C	222
C	150	20	100.0	185	13	AF521552	Human	ech	AF521552	Human	ech	AY342912	188	13	AY342912	20	100.0	C	223
C	151	20	100.0	185	13	AF521555	Human	ech	AF521555	Human	ech	AY342913	188	13	AY342913	20	100.0	C	224
C	152	20	100.0	185	13	AF521585	Human	ech	AY342851	Human	ech	AY342914	188	13	AY342914	20	100.0	C	225
C	153	20	100.0	185	13	AY342852	Human	ech	AY342852	Human	ech	AY342915	188	13	AY342915	20	100.0	C	226
C	154	20	100.0	185	13	AY342855	Human	ech	AY342855	Human	ech	AY342916	188	13	AY342916	20	100.0	C	227
C	155	20	100.0	186	13	AF521466	Human	ech	AF521466	Human	ech	AY342917	188	13	AY342917	20	100.0	C	228
C	156	20	100.0	186	13	AF521470	Human	cox	AF521470	Human	cox	AY342918	188	13	AY342918	20	100.0	C	229
C	157	20	100.0	186	13	AF521472	Human	cox	AF521472	Human	cox	AY342919	188	13	AY342919	20	100.0	C	230
C	158	20	100.0	186	13	AF521479	Human	ech	AF521479	Human	ech	AY342920	188	13	AY342920	20	100.0	C	231
C	159	20	100.0	187	13	AF521473	Human	ech	AY343032	Human	ech	AY342921	188	13	AY342921	20	100.0	C	232
C	160	20	100.0	188	13	AF521468	Human	ech	AF521468	Human	ech	AY342924	188	13	AY342924	20	100.0	C	233
C	161	20	100.0	188	13	AF521489	Human	ech	AF521489	Human	ech	AY342925	188	13	AY342925	20	100.0	C	234
C	162	20	100.0	188	13	AF521483	Human	ech	AF521483	Human	ech	AY342926	188	13	AY342926	20	100.0	C	235
C	163	20	100.0	188	13	AY342838	Human	ech	AY342838	Human	ech	AY342927	188	13	AY342927	20	100.0	C	236
C	164	20	100.0	188	13	AY342839	Human	cox	AY342839	Human	cox	AY342930	188	13	AY342930	20	100.0	C	237



C 384	20	100.0	315	13	AJ783774	Human pol	AJ783774	Human pol	C 457	20	100.0	628	6	I64591	164591 Sequence 5
C 385	20	100.0	316	13	ECV7335	Echovirus	AJ007335	Echovirus	C 458	20	100.0	629	13	EV4VPGEN	X89534 Echovirus 4
C 386	20	100.0	316	13	ECV7336	Echovirus	AJ007336	Echovirus	C 459	20	100.0	630	13	AF117626	AF117626 Enterovir
C 387	20	100.0	316	13	ECV7337	Echovirus	AJ007337	Echovirus	C 460	20	100.0	639	6	Q821453	Q821453 Sequence
C 388	20	100.0	316	13	ECV7338	Echovirus	AJ007338	Echovirus	C 461	20	100.0	641	13	CA22RNAPA	X87603 Coxsackievi
C 389	20	100.0	316	13	ECV7339	Echovirus	AJ007339	Echovirus	C 462	20	100.0	644	13	AY055125	AY055125 Human ent
C 390	20	100.0	316	13	ECV7341	Echovirus	AJ007341	Echovirus	C 463	20	100.0	644	13	AY055126	AY055126 Human ent
C 391	20	100.0	316	13	ECV7342	Echovirus	AJ007342	Echovirus	C 464	20	100.0	644	13	AY055127	AY055127 Human ent
C 392	20	100.0	316	13	ECV7343	Echovirus	AJ007343	Echovirus	C 465	20	100.0	644	13	AY055128	AY055128 Human ent
C 393	20	100.0	316	13	ECV7344	Echovirus	AJ007344	Echovirus	C 466	20	100.0	644	13	AY055129	AY055129 Human ent
C 394	20	100.0	317	13	ECV7340	Echovirus	AJ007340	Echovirus	C 467	20	100.0	644	13	AY055130	AY055130 Human ent
C 395	20	100.0	317	13	ECV7346	Echovirus	AJ007346	Echovirus	C 468	20	100.0	644	13	AY055131	AY055131 Human ent
C 396	20	100.0	319	13	HEC579639	Human ech	AJ579639	Human ech	C 469	20	100.0	644	13	AY055132	AY055132 Human ent
C 397	20	100.0	319	13	HEC579640	Human ech	AJ579640	Human ech	C 470	20	100.0	644	13	AY055133	AY055133 Human ent
C 398	20	100.0	338	6	Q964036	Sequence	Q964036	Sequence	C 471	20	100.0	644	13	AY055134	AY055134 Human ent
C 399	20	100.0	339	6	Q964030	Sequence	Q964030	Sequence	C 472	20	100.0	644	13	AY055135	AY055135 Human ent
C 400	20	100.0	340	6	Q964031	Sequence	Q964031	Sequence	C 473	20	100.0	644	13	AY055136	AY055136 Human ent
C 401	20	100.0	340	6	Q964032	Sequence	Q964032	Sequence	C 474	20	100.0	644	13	AY055137	AY055137 Human ent
C 402	20	100.0	340	6	Q964033	Sequence	Q964033	Sequence	C 475	20	100.0	644	13	AY055138	AY055138 Human ent
C 403	20	100.0	351	13	AJ635236	Human pol	AJ635236	Human pol	C 476	20	100.0	644	13	AY055139	AY055139 Human ent
C 404	20	100.0	361	13	AJ783787	Human pol	AJ783787	Human pol	C 477	20	100.0	644	13	AY055140	AY055140 Human ent
C 405	20	100.0	364	13	S76767	{5', non-tra	S76767 {5', non-tra		C 478	20	100.0	644	13	AY055141	AY055141 Human ent
C 406	20	100.0	379	13	AJ783728	Human pol	AJ783728	Human pol	C 479	20	100.0	644	13	AY055144	AY055144 Human ent
C 407	20	100.0	379	13	AJ783780	Human pol	AJ783780	Human pol	C 480	20	100.0	644	13	AY055145	AY055145 Human ent
C 408	20	100.0	381	13	AJ783772	Human pol	AJ783772	Human pol	C 481	20	100.0	645	13	AY055147	AY055147 Human ent
C 409	20	100.0	382	13	AJ783778	Human pol	AJ783778	Human pol	C 482	20	100.0	646	13	AY055146	AY055146 Human ent
C 410	20	100.0	384	13	AJ783773	Human pol	AJ783773	Human pol	C 483	20	100.0	646	13	AY055166	AY055166 Human ent
C 411	20	100.0	385	13	AJ783727	Human pol	AJ783727	Human pol	C 484	20	100.0	647	13	AF117632	AF117632 Enterovir
C 412	20	100.0	386	13	AJ783731	Human pol	AJ783731	Human pol	C 485	20	100.0	648	13	AF117635	AF117635 Enterovir
C 413	20	100.0	388	13	AJ634678	Human pol	AJ634678	Human pol	C 486	20	100.0	648	13	AF117635	AF117635 Enterovir
C 414	20	100.0	388	13	AY599875	Human cox	AY599875	Human cox	C 487	20	100.0	648	13	AY055152	AY055152 Human ent
C 415	20	100.0	389	13	AJ783776	Human pol	AJ783776	Human pol	C 488	20	100.0	648	13	AY055153	AY055153 Human ent
C 416	20	100.0	389	13	AY599872	Human cox	AY599872	Human cox	C 489	20	100.0	648	13	AY055154	AY055154 Human ent
C 417	20	100.0	389	13	AY599874	Human cox	AY599874	Human cox	C 490	20	100.0	648	13	AY055155	AY055155 Human ent
C 418	20	100.0	390	13	AJ783730	Human pol	AJ783730	Human pol	C 491	20	100.0	648	13	AY055156	AY055156 Human ent
C 419	20	100.0	390	13	AJ783773	Human pol	AJ783773	Human pol	C 492	20	100.0	648	13	AY055157	AY055157 Human ent
C 420	20	100.0	391	13	AJ783739	Human pol	AJ783739	Human pol	C 493	20	100.0	648	13	AY055158	AY055158 Human ent
C 421	20	100.0	392	13	AJ783729	Human pol	AJ783729	Human pol	C 494	20	100.0	648	13	AY055159	AY055159 Human ent
C 422	20	100.0	393	13	E70278125	Enterovirus	Z78125 Enterovirus		C 495	20	100.0	648	13	AY055160	AY055160 Human ent
C 423	20	100.0	394	13	E70278127	Enterovirus	Z78127 Enterovirus		C 496	20	100.0	648	13	AY055161	AY055161 Human ent
C 424	20	100.0	394	13	E70278133	Enterovirus	Z78133 Enterovirus		C 497	20	100.0	648	13	AY055162	AY055162 Human ent
C 425	20	100.0	394	13	E70278137	Enterovirus	Z78137 Enterovirus		C 498	20	100.0	648	13	AY055163	AY055163 Human ent
C 426	20	100.0	394	13	E70278139	Enterovirus	Z78139 Enterovirus		C 499	20	100.0	648	13	AY055164	AY055164 Human ent
C 427	20	100.0	395	13	AJ783771	Human pol	AJ783771	Human pol	C 500	20	100.0	648	13	AY055165	AY055165 Human ent
C 428	20	100.0	397	13	AJ783732	Human pol	AJ783732	Human pol							
C 429	20	100.0	400	13	AJ783725	Human pol	AJ783725	Human pol							
C 430	20	100.0	404	13	AJ783724	Human pol	AJ783724	Human pol							
C 431	20	100.0	404	13	S76769	{5', non-tra	S76769 {5', non-tra								
C 432	20	100.0	405	13	S76768	{5', non-tra	S76768 {5', non-tra								
C 433	20	100.0	413	13	AJ783721	Human pol	AJ783721	Human pol							
C 434	20	100.0	421	13	AJ783786	Human pol	AJ783786	Human pol							
C 435	20	100.0	466	13	CA1RNAPA	Coxsackievi	X87584 Coxsackievi								
C 436	20	100.0	467	13	HEC295173	Human ech	AJ295173 Human ech								
C 437	20	100.0	472	13	AJ783722	Human pol	AJ783722	Human pol							
C 438	20	100.0	477	13	CABRNAPA	Coxsackievi	X87590 Coxsackievi								
C 439	20	100.0	497	13	HEC295183	Human ech	AJ295183 Human ech								
C 440	20	100.0	499	13	AF108167	Human rhi	AF108167 Human rhi								
C 441	20	100.0	501	13	AJ783726	Human pol	AJ783726	Human pol							
C 442	20	100.0	511	13	AF108177	Human rhi	AF108177 Human rhi								
C 443	20	100.0	570	13	PEN295169	Porcine e	AJ295169 Porcine e								
C 444	20	100.0	587	13	CA20ARNAP	Coxsackievi	X87601 Coxsackievi								
C 445	20	100.0	589	13	HEC295177	Human ech	AJ295177 Human ech								
C 446	20	100.0	595	13	AF447481	Human ech	AF447481 Human ech								
C 447	20	100.0	595	13	AF447487	Human ech	AF447487 Human ech								
C 448	20	100.0	597	13	AF447479	Human ech	AF447479 Human ech								
C 449	20	100.0	598	13	AF447484	Human ech	AF447484 Human ech								
C 450	20	100.0	598	13	AF447485	Human ech	AF447485 Human ech								
C 451	20	100.0	598	13	AF447486	Human ech	AF447486 Human ech								
C 452	20	100.0	617	13	AB059823	Enterovir	AB059823 Enterovir								
C 453	20	100.0	617	13	AB059825	Enterovir	AB059825 Enterovir								
C 454	20	100.0	617	13	AB059826	Enterovir	AB059826 Enterovir								
C 455	20	100.0	628	6	A37539	Sequence 5	A37539 Sequence 5								
C 456	20	100.0	628	6	A37564	Sequence 5	A37564 Sequence 5								

ALIGNMENTS

RESULT 1	AY189930/c	AY189930	73 bp	RNA	linear	VRL 08-MAY-2003
LOCUS	Human enterovirus B isolate NSW/51/97 5'	Human enterovirus B isolate NSW/51/97 5'	73 bp	RNA	linear	VRL 08-MAY-2003
DEFINITION	partial sequence.	partial sequence.				
ACCESSION	AY189930	AY189930.1	GI:28395429			
VERSION	AY189930.1	GI:28395429				
KEYWORDS	Human enterovirus B	Human enterovirus B				
SOURCE	Viruses; ssRNA positive-strand viruses, no DNA stage;	Viruses; ssRNA positive-strand viruses, no DNA stage;				
ORGANISM	Picornaviridae; Enterovirus.	Picornaviridae; Enterovirus.				
REFERENCE	1 (bases 1 to 73)	1 (bases 1 to 73)				
AUTHORS	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.				
TITLE	Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1	Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1				
JOURNAL	Diabetes Associated with Enterovirus RNA	Diabetes Associated with Enterovirus RNA				
PUBMED	J. Infect. Dis. 187 (10), 1562-1570 (2003)	J. Infect. Dis. 187 (10), 1562-1570 (2003)				
REFERENCE	2 (bases 1 to 73)	2 (bases 1 to 73)				
AUTHORS	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.	Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.				
TITLE	Direct Submission	Direct Submission				
JOURNAL	Submitted (03-DEC-2002) Virology Division, University of New South	Submitted (03-DEC-2002) Virology Division, University of New South				
	Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,	Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,				
	Australia	Australia				

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QY 1 AAGGAACACGACACCCAA 20
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Db 61 AAGGAACACGACACCCAA 42

RESULT 2
AY189933/c
LOCUS      73 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/167/97 5' untranslated region,
partial sequence.
ACCESSION  AY189933
VERSION     AY189933.1 GI:28395432
KEYWORDS
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
REFERENCE   1 (bases 1 to 73)
AUTHORS     Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 73)
AUTHORS     Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE       Direct Submission
JOURNAL     Submitted (03-DEC-2002) Virology Division, University of New South
Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,
Australia
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    |||||
Db 61 AAGGAACACGACACCCAA 42

RESULT 3
ESU55869/c
LOCUS      103 bp RNA linear VRL 23-MAY-1996
DEFINITION Enterovirus sp. 5' NTR sequence from patient A27.
ACCESSION  U55869
VERSION     U55869.1 GI:1330334
KEYWORDS
SOURCE      Enterovirus sp.
ORGANISM    Enterovirus sp.
REFERENCE   1 (bases 1 to 103)
AUTHORS     Muir, P., Nicholson, F., Spencer, G.T., Ajetunmbi, J.F., Starkey, W.G.,
Khan, M., Archard, L.C., Cairns, N.J., Anderson, V.E.R., Leigh, P.N.,
Howard, R.S. and Banatvala, J.E.
TITLE       Enterovirus infection of the central nervous system of humans: lack
of association with chronic neurological disease
J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
PUBMED     8757988
REFERENCE   2 (bases 1 to 103)
AUTHORS     Muir, P.
TITLE       Direct Submission
JOURNAL     Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
Road, London SE1 7EH, UK
FEATURES
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  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
    |||||
Db 91 AAGGAACACGACACCCAA 72

RESULT 4
AY049767/c
LOCUS      109 bp RNA linear VRL 08-DEC-2001
DEFINITION Enterovirus sp. clone Entero-1 5' untranslated region, partial
sequence.
ACCESSION  AY049767
VERSION     AY049767.1 GI:17426413
KEYWORDS
SOURCE      Enterovirus sp.
ORGANISM    Enterovirus sp.
REFERENCE   1 (bases 1 to 109)
AUTHORS     Kawashima, H., Kasaiwagi, Y. and Mori, T.
TITLE       Direct Submission
JOURNAL     Submitted (02-AUG-2001) Pediatrics, Tokyo Medical University, 6-7-1
Nishishinjuku, Shinjuku-ku, Tokyo 160-0023, Japan
FEATURES
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    /note="from cerebrospinal fluid"
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  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
    |||||
Db 97 AAGGAACACGACACCCAA 78

RESULT 5
E7U00872/c
LOCUS      109 bp DNA linear VRL 26-MAR-1997
DEFINITION Enterovirus E71 H 5' untranslated region.
ACCESSION  U00872
VERSION     U00872.1 GI:405115
KEYWORDS
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71

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Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 109)
Zheng,Z.M., He,P.J., Caueffield,D., Neumann,M., Specter,S.,
Baker,C.C. and Bankowski,M.J.
Enterovirus 71 isolated from China is serologically similar to the
prototype E71 BrCr strain but differs in the 5'-noncoding region
J. Med. Virol. 47 (2), 161-167 (1995)
JOURNAL
PUBMED 8830120
REFERENCE 2 (bases 1 to 109)
AUTHORS Bankowski,M.J.
TITLE Direct Submission
JOURNAL Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 97 AAGGAAACACGGACACCCAA 78

RESULT 6
AY189929/c
LOCUS Human enterovirus B isolate NSW/47/97 5' linear VRL 08-MAY-2003
DEFINITION partial sequence.
ACCESSION AY189929
VERSION AY189929.1 GI:28395428
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 112)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 112)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Virology Division, University of New South
Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,
Australia
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Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 7
AY189177/c
LOCUS Human poliovirus 1 strain Sabin isolate NSW/84/97 5' linear VRL 08-MAY-2003
DEFINITION sequence.
ACCESSION AY189177
VERSION AY189177.1 GI:28274400
KEYWORDS
SOURCE Human poliovirus 1 strain Sabin
ORGANISM Human poliovirus 1 strain Sabin
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 115)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 8
AY189178/c
LOCUS Human poliovirus 1 strain Sabin isolate NSW/96/97 5' linear VRL 08-MAY-2003
DEFINITION sequence.
ACCESSION AY189178
VERSION AY189178.1 GI:28274401
KEYWORDS
SOURCE Human poliovirus 1 strain Sabin
ORGANISM Human poliovirus 1 strain Sabin
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 115)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 115)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 9
AY189210/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/227/99 5' UTR, partial sequence.
ACCESSION AY189210
VERSION AY189210.1 GI:28274433
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 10
AY189213/c
LOCUS
DEFINITION Human enterovirus A isolate NSW/255/99 5' UTR, partial sequence.
ACCESSION AY189213
VERSION AY189213.1 GI:28274436
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936

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REFERENCE 2 (bases 1 to 115)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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    |||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 11
PEN295168/c
LOCUS
DEFINITION Porcine enterovirus 9 genomic RNA for partial 5'UTR, isolate
ITA93-766BE93.
ACCESSION AJ295168
VERSION AJ295168.1 GI:14140111
KEYWORDS
SOURCE Porcine enterovirus 9
ORGANISM Porcine enterovirus 9
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1
AUTHORS Muscillo,M., La Rosa,G. and Marianelli,C.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 115)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
FEATURES
source
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/db_xref="taxon:64141"
/notes="viral particles isolated from serum of swine"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 103 AAGGAAACACGGACACCCAA 84

RESULT 12
AY189158/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/01/97 5' UTR, partial sequence.
ACCESSION AY189158
VERSION AY189158.1 GI:28274381
KEYWORDS

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SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL    J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 13
AY189160/c
LOCUS      Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.
ACCESSION  AY189160
VERSION     AY189160.1 GI:28274383
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL    J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

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RESULT 14
AY189161/c
LOCUS      Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
DEFINITION Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
ACCESSION  AY189161
VERSION     AY189161.1 GI:28274384
KEYWORDS
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL    J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
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            /note="Human enterovirus 71"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 15
AY189162/c
LOCUS      Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
ACCESSION  AY189162
VERSION     AY189162.1 GI:28274385
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL    J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED     12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS    Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE      Direct Submission
JOURNAL    Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
            source
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            /isolate="NSW/14/97"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAAC 20
    |||||
Db 104 AAGGAACACGACGCCAAC 85

RESULT 16
AY189163/c
LOCUS AY189163 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/16/97 5' UTR, partial sequence.
ACCESSION AY189163
VERSION AY189163.1 GI:28274386
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL
SUBMITTED (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Db 104 AAGGAACACGACGCCAAC 85

RESULT 17
AY189164/c
LOCUS AY189164 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
ACCESSION AY189164
VERSION AY189164.1 GI:28274387
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
```

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JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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RESULT 18
AY189165/c
LOCUS AY189165 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/19/97 5' UTR, partial sequence.
ACCESSION AY189165
VERSION AY189165.1 GI:28274388
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL
SUBMITTED (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
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/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 104 AAGGAACACGACGCCAAC 85

RESULT 19
AY189166/c
LOCUS AY189166 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/23/97 5' UTR, partial sequence.
ACCESSION AY189166
VERSION AY189166.1 GI:28274389
KEYWORDS
SOURCE Human enterovirus NSW/23/97
ORGANISM Human enterovirus NSW/23/97
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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REFERENCE
AUTHORS      1 (bases 1 to 116)
TITLE        Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
             Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      104 AAGGAACACGGACACCCAA 85

RESULT 20
AY189170/c
LOCUS      AY189170      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/48/97 5' UTR, partial sequence.
ACCESSION  AY189170
VERSION     AY189170.1 GI:28274393
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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       |||||||
Db      104 AAGGAACACGGACACCCAA 85

REFERENCE
AUTHORS      1 (bases 1 to 116)
TITLE        Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
             Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
       |||||||
Db      104 AAGGAACACGGACACCCAA 85

RESULT 21
AY189171/c
LOCUS      AY189171      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
ACCESSION  AY189171
VERSION     AY189171.1 GI:28274394
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 30;
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Qy      1 AAGGAACACGGACACCCAA 20
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Db      104 AAGGAACACGGACACCCAA 85

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LOCUS      AY189171      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
ACCESSION  AY189171
VERSION     AY189171.1 GI:28274394
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAACACGGACACCCAA 20
       |||||||
Db      104 AAGGAACACGGACACCCAA 85

RESULT 22
AY189172/c
LOCUS      AY189172      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus C isolate NSW/68/97 5' UTR, partial sequence.
ACCESSION  AY189172
VERSION     AY189172.1 GI:28274395
KEYWORDS
SOURCE      Human enterovirus C
ORGANISM    Human enterovirus C
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
             Diabetes Associated with Enterovirus RNA
JOURNAL      J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED       12721936
REFERENCE     2 (bases 1 to 116)
AUTHORS      Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE        Direct Submission
JOURNAL      Submitted (29-NOV-2002) Virology Division, South Eastern Area
             Laboratory Services, University of New South Wales/Prince of Wales
             Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES     Location/Qualifiers
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Db      104 AAGGAACACGGACACCCAA 85

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
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Db 104 AAGGAAACACGACACCCAA 85

RESULT 23  
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LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Human enterovirus B  
Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
12721936  
2 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Direct Submission  
Submitted (29-NOV-2002) Virology Division, South Eastern Area  
Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia  
Location/Qualifiers

FEATURES  
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Db 104 AAGGAAACACGACACCCAA 85

RESULT 24  
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DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Human enterovirus B  
Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
12721936  
2 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Direct Submission  
Submitted (29-NOV-2002) Virology Division, South Eastern Area  
Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia  
Location/Qualifiers

FEATURES  
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Db 104 AAGGAAACACGACACCCAA 85

RESULT 25  
AY189176/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Human enterovirus B  
Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
12721936  
2 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Direct Submission  
Submitted (29-NOV-2002) Virology Division, South Eastern Area  
Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia  
Location/Qualifiers

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/isolate="NSW/83/97"  
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<1..>116

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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 104 AAGGAAACACGACACCCAA 85

RESULT 26  
AY189180/c  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Human enterovirus B  
Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 116)  
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)

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12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
source
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/organism="Human enterovirus B"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 27
AY189181/c
LOCUS AY189181 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/135/98 5' UTR, partial sequence.
ACCESSION AY189181
VERSION AY189181.1 GI:28274404
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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/mol_type="genomic RNA"
/isolate="NSW/135/98"
/db_xref="taxon:138949"
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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 28
AY189182/c
LOCUS AY189182 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 70 NSW/140/98 5' UTR, partial sequence.
ACCESSION AY189182
VERSION AY189182.1 GI:28274405
KEYWORDS

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Human enterovirus 70
Human enterovirus 70
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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/isolate="NSW/140/98"
/db_xref="taxon:12090"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

RESULT 29
AY189183/c
LOCUS AY189183 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.
ACCESSION AY189183
VERSION AY189183.1 GI:28274406
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
|||||
Db 104 AAGGAAACACGGACACCCAA 85

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RESULT 30
AY189184/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.
ACCESSION AY189184
VERSION AY189184.1 GI:28274407
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
12721936
PUBMED
REFERENCE
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
JOURNAL
Location/Qualifiers
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/mol_type="genomic RNA"
/isolate="NSW/143/98"
/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
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104 AAGGAACACGACACCCAA 85
Db

RESULT 31
AY189186/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.
ACCESSION AY189186
VERSION AY189186.1 GI:28274409
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
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JOURNAL
12721936
PUBMED
REFERENCE
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
JOURNAL
Location/Qualifiers
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/mol_type="genomic RNA"
/isolate="NSW/147/98"
/db_xref="taxon:138949"
<1. .>116
FEATURES
source
5'UTR
ORIGIN

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## ORIGIN

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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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104 AAGGAACACGACACCCAA 85
Db

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## RESULT 32

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AY189187/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/149/98 5' UTR, partial sequence.
ACCESSION AY189187
VERSION AY189187.1 GI:28274410
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
12721936
PUBMED
REFERENCE
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
JOURNAL
Location/Qualifiers
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/organism="Human enterovirus B"
/mol_type="genomic RNA"
/isolate="NSW/149/98"
/db_xref="taxon:138949"
<1. .>116
FEATURES
source
5'UTR
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Query Match 100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGACACCCAA 20
104 AAGGAACACGACACCCAA 85
Db

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## RESULT 33

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AY189188/c
LOCUS
DEFINITION Human enterovirus B isolate NSW/151/98 5' UTR, partial sequence.
ACCESSION AY189188
VERSION AY189188.1 GI:28274411
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
12721936
PUBMED
REFERENCE
2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
JOURNAL

```

Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia

## FEATURES

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/organism="Human enterovirus B"  
/mol\_type="genomic RNA"  
/isolate="NSW/151/98"  
/db\_xref="taxon:138949"  
<1. .>116

## 5'UTR

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

|||||  
Db 104 AAGGAAACACGGACACCCAA 85

## RESULT 34

AY189189/c  
LOCUS AY189189 116 bp RNA linear VRL 08-MAY-2003  
DEFINITION Human enterovirus 71 isolate NSW/153/98 5' UTR, partial sequence.  
ACCESSION AY189189  
VERSION AY189189.1 GI:28274412

## KEYWORDS

## SOURCE

Human enterovirus 71  
Human enterovirus 71  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

## REFERENCE

1 (bases 1 to 116)  
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA

## JOURNAL

## PUBMED

## REFERENCE

2 (bases 1 to 116)  
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.  
Direct Submission  
Submitted (29-NOV-2002) Virology Division, South Eastern Area  
Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia

## FEATURES

source  
1. .116  
/organism="Human enterovirus 71"  
/mol\_type="genomic RNA"  
/isolate="NSW/153/98"  
/db\_xref="taxon:39054"  
/note="Human enterovirus 71"  
<1. .>116

## 5'UTR

## ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

|||||  
Db 104 AAGGAAACACGGACACCCAA 85

## RESULT 35

AY189190/c  
LOCUS AY189190 116 bp RNA linear VRL 08-MAY-2003  
DEFINITION Human enterovirus NSW/154/98 5' UTR, partial sequence.  
ACCESSION AY189190  
VERSION AY189190.1 GI:28274413

## KEYWORDS

## SOURCE

Human enterovirus NSW/154/98  
Human enterovirus NSW/154/98  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

1 (bases 1 to 116)  
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.  
Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1  
Diabetes Associated with Enterovirus RNA

## 5'UTR

## ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 116;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

|||||  
Db 104 AAGGAAACACGGACACCCAA 85

## RESULT 36

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## FEATURES

## source

1 (bases 1 to 116)  
Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.  
Direct Submission  
Submitted (29-NOV-2002) Virology Division, South Eastern Area  
Laboratory Services, University of New South Wales/Prince of Wales  
Hospital, High Street, Randwick, NSW 2031, Australia

## 5'UTR

## ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 116;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

|||||  
Db 104 AAGGAAACACGGACACCCAA 85

## RESULT 37



AY189194/c  
 LOCUS  
 DEFINITION Human enterovirus NSW/161/98 5' UTR, partial sequence.  
 ACCESSION AY189194  
 VERSION AY189194.1 GI:28274417  
 KEYWORDS  
 SOURCE Human enterovirus NSW/161/98  
 ORGANISM Human enterovirus NSW/161/98  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
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 /organism="Human enterovirus NSW/161/98"  
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 Oy 1 AAGGAACACGACACCCAA 20  
 Db 104 AAGGAACACGACACCCAA 85  
 RESULT 38  
 LOCUS  
 DEFINITION Human enterovirus 71 isolate NSW/166/98 5' UTR, partial sequence.  
 ACCESSION AY189195  
 VERSION AY189195.1 GI:28274418  
 KEYWORDS  
 SOURCE Human enterovirus 71  
 ORGANISM Human enterovirus 71  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
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 /organism="Human enterovirus 71"  
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 /isolate="NSW/166/98"  
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 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AAGGAACACGACACCCAA 20  
 Db 104 AAGGAACACGACACCCAA 85  
 RESULT 39  
 LOCUS  
 DEFINITION Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.  
 ACCESSION AY189196  
 VERSION AY189196.1 GI:28274419  
 KEYWORDS  
 SOURCE Human enterovirus 71  
 ORGANISM Human enterovirus 71  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
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 Oy 1 AAGGAACACGACACCCAA 20  
 Db 104 AAGGAACACGACACCCAA 85  
 RESULT 40  
 LOCUS  
 DEFINITION Human enterovirus NSW/173/98  
 ACCESSION AY189197  
 VERSION AY189197.1 GI:28274420  
 KEYWORDS  
 SOURCE Human enterovirus NSW/173/98  
 ORGANISM Human enterovirus NSW/173/98  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
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 /organism="Human enterovirus 71"  
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 Db 104 AAGGAACACGACACCCAA 85  
 RESULT 39  
 LOCUS  
 DEFINITION Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.  
 ACCESSION AY189196  
 VERSION AY189196.1 GI:28274419  
 KEYWORDS  
 SOURCE Human enterovirus 71  
 ORGANISM Human enterovirus 71  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
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 /note="Human enterovirus 71"  
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 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AAGGAACACGACACCCAA 20  
 Db 104 AAGGAACACGACACCCAA 85  
 RESULT 40  
 LOCUS  
 DEFINITION Human enterovirus NSW/173/98  
 ACCESSION AY189197  
 VERSION AY189197.1 GI:28274420  
 KEYWORDS  
 SOURCE Human enterovirus NSW/173/98  
 ORGANISM Human enterovirus NSW/173/98  
 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.  
 REFERENCE 1 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
 JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)  
 PUBMED 12721936  
 REFERENCE 2 (bases 1 to 116)  
 AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area Laboratory Services, University of New South Wales/Prince of Wales

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FEATURES
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                /isolate="NSW/173/98"
                /db_xref="taxon:220411"
                <1..>116

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 41
AY189198/c
LOCUS AY189198 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
ACCESSION AY189198
VERSION AY189198.1 GI:28274421
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
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                /mol_type="genomic RNA"
                /isolate="NSW/180/98"
                /db_xref="taxon:39054"
                /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 42
AY189199/c
LOCUS AY189199 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/182/98 5' UTR, partial sequence.
ACCESSION AY189199
VERSION AY189199.1 GI:28274422
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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                /mol_type="genomic RNA"
                /isolate="NSW/180/98"
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                /note="Human enterovirus 71"
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Query Match      100.0%; Score 20; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 43
AY189200/c
LOCUS AY189200 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/189/99 5' UTR, partial sequence.
ACCESSION AY189200
VERSION AY189200.1 GI:28274423
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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                /mol_type="genomic RNA"
                /isolate="NSW/189/99"
                /db_xref="taxon:138949"
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
    |||||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 44
AY189202/c

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AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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5'UTR
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 43
AY189200/c
LOCUS AY189200 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/189/99 5' UTR, partial sequence.
ACCESSION AY189200
VERSION AY189200.1 GI:28274423
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
          Viruses; ssRNA positive-strand viruses, no DNA stage;
          Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES
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                /db_xref="taxon:138949"
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 44
AY189202/c

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LOCUS      AY189202              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/196/99 5' UTR, partial sequence.
ACCESSION  AY189202
VERSION     AY189202.1  GI:28274425
KEYWORDS
SOURCE      Human enterovirus 71
ORGANISM    Human enterovirus 71
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
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            /mol_type="genomic RNA"
            /isolate="NSW/196/99"
            /db_xref="taxon:39054"
            /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 45
LOCUS      AY189203/c              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/197/99 5' UTR, partial sequence.
ACCESSION  AY189203
VERSION     AY189203.1  GI:28274426
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
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            /mol_type="genomic RNA"
            /isolate="NSW/197/99"
            /db_xref="taxon:138949"
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5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
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Db      104 AAGGAACACGACACCCAA 85

RESULT 46
LOCUS      AY189204/c              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/198/99 5' UTR, partial sequence.
ACCESSION  AY189204
VERSION     AY189204.1  GI:28274427
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
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            /isolate="NSW/198/99"
            /db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AAGGAACACGACACCCAA 20
        |||||
Db      104 AAGGAACACGACACCCAA 85

RESULT 47
LOCUS      AY189206/c              116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/208/99 5' UTR, partial sequence.
ACCESSION  AY189206
VERSION     AY189206.1  GI:28274429
KEYWORDS
SOURCE      Human enterovirus B
ORGANISM    Human enterovirus B
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
            Diabetes Associated with Enterovirus RNA
JOURNAL     J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED      12721936
REFERENCE   2 (bases 1 to 116)
AUTHORS     Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE       Direct Submission
JOURNAL     Submitted (29-NOV-2002) Virology Division, South Eastern Area
            Laboratory Services, University of New South Wales/Prince of Wales
            Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES    source
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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|||||
Db 104 AAGGAACACGGACACCCAA 85

RESULT 48
AY189208/c
LOCUS Human enterovirus B isolate NSW/214/99 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/214/99 5' UTR, partial sequence.
ACCESSION AY189208
VERSION AY189208.1 GI:28274431
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCAA 20
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 49
AY189211/c
LOCUS Human enterovirus B isolate NSW/230/99 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/230/99 5' UTR, partial sequence.
ACCESSION AY189211
VERSION AY189211.1 GI:28274434
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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/organism="Human enterovirus B"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 50
AY189214/c
LOCUS Human enterovirus A isolate NSW/277/99 5' UTR, partial sequence.
DEFINITION Human enterovirus A isolate NSW/277/99 5' UTR, partial sequence.
ACCESSION AY189214
VERSION AY189214.1 GI:28274437
KEYWORDS
SOURCE Human enterovirus A
ORGANISM Human enterovirus A
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 104 AAGGAACACGGACACCCAA 85

RESULT 51
AY189215/c
LOCUS Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
DEFINITION Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
ACCESSION AY189215
VERSION AY189215.1 GI:28274438

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KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 12721936
AUTHORS 2 (bases 1 to 116)
TITLE Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
JOURNAL Direct Submission
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL Hospital, High Street, Randwick, NSW 2031, Australia
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/db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 104 AAGGAAACACGGACACCCAA 85
RESULT 52
AY189216/c
LOCUS Human enterovirus 71 isolate NSW/E71/99 5' UTR, partial sequence.
DEFINITION
ACCESSION AY189216
VERSION AY189216.1 GI:28274439
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 12721936
AUTHORS 2 (bases 1 to 116)
TITLE Craig, M.E., Howard, N.J., Sillink, M. and Rawlinson, W.D.
JOURNAL Direct Submission
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales
HOSPITAL Hospital, High Street, Randwick, NSW 2031, Australia
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/note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 104 AAGGAAACACGGACACCCAA 85
RESULT 53
AY183003/c
LOCUS Human enterovirus 71 genomic RNA, 5' UTR, partial sequence,
DEFINITION isolate: 2279/EV71/Hyogo/2003.
ACCESSION AB183003
VERSION AB183003.1 GI:49614920
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 117)
AUTHORS Fujimoto, T., Munemura, T. and Chikahira, M.
JOURNAL Direct Submission
TITLE Submitted (30-JUN-2004) Tsuguto Fujimoto, Hyogo Prefectural
Institute of Public Health and Environmental Sciences, Infectious
Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail: Tsuguto.Fujimoto@pref.hyogo.jp,
URL: http://www.iphes.pref.hyogo.jp/, Tel: 81-78-511-6640 (ex.236),
Fax: 81-78-531-7080)
FEATURES
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/organism="Human enterovirus 71"
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/country="Japan:Hyogo"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86
RESULT 54
S66302S1/c
LOCUS Human poliovirus 3
DEFINITION Human poliovirus 3
ACCESSION S66302
VERSION S66302.1 GI:435703
KEYWORDS
SEGMENT 1 of 2
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 119)
LCDC (Canadian Govt)
Genomic analysis of type 3 wild poliovirus isolates in southern
Alberta
Can. Commun. Dis. Rep. 19 (13), 96-99 (1993)
JOURNAL 8395279
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138833] from the original journal article.

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Db 104 AAGGAAACACGGACACCCAA 85
RESULT 53
AB183003/c
LOCUS Human enterovirus 71 genomic RNA, 5' UTR, partial sequence,
DEFINITION isolate: 2279/EV71/Hyogo/2003.
ACCESSION AB183003
VERSION AB183003.1 GI:49614920
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 117)
AUTHORS Fujimoto, T., Munemura, T. and Chikahira, M.
JOURNAL Direct Submission
TITLE Submitted (30-JUN-2004) Tsuguto Fujimoto, Hyogo Prefectural
Institute of Public Health and Environmental Sciences, Infectious
Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail: Tsuguto.Fujimoto@pref.hyogo.jp,
URL: http://www.iphes.pref.hyogo.jp/, Tel: 81-78-511-6640 (ex.236),
Fax: 81-78-531-7080)
FEATURES
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 105 AAGGAAACACGGACACCCAA 86
RESULT 54
S66302S1/c
LOCUS Human poliovirus 3
DEFINITION Human poliovirus 3
ACCESSION S66302
VERSION S66302.1 GI:435703
KEYWORDS
SEGMENT 1 of 2
SOURCE Human poliovirus 3
ORGANISM Human poliovirus 3
REFERENCE Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 119)
LCDC (Canadian Govt)
Genomic analysis of type 3 wild poliovirus isolates in southern
Alberta
Can. Commun. Dis. Rep. 19 (13), 96-99 (1993)
JOURNAL 8395279
PUBMED
REMARK GenBank staff at the National Library of Medicine created this
entry [NCBI gibbsq 138833] from the original journal article.

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  Best Local Similarity 100.0%; Pred. No. 30;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 101 AAGGAAACACGGACACCCAA 82

RESULT 55
AJ783777/c
LOCUS
DEFINITION Human poliovirus 1, partial 5'UTR, genomic RNA, isolate P20.
ACCESSION AJ783777
VERSION AJ783777.1 GI:72534022
KEYWORDS
SOURCE Human poliovirus 1
ORGANISM Human poliovirus 1
REFERENCE
  1 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
AUTHORS
  Pavlov,D.N.
TITLE Genomic mutations in oral poliovirus vaccine strains:Implications for the eradication of poliovirus
JOURNAL Unpublished
REFERENCE
  2 (bases 1 to 128)
AUTHORS Pavlov,D.N.
TITLE Direct Submission
JOURNAL Submitted (12-JUL-2004) Pavlov D.N., Medical Virology, University of Pretoria, P.O.Box 2034, Pretoria, Gauteng, 0001, SOUTH AFRICA
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Db 118 AAGGAAACACGGACACCCAA 99

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LOCUS
DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ra/Roma99.
ACCESSION AJ312090
VERSION AJ312090.1 GI:16555708
KEYWORDS
SOURCE Human coxsackievirus B2
ORGANISM Human coxsackievirus B2
REFERENCE
  1 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
  2 (bases 1 to 145)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy
FEATURES
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Db 121 AAGGAAACACGGACACCCAA 102

RESULT 57
HEN312091/c
LOCUS
DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ro/Roma99.
ACCESSION AJ312091
VERSION AJ312091.1 GI:16555709
KEYWORDS
SOURCE Human coxsackievirus B2
ORGANISM Human coxsackievirus B2
REFERENCE
  1 Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae; Enterovirus.
  2 (bases 1 to 145)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy
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        /lab_host="vero cell culture"
        /notes="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
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Qy 1 AAGGAAACACGGACACCCAA 20
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Db 121 AAGGAAACACGGACACCCAA 102

AUTHORS Manzara,S., Muscillo,M., La Rosa,G., Marianelli,C., Cattani,P. and Fadda,G.
TITLE Molecular identification and typing of enteroviruses isolated from clinical specimens
JOURNAL J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
PUBMED 12454151
REFERENCE 2 (bases 1 to 145)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy
FEATURES
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        /notes="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"
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Qy 1 AAGGAAACACGGACACCCAA 20
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Db 121 AAGGAAACACGGACACCCAA 102

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Query Match	100.0%; Score 20; DB 13; Length 145;	
Best Local Similarity	100.0%; Pred. No. 30;	
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 AAGGAAACACGGACACCCAA 20	
Db	120 AAGGAAACACGGACACCCAA 101	
RESULT 58		
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LOCUS	AF314006 147 bp mRNA linear VRL 31-JUL-2002	
DEFINITION	Enterovirus 5506/SIN/001309 5' UTR, partial sequence.	
ACCESSION	AF314006	
VERSION	AF314006.1 GI:12667229	
KEYWORDS		
SOURCE	Enterovirus 5506/SIN/001309	
ORGANISM	Enterovirus 5506/SIN/001309	
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage;	
AUTHORS	Picornaviridae; Enterovirus.	
TITLE	1 (bases 1 to 147)	
	Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.	
	Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens	
	from a Hand, Foot, and Mouth Disease Outbreak in Singapore by	
	Reverse Transcription-PCR with Universal Enterovirus and	
	EV71-Specific Primers	
JOURNAL	J. Clin. Microbiol. 40 (8), 2823-2827 (2002)	
PUBMED	12149336	
REFERENCE	2 (bases 1 to 107)	
AUTHORS	Singh, S., Chow, V.T.K. and Poh, C.L.	
TITLE	Direct Submission	
JOURNAL	Submitted (18-OCT-2000) Microbiology, National University of	
	Singapore, 5 Science Drive 2, Singapore 117597, Singapore	
FEATURES	Location/Qualifiers	
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Best Local Similarity	100.0%; Pred. No. 30;	
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Qy	1 AAGGAAACACGGACACCCAA 20	
Db	122 AAGGAAACACGGACACCCAA 103	
RESULT 59		
AF316322/c		
LOCUS	AF316322 147 bp mRNA linear VRL 31-JUL-2002	
DEFINITION	Enterovirus 71 isolate 5855/sin/000009 5'UTR, partial sequence.	
ACCESSION	AF316322	
VERSION	AF316322.1 GI:12744302	
KEYWORDS		
SOURCE	Human enterovirus 71	
ORGANISM	Human enterovirus 71	
REFERENCE	Viruses; ssRNA positive-strand viruses, no DNA stage;	
AUTHORS	Picornaviridae; Enterovirus.	
TITLE	1 (bases 1 to 147)	
	Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.	
	Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens	
	from a Hand, Foot, and Mouth Disease Outbreak in Singapore by	
	Reverse Transcription-PCR with Universal Enterovirus and	
	EV71-Specific Primers	
JOURNAL	J. Clin. Microbiol. 40 (8), 2823-2827 (2002)	
PUBMED	12149336	
REFERENCE	2 (bases 1 to 147)	
AUTHORS	Singh, S., Chow, V.T.K. and Poh, C.L.	
TITLE	Direct Submission	

JOURNAL		Submitted (24-OCT-2000) Department of Microbiology, National University of Singapore, 5, Science Drive 2, Singapore 117597, Singapore	
FEATURES	Location/Qualifiers		
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	/isolate="5855/sin/000009"		
	/db_xref="taxon:39054"		
	/note="Human enterovirus 71 derived from isolates collected from human mouth swab, saliva, lung, heart, brain, rectal swab, tonsils, spleen, foot swab, throat swab, intestine, and oral mucosa."		
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Best Local Similarity	100.0%;	Pred. No. 30;	
Matches	20;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
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Db	122 AAGGAAACACGGACACCCAA 103		
RESULT 60			
AF314004/c		153 bp	mRNA linear VRL 31-JUL-2002
LOCUS	AF314004		
DEFINITION	Enterovirus 589/SIN/001809 5' UTR, partial sequence.		
ACCESSION	AF314004		
VERSION	AF314004.2	GI:131111667	
KEYWORDS			
SOURCE	Enterovirus 589/SIN/001809		
ORGANISM	Enterovirus 589/SIN/001809		
	Viruses; ssRNA positive-strand viruses, no DNA stage;		
	Picornaviridae; Enterovirus.		
REFERENCE	1 (bases 1 to 153)		
AUTHORS	Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.		
TITLE	Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers		
JOURNAL	J. Clin. Microbiol. 40 (8), 2823-2827 (2002)		
PUBMED	12149336		
REFERENCE	2 (bases 1 to 153)		
AUTHORS	Singh,S., Chow,V.T.K. and Poh,C.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore		
REFERENCE	3 (bases 1 to 153)		
AUTHORS	Singh,S., Chow,V.T.K. and Poh,C.L.		
TITLE	Direct Submission		
JOURNAL	Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore		
REMARK	Sequence update by submitter		
COMMENT	On Feb 23, 2001 this sequence version replaced gi:12667227.		
FEATURES	Location/Qualifiers		
source	1. .153		
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ORIGIN			
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Qy	1 AAGGAAACACGGACACCCAA 20		
Db	122 AAGGAAACACGGACACCCAA 103		

RESULT 61  
AF314003/c  
LOCUS AF314003 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5627/SIN/002009 5' UTR, partial sequence.  
ACCESSION AF314003  
VERSION AF314003.2 GI:13111666  
KEYWORDS  
SOURCE Enterovirus 5627/SIN/002009  
ORGANISM Enterovirus 5627/SIN/002009  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
JOURNAL 12149336  
PUBMED 2 (bases 1 to 154)  
REFERENCE Singh, S., Chow, V.T.K. and Poh, C.L.  
AUTHORS Direct Submission  
TITLE Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
JOURNAL 3 (bases 1 to 154)  
REFERENCE Singh, S., Chow, V.T.K. and Poh, C.L.  
AUTHORS Direct Submission  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667226.  
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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
Db 122 AAGGAAACACGGACACCCAA 103  
RESULT 62  
AF314005/c  
LOCUS AF314005 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5656/SIN/002209 5' UTR, partial sequence.  
ACCESSION AF314005  
VERSION AF314005.2 GI:13111668  
KEYWORDS  
SOURCE Enterovirus 5656/SIN/002209  
ORGANISM Enterovirus 5656/SIN/002209  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
JOURNAL 12149336  
PUBMED 2 (bases 1 to 154)  
REFERENCE Singh, S., Chow, V.T.K. and Poh, C.L.  
AUTHORS Direct Submission  
TITLE Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667226.  
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/strain="5627/SIN/002009"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
Db 122 AAGGAAACACGGACACCCAA 103  
RESULT 63  
AF314007/c  
LOCUS AF314007 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5536/SIN/001409 5' UTR, partial sequence.  
ACCESSION AF314007  
VERSION AF314007.2 GI:13111669  
KEYWORDS  
SOURCE Enterovirus 5536/SIN/001409  
ORGANISM Enterovirus 5536/SIN/001409  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
JOURNAL 12149336  
PUBMED 2 (bases 1 to 154)  
REFERENCE Singh, S., Chow, V.T.K. and Poh, C.L.  
AUTHORS Direct Submission  
TITLE Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667230.  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
Db 122 AAGGAAACACGGACACCCAA 103

Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
3 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K. and Poh, C.L.  
TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667228.  
FEATURES  
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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
Db 122 AAGGAAACACGGACACCCAA 103  
RESULT 63  
AF314007/c  
LOCUS AF314007 154 bp mRNA linear VRL 31-JUL-2002  
DEFINITION Enterovirus 5536/SIN/001409 5' UTR, partial sequence.  
ACCESSION AF314007  
VERSION AF314007.2 GI:13111669  
KEYWORDS  
SOURCE Enterovirus 5536/SIN/001409  
ORGANISM Enterovirus 5536/SIN/001409  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 154)  
AUTHORS Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.  
TITLE Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens from a Hand, Foot, and Mouth Disease Outbreak in Singapore by Reverse Transcription-PCR with Universal Enterovirus and EV71-Specific Primers  
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)  
JOURNAL 12149336  
PUBMED 2 (bases 1 to 154)  
REFERENCE Singh, S., Chow, V.T.K. and Poh, C.L.  
AUTHORS Direct Submission  
TITLE Submitted (18-OCT-2000) Microbiology, National University of Singapore, 5 Science Drive 2, Singapore 117597, Singapore  
REMARK Sequence update by submitter  
COMMENT On Feb 23, 2001 this sequence version replaced gi:12667230.  
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Qy 1 AAGGAAACACGGACACCCAA 20  
Db 122 AAGGAAACACGGACACCCAA 103



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RESULT 64
AY027864/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY027864
Enterovirus TS/SIN/001002 154 bp RNA linear VRL 31-JUL-2002
partial sequence.
AY027864
AY027864.1 GI:13591397
Enterovirus TS/SIN/001002
Enterovirus TS/SIN/001002
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 154)
Singh, S., Chow, V.T.K., Phoon, M.C., Chan, K.P. and Poh, C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand, Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
12149336
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (22-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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/organism="Enterovirus TS/SIN/001002"
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/strain="TS/SIN/001002"
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5'UTR
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
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Db 122 AAGGAACACGACACCCAA 103

RESULT 65
AY027865/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AY027865
Enterovirus TF/SIN/000704 154 bp RNA linear VRL 10-APR-2001
partial sequence.
AY027865
AY027865.1 GI:13591398
Enterovirus TF/SIN/000704
Enterovirus TF/SIN/000704
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Enterovirus strains from an outbreak of Hand, Foot and Mouth
disease in Singapore (2000)
Unpublished
2 (bases 1 to 154)
Singh, S., Chow, V.T.K. and Poh, C.L.
Direct Submission
Submitted (22-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Location/Qualifiers
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/organism="Enterovirus TF/SIN/000704"
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5'UTR
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
|||||
Db 122 AAGGAACACGACACCCAA 103

RESULT 66
HCO295181/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HCO295181
Human coxsackievirus B2 171 bp RNA linear VRL 15-MAY-2001
171 bp RNA linear VRL 15-MAY-2001
HCO295181
HCO295181.1 GI:14139958
Human coxsackievirus B2
Human coxsackievirus B2
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1
Muscullo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,

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5'UTR  
ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 154;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
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 Db 122 AAGGAACACGACACCCAA 103

RESULT 66  
 HEN312089/c

LOCUS  
 DEFINITION Human coxsackievirus B2 partial 5'UTR, strain /ia/Roma9.  
 ACCESSION AJ312089  
 VERSION AJ312089.1 GI:16555707  
 KEYWORDS  
 SOURCE Human coxsackievirus B2  
 ORGANISM Human coxsackievirus B2

Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.  
 1  
 Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and  
 Fadda, G.  
 Molecular identification and typing of enteroviruses isolated from  
 clinical specimens  
 J. Clin. Microbiol. 40 (12), 4554-4560 (2002)  
 12454151  
 2 (bases 1 to 155)  
 Muscillo, M.  
 Direct Submission  
 Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,  
 Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM  
 00161, Italy  
 Location/Qualifiers  
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 /note="throat swab from child with aseptic meningitis.  
 identified by immunofluorescence assay"  
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REFERENCE  
 AUTHORS

TITLE

JOURNAL  
 PUBMED  
 12454151

REFERENCE  
 2 (bases 1 to 155)

AUTHORS  
 Muscillo, M.

TITLE  
 Direct Submission

JOURNAL  
 Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,  
 Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM  
 00161, Italy

FEATURES  
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 identified by immunofluorescence assay"  
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5'UTR  
 ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 122 AAGGAACACGACACCCAA 103

RESULT 67  
 HCO295181/c

LOCUS  
 DEFINITION Human coxsackievirus B5 genomic RNA for partial 5'UTR, isolate  
 ITA99-21.  
 ACCESSION AJ295181  
 VERSION AJ295181.1 GI:14139958  
 KEYWORDS  
 SOURCE Human coxsackievirus B5  
 ORGANISM Human coxsackievirus B5

Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.  
 1  
 Muscillo, M., La Rosa, G., Marianelli, C., Capobianchi, M.R.,

REFERENCE  
 AUTHORS

Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and Ticca,F.

A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools

JOURNAL  
REFERENCE 2 (bases 1 to 171)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

1..171  
/organism="Human coxsackievirus B5"  
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/strain="F/Roma99"  
/isolate="ITA99-21"  
/specific\_host="Homo sapiens"  
/db\_xref="taxon:12074"  
/note="sporadic case of aseptic meningitis; BGM cell culture of stools from a four years old child"  
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5'UTR

ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 171;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 41 AAGGAACACGGACACCCAA 60

RESULT 68

HEN312088/c

LOCUS HEN312088

172 bp RNA linear VRL 02-JUL-2003

DEFINITION Human enterovirus 71 partial 5'UTR, strain /di/Roma98.

ACCESSION AJ312088

VERSION AJ312088.1 GI:16555706

SOURCE Human enterovirus 71

ORGANISM Human enterovirus 71

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1

AUTHORS Manzara,S., Muscillo,M., La Rosa,G., Marianelli,C., Cattani,P. and Fadda,G.

Molecular identification and typing of enteroviruses isolated from clinical specimens

J. Clin. Microbiol. 40 (12), 4554-4560 (2002)

REFERENCE 2 (bases 1 to 172)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

1..172  
/organism="Human enterovirus 71"  
/viroion  
/mol\_type="genomic RNA"  
/strain="di/Roma98"  
/isolate="IT98-5114"  
/db\_xref="taxon:39054"  
/lab\_hosts="vero cell cultures"  
/note="throat swab from child with aseptic meningitis, identified by immunofluorescence assay"  
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ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 172;

Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 120 AAGGAACACGGACACCCAA 101

RESULT 69

ESP295207

LOCUS ESP295207

DEFINITION Echovirus sp.

ACCESSION AJ295207

VERSION AJ295207.1

KEYWORDS GI:14140008

SOURCE Echovirus sp.

ORGANISM Echovirus sp.

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1

AUTHORS Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R., Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and Ticca,F.

TITLE A phylogenetic analysis of the two echovirus 30 isolated in Rome (Italy) in 1997 from an outbreak of aseptic meningitis associated with swimming pools

Unpublished

REFERENCE 2 (bases 1 to 177)

AUTHORS Muscillo,M.

TITLE Direct Submission

JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM 00161, Italy

FEATURES Location/Qualifiers

source

1..177

/organism="Echovirus sp."

/viroion

/mol\_type="genomic RNA"

/strain="Bastiani"

/isolate="ATCC VR-322"

/db\_xref="taxon:145390"

/note="isolated from fecal specimen of 10-year-old boy with symptoms of headache, stiff neck, fever"

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ORIGIN

Query Match 100.0%; Score 20; DB 13; Length 177;

Best Local Similarity 100.0%; Pred. No. 30;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 58 AAGGAACACGGACACCCAA 77

RESULT 70

AF521491/c

LOCUS AF521491

DEFINITION Human echovirus 13

ACCESSION AF521491

VERSION AF521491.1

KEYWORDS GI:31790833

SOURCE Human echovirus 13

ORGANISM Human echovirus 13

Viruses; ssRNA positive-strand viruses, no DNA stage;

Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 184)

AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselink,K., Lindberg,A.M. and Van Ranst,M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

JOURNAL

```

PUBMED
REFERENCE 12767006
AUTHORS 2 (bases 1 to 184)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
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    /vifion
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    /isolate="BE00-82"
    /isolation_source="patient 82 - zipcode Belgium 8560"
    /db_xref="taxon:47501"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
Db 128 AAGGAACACGACGCCAA 109

RESULT 71
AF521433/c
LOCUS AF521433 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
ACCESSION AF521433
VERSION AF521433.1 GI:31790775
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
    source Location/Qualifiers
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    /vifion
    /mol_type="genomic RNA"
    /isolate="BE00-14"
    /isolation_source="patient 14 - zipcode Belgium 9310"
    /db_xref="taxon:41846"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20

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Db 128 AAGGAACACGACGCCAA 109

RESULT 72
AF521434/c
LOCUS AF521434 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-15 5' UTR, partial sequence.
ACCESSION AF521434
VERSION AF521434.1 GI:31790776
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
        Virology, Department of Microbiology and Immunology, Rega Institute
        for Medical Research, University of Leuven, Minderbroedersstraat
        10, Leuven BE-3000, Belgium
FEATURES
    source Location/Qualifiers
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    /vifion
    /mol_type="genomic RNA"
    /isolate="BE00-15"
    /isolation_source="patient 15 - zipcode Belgium 9820"
    /db_xref="taxon:12074"
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20
Db 128 AAGGAACACGACGCCAA 109

RESULT 73
AF521435/c
LOCUS AF521435 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-1 5' UTR, partial sequence.
ACCESSION AF521435
VERSION AF521435.1 GI:31790777
KEYWORDS
SOURCE Human coxsackievirus B5
ORGANISM Human coxsackievirus B5
REFERENCE 1 (bases 1 to 185)
        Viruses; ssRNA positive-strand viruses, no DNA stage;
        Picornaviridae; Enterovirus.
AUTHORS Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
        an outbreak of aseptic meningitis in Belgium during the summer of
        2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
AUTHORS 2 (bases 1 to 185)
        Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
        Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission

```

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

# FEATURES

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Location/Qualifiers  
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/viroion  
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/db\_xref="taxon:12074"  
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# 5'UTR

ORIGIN  
Query Match 100.0%; Score 20; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

# RESULT 74

AF521436/c AF521436 185 bp RNA linear VRL 17-JUN-2003  
LOCUS Human echovirus 30 isolate BE00-2 5' UTR, partial sequence.  
DEFINITION AF521436  
ACCESSION AF521436  
VERSION AF521436.1 GI:31790778

# SOURCE

Human echovirus 30  
Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.  
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

# FEATURES

source  
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Location/Qualifiers  
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/db\_xref="taxon:41846"  
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# 5'UTR

ORIGIN  
Query Match 100.0%; Score 20; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

# RESULT 75

AF521440/c

LOCUS AF521440 185 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-6 5' UTR, partial sequence.  
ACCESSION AF521440  
VERSION AF521440.1 GI:31790782

# KEYWORDS

Human echovirus 30  
Human echovirus 30

ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

# FEATURES

source  
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Location/Qualifiers  
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/viroion  
/mol\_type="genomic RNA"  
/isolate="BE00-6"  
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/db\_xref="taxon:41846"  
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# 5'UTR

ORIGIN  
Query Match 100.0%; Score 20; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 128 AAGGAACACGGACACCCAA 109

# RESULT 76

AF521444/c

LOCUS AF521444 185 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-11 5' UTR, partial sequence.

ACCESSION AF521444

VERSION AF521444.1 GI:31790786

# KEYWORDS

Human echovirus 30  
Human echovirus 30

ORGANISM  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

# REFERENCE

1 (bases 1 to 185)  
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.

Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

J. Med. Virol. 70 (3), 420-429 (2003)

12767006

2 (bases 1 to 185)

Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.

Direct Submission

Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

# FEATURES

Location/Qualifiers

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db 128 AAGGAACACGGACACCCAA 109

RESULT 77
AF521445/c
LOCUS AF521445 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-12 5' UTR, partial sequence.
ACCESSION AF521445
VERSION AF521445.1 GI:31790787
KEYWORDS
SOURCE
ORGANISM
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
/organism="Human echovirus 30"
/virion
/mol_type="genomic RNA"
/isolate="BE00-12"
/isolation_source="patient 12 - zipcode Belgium 9402"
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Qy 1 AAGGAACACGGACACCCAA 20
|||||
Db 128 AAGGAACACGGACACCCAA 109

RESULT 78
AF521446/c
LOCUS AF521446 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 16 isolate BE00-13 5' UTR, partial sequence.
ACCESSION AF521446
VERSION AF521446.1 GI:31790789
KEYWORDS
SOURCE
ORGANISM
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
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|||||
Db 128 AAGGAACACGGACACCCAA 109

RESULT 79
AF521447/c
LOCUS AF521447 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
ACCESSION AF521447
VERSION AF521447.1 GI:31790789
KEYWORDS
SOURCE
ORGANISM
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
Location/Qualifiers
1. .185
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/isolate="BE00-30"

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SOURCE
ORGANISM
Human echovirus 16
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 AAGGAACACGGACACCCAA 109

RESULT 79
AF521447/c
LOCUS AF521447 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-30 5' UTR, partial sequence.
ACCESSION AF521447
VERSION AF521447.1 GI:31790789
KEYWORDS
SOURCE
ORGANISM
Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
10, Leuven BE-3000, Belgium
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/virion
/mol_type="genomic RNA"
/isolate="BE00-30"

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Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 80
AF521448/c
LOCUS AF521448 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human coxsackievirus B5 isolate BE00-31 5' UTR, partial sequence.
ACCESSION AF521448
VERSION AF521448.1 GI:31790790
KEYWORDS Human coxsackievirus B5
SOURCE Human coxsackievirus B5
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
FEATURES
source
Location/Qualifiers
1..185
/organism="Human coxsackievirus B5"
/virion
/mol_type="genomic RNA"
/isolate="BE00-31"
/isolation_source="patient 31 - zipcode Belgium 9320"
/db_xref="taxon:12074"
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ORIGIN
Query Match      100.0%; Score 20; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 128 AAGGAAACACGGACACCCAA 109

RESULT 81
AF521449/c
LOCUS AF521449 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-32 5' UTR, partial sequence.
ACCESSION AF521449
VERSION AF521449.1 GI:31790791
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)

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AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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ACCESSION AF521450
VERSION AF521450.1 GI:31790792
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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DEFINITION AF521451  
ACCESSION AF521451.1 GI:31790793  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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/viral protein  
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ACCESSION AF521458.1 GI:31790800  
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SOURCE  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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Db 128 AAGGAAACACGGACACCCAA 109

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DEFINITION AF521461  
ACCESSION AF521461.1 GI:31790803  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000

J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium

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AF521474/c
LOCUS       AF521474               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
ACCESSION    AF521474
VERSION      AF521474.1  GI:31790816
KEYWORDS     .
SOURCE       Human echovirus 30
ORGANISM     Human echovirus 30
REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS      1 (bases 1 to 185)
              Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
              Lindberg, A.M. and Van Ranst, M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
              Lindberg, M.A. and Van Ranst, M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
FEATURES     Location/Qualifiers
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Db 128 AAGGAAACACGGACACCCCAA 109

RESULT 90
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LOCUS       AF521475               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.
ACCESSION    AF521475
VERSION      AF521475.1  GI:31790817
KEYWORDS     .
SOURCE       Human echovirus 30
ORGANISM     Human echovirus 30
REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS      1 (bases 1 to 185)
              Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
              Lindberg, A.M. and Van Ranst, M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
              Lindberg, M.A. and Van Ranst, M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium

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FEATURES     Location/Qualifiers
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Db 128 AAGGAAACACGGACACCCCAA 109

RESULT 91
AF521476/c
LOCUS       AF521476               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.
ACCESSION    AF521476
VERSION      AF521476.1  GI:31790818
KEYWORDS     .
SOURCE       Human echovirus 30
ORGANISM     Human echovirus 30
REFERENCE    Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS      1 (bases 1 to 185)
              Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
              Lindberg, A.M. and Van Ranst, M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
              Lindberg, M.A. and Van Ranst, M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
FEATURES     Location/Qualifiers
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Db 128 AAGGAAACACGGACACCCCAA 109

RESULT 92
AF521477/c
LOCUS       AF521477               185 bp    RNA        linear    VRL 17-JUN-2003
DEFINITION   Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.
ACCESSION    AF521477
VERSION      AF521477.1  GI:31790819

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KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Viruses; ssRNA positive-strand viruses, no DNA stage;
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REFERENCE
AUTHORS     1 (bases 1 to 185)
            Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE       Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL     J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED      12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS     Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Db 128 AAGGAAACACGGACACCCAA 109

RESULT 94
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LOCUS        AF521480                185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION   Human coxsackievirus B5 isolate BE00-27 5' UTR, partial sequence.
ACCESSION    AF521480
VERSION      AF521480.1 GI:31790822
KEYWORDS     .
ORGANISM     Human coxsackievirus B5
SOURCE       Human coxsackievirus B5
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE    1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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DEFINITION   Human echovirus 16 isolate BE00-72 5' UTR, partial sequence.
ACCESSION    AF521481
VERSION      AF521481.1 GI:31790823
KEYWORDS     .
ORGANISM     Human echovirus 16
SOURCE       Human echovirus 16
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.

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REFERENCE
AUTHORS      1 (bases 1 to 185)
              Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
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TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
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DEFINITION
ACCESSION  AF521482
VERSION     AF521482.1 GI:31790824
KEYWORDS
SOURCE      Human echovirus 13
ORGANISM    Human echovirus 13
REFERENCE    1 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
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DB 128 AAGGAAACACGGACACCCAA 109

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DEFINITION
ACCESSION  AF521483
VERSION     AF521483.1 GI:31790825
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
REFERENCE    1 (bases 1 to 185)
              Picornaviridae; Enterovirus.
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000
JOURNAL      J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED       12767006
REFERENCE    2 (bases 1 to 185)
AUTHORS      Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
              Lindberg,M.A. and Van Ranst,M.
TITLE        Direct Submission
JOURNAL      Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
              Virology, Department of Microbiology and Immunology, Rega Institute
              for Medical Research, University of Leuven, Minderbroedersstraat
              10, Leuven BE-3000, Belgium
FEATURES     Location/Qualifiers
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DB 128 AAGGAAACACGGACACCCAA 109

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DEFINITION
ACCESSION  AF521484
VERSION     AF521484.1 GI:31790826
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SOURCE      Human echovirus 16
ORGANISM    Human echovirus 16
REFERENCE    1 (bases 1 to 185)
              Picornaviridae; Enterovirus.
AUTHORS      Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
              Lindberg,A.M. and Van Ranst,M.
TITLE        Molecular typing and epidemiology of enteroviruses identified from
              an outbreak of aseptic meningitis in Belgium during the summer of
              2000

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OM nucleic - nucleic search, using sw model

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468.258 Million cell updates/sec

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+-----+

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Searched: 1303057 seqs, 888780828 residues

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Listing first 500 summaries

Database : Issued Patents NA.\*

- 1: /cgn2\_6/ptodata/1/ina/1 COMB.seq.\*
- 2: /cgn2\_6/ptodata/1/ina/5 COMB.seq.\*
- 3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*
- 4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*
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- 6: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*
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- 8: /cgn2\_6/ptodata/1/ina/RE COMB.seq.\*
- 9: /cgn2\_6/ptodata/1/ina/backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	20	100.0	628	2	US-08-387-845-5
C 2	20	100.0	628	2	US-08-778-275-5
C 3	20	100.0	628	3	US-08-867-352-5
C 4	20	100.0	1220	3	US-09-116-032-2
C 5	20	100.0	2320	3	US-09-202-904A-10
C 6	20	100.0	7400	3	US-09-116-032-1
C 7	20	100.0	7432	2	US-07-852-260-1
C 8	20	100.0	7432	2	US-08-461-503-1
C 9	20	100.0	7432	2	US-08-465-250-1
C 10	20	100.0	7441	3	US-09-284-349B-1
C 11	19.2	100.0	28	3	US-09-724-678D-11
C 12	18.4	92.0	1560	3	US-09-724-678D-16
C 13	17	85.0	33	3	US-09-129-686-20
C 14	17	85.0	33	3	US-09-566-581-20
C 15	17	85.0	39	3	US-09-061-273-8
C 16	17	85.0	627	2	US-08-221-816B-31
C 17	17	85.0	627	3	US-10-112-547-31
C 18	17	85.0	627	3	US-10-112-241-31
C 19	17	85.0	627	3	US-10-104-611-31
C 20	17	85.0	627	3	US-10-109-368-31
C 21	17	85.0	627	3	US-09-724-380-31
C 22	16.8	84.0	601	3	US-09-949-016-78843
C 23	16.8	84.0	601	3	US-09-949-016-78844
C 24	16.8	84.0	784019	3	US-09-949-016-14033

25	16.8	84.0	828152	3	US-09-949-016-12777	Sequence 12777, A
26	16.4	82.0	601	3	US-09-949-016-78842	Sequence 78842, A
27	16	80.0	601	3	US-09-949-016-194126	Sequence 194126, A
C 28	16	80.0	18568	3	US-09-949-016-16963	Sequence 16963, A
C 29	16	80.0	137949	3	US-09-949-016-12196	Sequence 12196, A
C 30	16	80.0	137956	3	US-09-949-016-17260	Sequence 17260, A
C 31	15.8	79.0	601	3	US-09-949-016-56995	Sequence 56995, A
C 32	15.8	79.0	1560	3	US-09-134-000C-1077	Sequence 1077, Ap
C 33	15.8	79.0	1817	2	US-08-743-637B-1	Sequence 1, Appl
C 34	15.8	79.0	1817	2	US-08-526-840B-1	Sequence 1, Appl
C 35	15.8	79.0	16434	3	US-09-949-016-13235	Sequence 13235, A
C 36	15.8	79.0	40091	3	US-09-949-016-16011	Sequence 16011, A
C 37	15.8	79.0	46626	3	US-09-949-016-13390	Sequence 13390, A
C 38	15.4	77.0	2053	3	US-09-270-767-247	Sequence 247, App
C 39	15.4	77.0	2053	3	US-09-270-767-15529	Sequence 15529, A
C 40	15.4	77.0	2690	3	US-09-999-833A-514	Sequence 514, App
C 41	15.4	77.0	2690	3	US-10-020-445A-514	Sequence 514, App
C 42	15.4	77.0	300598	3	US-09-949-016-11868	Sequence 11868, A
C 43	15.4	77.0	302604	3	US-09-949-016-14588	Sequence 14588, A
C 44	15.4	77.0	302604	3	US-09-949-016-14589	Sequence 14589, A
C 45	15.2	76.0	308362	3	US-09-949-016-17119	Sequence 17119, A
C 46	15.2	76.0	507	3	US-09-107-532A-826	Sequence 826, App
C 47	15.2	76.0	601	3	US-09-949-016-26382	Sequence 26382, A
C 48	15.2	76.0	601	3	US-09-949-016-26383	Sequence 26383, A
C 49	15.2	76.0	601	3	US-09-949-016-58446	Sequence 58446, A
C 50	15.2	76.0	601	3	US-09-949-016-58447	Sequence 58447, A
C 51	15.2	76.0	601	3	US-09-949-016-58448	Sequence 58448, A
C 52	15.2	76.0	601	3	US-09-949-016-58449	Sequence 58449, A
C 53	15.2	76.0	601	3	US-09-949-016-58450	Sequence 58450, A
C 54	15.2	76.0	601	3	US-09-949-016-110157	Sequence 110157, A
C 55	15.2	76.0	601	3	US-09-949-016-110158	Sequence 110158, A
C 56	15.2	76.0	601	3	US-09-949-016-110159	Sequence 110159, A
C 57	15.2	76.0	601	3	US-09-949-016-138287	Sequence 138287, A
C 58	15.2	76.0	601	3	US-09-949-016-138288	Sequence 138288, A
C 59	15.2	76.0	601	3	US-09-949-016-149759	Sequence 149759, A
C 60	15.2	76.0	675	3	US-09-533-559-6526	Sequence 6526, Ap
C 61	15.2	76.0	1455	3	US-09-248-796A-4726	Sequence 4726, Ap
C 62	15.2	76.0	1622	2	US-08-631-200-13	Sequence 13, Appl
C 63	15.2	76.0	1622	2	US-08-829-553-13	Sequence 13, Appl
C 64	15.2	76.0	1622	2	US-08-922-607A-13	Sequence 13, Appl
C 65	15.2	76.0	1622	2	US-08-936-707A-13	Sequence 13, Appl
C 66	15.2	76.0	1622	2	US-08-936-706A-13	Sequence 13, Appl
C 67	15.2	76.0	1622	3	US-09-248-203-13	Sequence 13, Appl
C 68	15.2	76.0	1622	3	US-09-406-071-13	Sequence 13, Appl
C 69	15.2	76.0	1622	3	US-09-814-986-13	Sequence 13, Appl
C 70	15.2	76.0	1987	2	US-08-990-379-2	Sequence 1, Appl
C 71	15.2	76.0	1993	2	US-08-990-379-2	Sequence 2, Appl
C 72	15.2	76.0	2391	3	US-09-555-820A-1	Sequence 1, Appl
C 73	15.2	76.0	2391	3	US-09-555-820A-2	Sequence 2, Appl
C 74	15.2	76.0	4983	3	US-09-270-767-12587	Sequence 12587, A
C 75	15.2	76.0	17353	3	US-09-949-016-13437	Sequence 13437, A
C 76	15.2	76.0	54463	3	US-09-949-016-14781	Sequence 14781, A
C 77	15.2	76.0	57178	3	US-09-949-016-12838	Sequence 12838, A
C 78	15.2	76.0	57178	3	US-09-949-016-17458	Sequence 17458, A
C 79	15.2	76.0	75929	3	US-09-949-016-15543	Sequence 15543, A
C 80	15.2	76.0	75929	3	US-09-949-016-15544	Sequence 15544, A
C 81	15.2	76.0	98439	3	US-09-949-016-13597	Sequence 13597, A
C 82	15.2	76.0	105050	3	US-09-949-016-15953	Sequence 15953, A
C 83	15.2	76.0	119594	3	US-09-949-016-12080	Sequence 12080, A
C 84	15.2	76.0	119601	3	US-09-949-016-15952	Sequence 15952, A
C 85	15.2	76.0	133642	3	US-09-949-016-12174	Sequence 12174, A
C 86	15.2	76.0	153643	3	US-09-949-016-15635	Sequence 15635, A
C 87	15.2	76.0	455726	3	US-09-949-016-14157	Sequence 14157, A
C 88	15.2	76.0	481115	3	US-09-949-016-11940	Sequence 11940, A
C 89	15	75.0	34	2	US-08-361-337-12	Sequence 12, Appl
C 90	15	75.0	2497	3	US-09-396-149-1	Sequence 1, Appl
C 91	15	75.0	767677	3	US-09-949-016-12147	Sequence 12147, A
C 92	15	75.0	767677	3	US-09-949-016-17361	Sequence 17361, A
C 93	14.8	74.0	577	3	US-09-621-976-1696	Sequence 1696, Ap
C 94	14.8	74.0	751	3	US-09-270-767-8728	Sequence 8728, Ap
C 95	14.8	74.0	751	3	US-09-270-767-24010	Sequence 24010, A
C 96	14.8	74.0	1049	3	US-09-023-655-195	Sequence 195, App
C 97	14.8	74.0	1281	3	US-09-107-532A-3518	Sequence 3518, Ap

c 98	14.8	74.0	1635	3	US-09-722-377-12	Sequence 12, Appl	c 171	14.2	71.0	490	3	US-09-573-080A-400	Sequence 400, App
c 99	14.8	74.0	1888	3	US-09-599-360B-38	Sequence 38, Appl	172	14.2	71.0	601	3	US-09-949-016-29230	Sequence 29230, A
c 100	14.8	74.0	2281	3	US-09-722-377-6	Sequence 1965, A	173	14.2	71.0	601	3	US-09-949-016-29325	Sequence 29325, A
c 101	14.8	74.0	2621	3	US-09-270-767-11965	Sequence 11965, A	174	14.2	71.0	601	3	US-09-949-016-29325	Sequence 29325, A
c 102	14.8	74.0	4105	3	US-09-722-377-10	Sequence 10, Appl	175	14.2	71.0	601	3	US-09-949-016-32797	Sequence 32797, A
c 103	14.8	74.0	5080	3	US-09-976-594-495	Sequence 495, App	176	14.2	71.0	601	3	US-09-949-016-32856	Sequence 32856, A
c 104	14.8	74.0	5493	3	US-09-949-016-619	Sequence 619, App	177	14.2	71.0	601	3	US-09-949-016-50714	Sequence 50714, A
c 105	14.8	74.0	5494	3	US-09-910-864-10	Sequence 10, Appl	178	14.2	71.0	601	3	US-09-949-016-50773	Sequence 50773, A
c 106	14.8	74.0	5494	3	US-09-949-016-1307	Sequence 1307, App	179	14.2	71.0	601	3	US-09-949-016-53652	Sequence 53652, A
c 107	14.8	74.0	5510	2	US-08-483-278-7	Sequence 7, Appl	180	14.2	71.0	601	3	US-09-949-016-55760	Sequence 55760, A
c 108	14.8	74.0	5510	2	US-08-483-278-7	Sequence 7, Appl	181	14.2	71.0	601	3	US-09-949-016-55763	Sequence 55763, A
c 109	14.8	74.0	8346	3	US-09-949-016-14497	Sequence 14497, A	182	14.2	71.0	601	3	US-09-949-016-56416	Sequence 56416, A
c 110	14.8	74.0	13361	3	US-09-949-016-12478	Sequence 12478, A	183	14.2	71.0	601	3	US-09-949-016-56437	Sequence 56437, A
c 111	14.8	74.0	13785	3	US-09-949-016-15631	Sequence 15631, A	184	14.2	71.0	601	3	US-09-949-016-56458	Sequence 56458, A
c 112	14.8	74.0	26769	3	US-09-949-016-14934	Sequence 14934, A	185	14.2	71.0	601	3	US-09-949-016-62909	Sequence 62909, A
c 113	14.8	74.0	55135	3	US-09-949-016-16587	Sequence 16587, A	186	14.2	71.0	601	3	US-09-949-016-74304	Sequence 74304, A
c 114	14.8	74.0	64610	3	US-09-949-016-12214	Sequence 12214, A	187	14.2	71.0	601	3	US-09-949-016-83261	Sequence 83261, A
c 115	14.8	74.0	69874	3	US-09-949-016-12361	Sequence 12361, A	188	14.2	71.0	601	3	US-09-949-016-83262	Sequence 83262, A
c 116	14.8	74.0	69874	3	US-09-949-016-13049	Sequence 13049, A	189	14.2	71.0	601	3	US-09-949-016-83922	Sequence 83922, A
c 117	14.8	74.0	108440	3	US-09-949-016-12065	Sequence 12065, A	190	14.2	71.0	601	3	US-09-949-016-83923	Sequence 83923, A
c 118	14.8	74.0	108441	3	US-09-949-016-14090	Sequence 14090, A	191	14.2	71.0	601	3	US-09-949-016-109648	Sequence 109648, A
c 119	14.8	74.0	194889	3	US-09-949-016-15654	Sequence 15654, A	192	14.2	71.0	601	3	US-09-949-016-109649	Sequence 109649, A
c 120	14.4	72.0	25	3	US-09-396-196G-33476	Sequence 33476, A	193	14.2	71.0	601	3	US-09-949-016-109650	Sequence 109650, A
c 121	14.4	72.0	345	3	US-09-991-789A-214	Sequence 214, App	194	14.2	71.0	601	3	US-09-949-016-121877	Sequence 121877, A
c 122	14.4	72.0	345	3	US-09-062-451-214	Sequence 214, App	195	14.2	71.0	601	3	US-09-949-016-122370	Sequence 122370, A
c 123	14.4	72.0	345	3	US-09-598-326-214	Sequence 214, App	196	14.2	71.0	601	3	US-09-949-016-131409	Sequence 131409, A
c 124	14.4	72.0	345	3	US-09-289-198-214	Sequence 214, App	197	14.2	71.0	601	3	US-09-949-016-156685	Sequence 156685, A
c 125	14.4	72.0	345	3	US-09-429-755-214	Sequence 214, App	198	14.2	71.0	601	3	US-09-949-016-156686	Sequence 156686, A
c 126	14.4	72.0	345	3	US-09-699-295-214	Sequence 214, App	199	14.2	71.0	601	3	US-09-949-016-170866	Sequence 170866, A
c 127	14.4	72.0	345	3	US-09-534-825A-214	Sequence 214, App	200	14.2	71.0	601	3	US-09-949-016-170867	Sequence 170867, A
c 128	14.4	72.0	473	3	US-09-513-999C-26008	Sequence 26008, A	201	14.2	71.0	601	3	US-09-949-016-177100	Sequence 177100, A
c 129	14.4	72.0	515	3	US-09-270-767-10716	Sequence 10716, A	202	14.2	71.0	601	3	US-09-949-016-177101	Sequence 177101, A
c 130	14.4	72.0	548	3	US-09-533-559-224	Sequence 224, App	203	14.2	71.0	601	3	US-09-949-016-177102	Sequence 177102, A
c 131	14.4	72.0	591	3	US-09-270-767-8649	Sequence 8649, App	204	14.2	71.0	601	3	US-09-949-016-187531	Sequence 187531, A
c 132	14.4	72.0	591	3	US-09-270-767-23931	Sequence 23931, A	205	14.2	71.0	601	3	US-09-949-016-187532	Sequence 187532, A
c 133	14.4	72.0	601	3	US-09-949-016-67259	Sequence 67259, A	206	14.2	71.0	601	3	US-09-949-016-187533	Sequence 187533, A
c 134	14.4	72.0	601	3	US-09-949-016-67260	Sequence 67260, A	207	14.2	71.0	601	3	US-09-270-767-12446	Sequence 12446, A
c 135	14.4	72.0	601	3	US-09-949-016-112622	Sequence 112622, A	208	14.2	71.0	893	3	US-09-270-767-12446	Sequence 12446, A
c 136	14.4	72.0	601	3	US-09-949-016-112623	Sequence 112623, A	209	14.2	71.0	936	3	US-09-533-559-1512	Sequence 1512, App
c 137	14.4	72.0	601	3	US-09-949-016-112624	Sequence 112624, A	210	14.2	71.0	936	3	US-09-533-559-1512	Sequence 1512, App
c 138	14.4	72.0	601	3	US-09-949-016-112625	Sequence 112625, A	211	14.2	71.0	1107	3	US-09-509-712B-61	Sequence 61, Appl
c 139	14.4	72.0	601	3	US-09-949-016-112626	Sequence 112626, A	212	14.2	71.0	1107	3	US-09-509-712B-110	Sequence 110, App
c 140	14.4	72.0	601	3	US-09-949-016-143653	Sequence 143653, A	213	14.2	71.0	1186	3	US-09-148-545-58	Sequence 58, Appl
c 141	14.4	72.0	601	3	US-09-949-016-143654	Sequence 143654, A	214	14.2	71.0	1186	3	US-09-148-545-58	Sequence 58, Appl
c 142	14.4	72.0	601	3	US-09-949-016-143655	Sequence 143655, A	215	14.2	71.0	1259	3	US-09-621-011-58	Sequence 58, Appl
c 143	14.4	72.0	601	3	US-09-949-016-143656	Sequence 143656, A	216	14.2	71.0	1381	3	US-09-270-767-31484	Sequence 31484, A
c 144	14.4	72.0	1306	3	US-09-270-767-28611	Sequence 28611, A	217	14.2	71.0	1398	3	US-09-594-506-25	Sequence 25, Appl
c 145	14.4	72.0	1404	3	US-09-902-540-4821	Sequence 4821, App	218	14.2	71.0	1446	3	US-09-533-559-4423	Sequence 4423, App
c 146	14.4	72.0	1452	3	US-09-693-746-23	Sequence 23, Appl	219	14.2	71.0	1488	3	US-09-248-796A-7742	Sequence 7742, App
c 147	14.4	72.0	1595	3	US-09-270-767-12787	Sequence 12787, A	220	14.2	71.0	1607	3	US-09-328-857A-1	Sequence 1, Appli
c 148	14.4	72.0	26659	3	US-09-902-540-12337	Sequence 12337, App	221	14.2	71.0	1720	3	US-09-919-932A-1	Sequence 1, Appli
c 149	14.4	72.0	30444	3	US-09-949-016-14997	Sequence 14997, A	222	14.2	71.0	1792	3	US-09-270-767-15162	Sequence 15162, A
c 150	14.4	72.0	59977	3	US-09-949-016-12259	Sequence 12259, A	223	14.2	71.0	1927	3	US-09-786-240-19	Sequence 19, Appl
c 151	14.4	72.0	59978	3	US-09-949-016-15397	Sequence 15397, A	224	14.2	71.0	2047	3	US-09-202-904A-14	Sequence 14, Appl
c 152	14.4	72.0	60304	3	US-09-949-016-12218	Sequence 12218, A	225	14.2	71.0	2143	3	US-09-919-039-126	Sequence 126, App
c 153	14.4	72.0	60305	3	US-09-949-016-15791	Sequence 15791, A	226	14.2	71.0	2230	3	US-09-919-039-125	Sequence 125, App
c 154	14.4	72.0	67156	3	US-09-949-016-12284	Sequence 12284, A	227	14.2	71.0	2272	2	US-08-726-228-1	Sequence 1, Appli
c 155	14.4	72.0	67157	3	US-09-949-016-16558	Sequence 16558, A	228	14.2	71.0	2272	3	US-08-870-815-1	Sequence 1, Appli
c 156	14.4	72.0	72504	3	US-09-949-016-14855	Sequence 14855, A	229	14.2	71.0	2272	3	US-08-949-004-1	Sequence 51, Appl
c 157	14.4	72.0	100463	3	US-09-949-016-12511	Sequence 12511, A	230	14.2	71.0	2491	3	US-09-533-029-51	Sequence 87, Appl
c 158	14.4	72.0	100468	3	US-09-949-016-13725	Sequence 13725, A	231	14.2	71.0	2498	3	US-09-949-002-87	Sequence 87, Appl
c 159	14.2	71.0	50	3	US-10-131-827-7792	Sequence 7792, App	232	14.2	71.0	2518	3	US-09-949-002-211	Sequence 211, App
c 160	14.2	71.0	158	3	US-09-270-767-2490	Sequence 2490, App	233	14.2	71.0	2622	3	US-10-104-047-1005	Sequence 1005, App
c 161	14.2	71.0	158	3	US-09-270-767-17772	Sequence 17772, A	234	14.2	71.0	2625	3	US-10-070-634-20	Sequence 20, Appl
c 162	14.2	71.0	162	3	US-09-513-999C-8384	Sequence 8384, App	235	14.2	71.0	3122	3	US-09-042-353-152	Sequence 152, App
c 163	14.2	71.0	241	3	US-09-090-672B-27	Sequence 27, Appl	236	14.2	71.0	3122	3	US-08-758-417A-416	Sequence 416, App
c 164	14.2	71.0	241	3	US-09-730-559B-28	Sequence 28, Appl	237	14.2	71.0	3301	2	US-08-447-430A-42	Sequence 42, Appl
c 165	14.2	71.0	270	3	US-09-252-991A-6544	Sequence 6544, App	238	14.2	71.0	3301	2	US-09-342-673-42	Sequence 42, Appl
c 166	14.2	71.0	400	3	US-08-956-171E-970	Sequence 970, App	239	14.2	71.0	3423	2	US-08-447-430A-40	Sequence 40, Appl
c 167	14.2	71.0	400	3	US-08-781-986A-970	Sequence 970, App	240	14.2	71.0	3423	3	US-09-485-737B-86	Sequence 86, Appl
c 168	14.2	71.0	465	3	US-09-248-796A-5956	Sequence 5956, App	241	14.2	71.0	3423	3	US-09-342-673-40	Sequence 40, Appl
c 169	14.2	71.0	468	3	US-09-621-976-11015	Sequence 11015, A	242	14.2	71.0	3423	3	US-10-071-485-86	Sequence 86, Appl
c 170	14.2	71.0	479	3	US-09-533-559-2886	Sequence 2886, App	243	14.2	71.0	3427	3	US-09-023-655-1400	Sequence 1400, App

C 244	14.2	71.0	3427	3	US-09-949-016-828	Sequence 828, App	Sequence 828, App	317	14.2	71.0	4977	2	US-08-451-233-14	Sequence 14, Appl
C 245	14.2	71.0	3474	2	US-08-447-430A-41	Sequence 41, Appl	Sequence 41, Appl	318	14.2	71.0	4977	2	US-08-451-233-17	Sequence 17, Appl
C 246	14.2	71.0	3474	2	US-08-318-837-10	Sequence 10, Appl	Sequence 10, Appl	319	14.2	71.0	4977	2	US-08-450-236-14	Sequence 14, Appl
C 247	14.2	71.0	3474	3	US-08-122-458D-8	Sequence 8, Appl	Sequence 8, Appl	320	14.2	71.0	4977	3	US-08-450-236-17	Sequence 17, Appl
C 248	14.2	71.0	3474	3	US-09-342-673-41	Sequence 41, Appl	Sequence 41, Appl	321	14.2	71.0	4977	3	US-08-235-403-14	Sequence 14, Appl
C 249	14.2	71.0	3618	3	US-09-042-353-224	Sequence 224, App	Sequence 224, App	322	14.2	71.0	4977	3	US-08-235-403-17	Sequence 17, Appl
C 250	14.2	71.0	3618	3	US-08-758-417A-72	Sequence 72, App	Sequence 72, App	323	14.2	71.0	5005	3	US-09-695-437A-60	Sequence 60, Appl
C 251	14.2	71.0	3698	2	US-07-834-539A-49	Sequence 49, Appl	Sequence 49, Appl	324	14.2	71.0	5018	3	US-09-813-718-9	Sequence 9, Appl
C 252	14.2	71.0	3698	2	US-08-800-353-49	Sequence 49, Appl	Sequence 49, Appl	C 325	14.2	71.0	5076	3	US-09-991-258-8	Sequence 8, Appl
C 253	14.2	71.0	3698	6	PCT-US92-06185-49	Sequence 49, Appl	Sequence 49, Appl	C 326	14.2	71.0	5096	3	US-08-106-433A-3	Sequence 3, Appl
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C 261	14.2	71.0	3754	3	US-08-379-611-17	Sequence 17, Appl	Sequence 17, Appl	C 334	14.2	71.0	5110	2	US-08-106-433A-4	Sequence 4, Appl
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C 263	14.2	71.0	3887	3	US-09-976-594-660	Sequence 660, App	Sequence 660, App	C 336	14.2	71.0	5110	2	US-08-106-433A-6	Sequence 6, Appl
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C 266	14.2	71.0	4100	3	US-09-813-718-5	Sequence 5, Appl	Sequence 5, Appl	C 339	14.2	71.0	5110	2	US-08-106-433A-9	Sequence 9, Appl
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C 268	14.2	71.0	4200	2	US-07-841-654B-1	Sequence 1, Appl	Sequence 1, Appl	C 341	14.2	71.0	5110	2	US-08-106-433A-11	Sequence 11, Appl
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C 272	14.2	71.0	4200	6	PCT-US93-01560-1	Sequence 1, Appl	Sequence 1, Appl	C 345	14.2	71.0	5115	3	US-08-106-433A-15	Sequence 15, Appl
C 273	14.2	71.0	4245	2	US-08-929-967-4	Sequence 4, Appl	Sequence 4, Appl	C 346	14.2	71.0	5115	3	US-08-825-852-19	Sequence 19, Appl
C 274	14.2	71.0	4342	3	US-09-943-016-575	Sequence 575, App	Sequence 575, App	C 347	14.2	71.0	5115	3	US-08-052-888-19	Sequence 19, Appl
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C 276	14.2	71.0	4378	3	US-08-586-740A-9	Sequence 9, Appl	Sequence 9, Appl	C 349	14.2	71.0	5115	3	US-09-723-901-19	Sequence 19, Appl
C 277	14.2	71.0	4451	3	US-09-303-064-45	Sequence 45, Appl	Sequence 45, Appl	C 350	14.2	71.0	5115	3	US-09-724-547-19	Sequence 19, Appl
C 278	14.2	71.0	4451	3	US-09-086-503-45	Sequence 45, Appl	Sequence 45, Appl	C 351	14.2	71.0	5115	3	US-09-724-127-19	Sequence 19, Appl
C 279	14.2	71.0	4481	3	US-08-867-611-1	Sequence 1, Appl	Sequence 1, Appl	C 352	14.2	71.0	5115	3	US-09-723-931-19	Sequence 19, Appl
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C 281	14.2	71.0	4481	6	PCT-US92-06965A-6	Sequence 6, Appl	Sequence 6, Appl	C 354	14.2	71.0	5115	3	US-09-724-114-19	Sequence 19, Appl
C 282	14.2	71.0	4584	2	US-08-901-200A-15	Sequence 15, Appl	Sequence 15, Appl	C 355	14.2	71.0	5115	3	US-09-723-912-19	Sequence 19, Appl
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C 310	14.2	71.0	4910	3	US-09-086-503-40	Sequence 40, Appl	Sequence 40, Appl	C 383	14.2	71.0	5248	3	US-08-487-283A-18	Sequence 18, Appl
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C 312	14.2	71.0	4977	2	US-08-450-257-17	Sequence 17, Appl	Sequence 17, Appl	C 385	14.2	71.0	5249	2	US-08-688-649-3	Sequence 3, Appl
C 313	14.2	71.0	4977	2	US-08-450-257-14	Sequence 14, Appl	Sequence 14, Appl	C 386	14.2	71.0	5249	2	US-08-688-649-4	Sequence 4, Appl
C 314	14.2	71.0	4977	2	US-08-450-246-17	Sequence 17, Appl	Sequence 17, Appl	C 387	14.2	71.0	5258	3	US-09-303-064-48	Sequence 48, Appl
C 315	14.2	71.0	4977	2	US-08-450-246-17	Sequence 17, Appl	Sequence 17, Appl	C 388	14.2	71.0	5258	3	US-09-086-503-48	Sequence 48, Appl
C 316	14.2	71.0	4977	2	US-08-450-098-14	Sequence 14, Appl	Sequence 14, Appl	C 389	14.2	71.0	5312	3	US-10-263-103-35	Sequence 35, Appl
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; OTHER INFORMATION: /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at position 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-387-845-5

Query Match      100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      565 AAGGAAACACGGACACCCAA 546

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; Sequence 5, Application US/08778275
; Patent No. 5935819
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a
; TITLE OF INVENTION: bicistronic vector system in mammalian cells
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/778,275
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,845
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
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; NAME/KEY: -
; LOCATION: 1..628
; OTHER INFORMATION: /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
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; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at position 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-867-352-5

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Best Local Similarity 100.0%; Pred. No. 2.7;
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; DATE: 1989
US-08-778-275-5

Query Match      100.0%; Score 20; DB 2; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
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Qy      1 AAGGAAACACGGACACCCAA 20
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; Sequence 5, Application US/08867352
; Patent No. 6060273
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Multicistronic expression units and their use
; NUMBER OF SEQUENCES: 25
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,352
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/387,847
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)
; IMMEDIATE SOURCE:
; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..628
; OTHER INFORMATION: /note= "shown are the first
; OTHER INFORMATION: 628 nt of the 5' non-translated region of
; OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"
; FEATURE:
; NAME/KEY: -
; LOCATION: 610
; OTHER INFORMATION: /note= "non-authentic sequence
; OTHER INFORMATION: due to a base pair substitution from C to G
; OTHER INFORMATION: at Location 610"
; PUBLICATION INFORMATION:
; AUTHORS: Sarnow, P.
; JOURNAL: J. Virol.
; VOLUME: 63
; PAGES: 467-470
; DATE: 1989
US-08-867-352-5

Query Match      100.0%; Score 20; DB 3; Length 628;
Best Local Similarity 100.0%; Pred. No. 2.7;
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## RESULT 4

US-09-116-032-2/c

; Sequence 2, Application US/09116032

; Patent No. 6200576

; GENERAL INFORMATION:

; APPLICANT: HWONG, CHING LONG

; APPLICANT: LO, CHENG-KAI

; APPLICANT: YANG, YING-CHUAN

; APPLICANT: JENG, KING-SONG

; APPLICANT: CHANG, EDWARD L.

; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY

; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND

; FILE REFERENCE: 9751.79US01

; CURRENT APPLICATION NUMBER: US/09/116.032

; CURRENT FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: CHINA 86105814

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 1220

; TYPE: DNA

; ORGANISM: SWINE VESICULAR DISEASE VIRUS

US-09-116-032-2

## Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 1220;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 568 AAGGAAACACGGACACCCAA 549

## RESULT 5

US-09-202-904A-10/c

; Sequence 10, Application US/09202904A

; Patent No. 6395471

; GENERAL INFORMATION:

; APPLICANT: Kang, Sung Key

; APPLICANT: Hahn, Bumsuk

; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing

; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant

; FILE REFERENCE: A32210-PCT-USA 072944.0104

; CURRENT APPLICATION NUMBER: US/09/202,904A

; CURRENT FILING DATE: 2001-01-22

; PRIOR APPLICATION NUMBER: PCT/KR97/00120

; PRIOR FILING DATE: 1997-06-25

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 10

; LENGTH: 2320

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Genetically engineered virus derived from

; OTHER INFORMATION: poliovirus and hepatitis C virus

US-09-202-904A-10

## Query Match

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 565 AAGGAAACACGGACACCCAA 546

## RESULT 6

US-09-116-032-1/c

; Sequence 1, Application US/09116032

; Patent No. 6200576

; GENERAL INFORMATION:

; APPLICANT: HWONG, CHING LONG

; APPLICANT: LO, CHENG-KAI

; APPLICANT: YANG, YING-CHUAN

; APPLICANT: JENG, KING-SONG

; APPLICANT: CHANG, EDWARD L.

; APPLICANT: DEVELOPMENT CENTER FOR BIOTECHNOLOGY

; TITLE OF INVENTION: SWINE VESICULAR DISEASE VIRUS AND MUTANT STRAINS AND

; FILE REFERENCE: 9751.79US01

; CURRENT APPLICATION NUMBER: US/09/116.032

; CURRENT FILING DATE: 1998-07-15

; EARLIER APPLICATION NUMBER: CHINA 86105814

; EARLIER FILING DATE: 1997-05-01

; NUMBER OF SEQ ID NOS: 39

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 1

; LENGTH: 7400

; TYPE: DNA

; ORGANISM: SWINE VESICULAR DISEASE VIRUS

US-09-116-032-1

## Query Match

Best Local Similarity 100.0%; Score 20; DB 3; Length 7400;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 568 AAGGAAACACGGACACCCAA 549

## RESULT 7

US-07-852-260-1/c

; Sequence 1, Application US/07852260

; Patent No. 5525715

; GENERAL INFORMATION:

; APPLICANT: Racaniallo, Vincent

; APPLICANT: Tatem, Joanne M.

; APPLICANT: Weeks-Levy, Carolyn L.

; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM

; TITLE OF INVENTION: CDNA

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper &amp; Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: U.S.A.

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA: US/07/852,260

; APPLICATION NUMBER: 19920619

; FILING DATE: 19920619

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John P.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 977-9550

; TELEFAX: (212) 664-0525

; TELEX: 422523 COOP UI

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7432 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: single

; TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 743..7361  
US-07-852-260-1

Query Match 100.0%; Score 20; DB 2; Length 7432;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 568 AAGGAAACACGGACACCCAA 549

## RESULT 8

US-08-461-503-1/c  
Sequence 1, Application US/08461503  
Patent No. 5834302  
GENERAL INFORMATION:  
APPLICANT: Racaniello, Vincent  
APPLICANT: Tatem, Joanne M.  
APPLICANT: Weeks-Levy, Carolyn L.  
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES  
TITLE OF INVENTION: FROM CDNA  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10112

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/461,503  
FILING DATE: 5-JUN-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 36607-D-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX: 422523 COOP UI

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7432 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 743..7361  
US-08-461-503-1

Query Match 100.0%; Score 20; DB 2; Length 7432;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 568 AAGGAAACACGGACACCCAA 549

## RESULT 9

US-08-465-250-1/c  
Sequence 1, Application US/08465250  
Patent No. 6136570  
GENERAL INFORMATION:  
APPLICANT: Racaniello, Vincent  
APPLICANT: Tatem, Joanne M.  
APPLICANT: Weeks-Levy, Carolyn L.  
TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM  
TITLE OF INVENTION: CDNA  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper & Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release 1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,250  
FILING DATE: 6-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 36607-E-PCT-US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 278-0400  
TELEFAX: (212) 391-0525  
TELEX:

INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7432 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 743..7361  
US-08-465-250-1

Query Match 100.0%; Score 20; DB 3; Length 7432;  
Best Local Similarity 100.0%; Pred. No. 3.5;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 568 AAGGAAACACGGACACCCAA 549

## RESULT 10

US-09-284-349B-1/c  
Sequence 1, Application US/09284349B  
Patent No. 6696289  
GENERAL INFORMATION:  
APPLICANT: Yong Soo, Bae  
APPLICANT: Jung, Hye Rhan  
TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain  
FILE REFERENCE: Docket No. 6696289; 4220-109 US  
CURRENT APPLICATION NUMBER: US/09/284,349B  
CURRENT FILING DATE: 1999-06-04  
PRIOR APPLICATION NUMBER: PCT/KR98/00242  
PRIOR FILING DATE: 1998-07-08

```
; PRIOR APPLICATION NUMBER: KR 97/37812
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 7441
; TYPE: DNA
; ORGANISM: Human poliovirus 1
US-09-284-349B-1

Query Match      100.0%; Score 20; DB 3; Length 7441;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 565 AAGGAAACACGGACACCCAA 546

RESULT 11
US-09-724-678D-11/c
; Sequence 11, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence is Synthesized
; Patent No. 6818397
US-09-724-678D-11

Query Match      100.0%; Score 20; DB 3; Length 28;
Best Local Similarity 95.0%; Pred. No. 4.7;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 24 AAGGAAACACGGACACCCAA 5

RESULT 12
US-09-724-678D-16/c
; Sequence 16, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and Probes Therefor
; FILE REFERENCE: TAI 316
; CURRENT APPLICATION NUMBER: US/09/724,678D
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-09-724-678D-16

Query Match      92.0%; Score 18.4; DB 3; Length 1560;
Best Local Similarity 95.0%; Pred. No. 17;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 570 AAGGAAACACGGACACCCAA 551

RESULT 13
US-09-129-686-20
; Sequence 20, Application US/09129686A
; Patent No. 6264940
; GENERAL INFORMATION:
; APPLICANT: Gromeier PhD, Matthias
; APPLICANT: Wimmer Prof, Eckard
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/09/129,686A
; CURRENT FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Human rhinovirus 2
US-09-129-686-20

Query Match      85.0%; Score 17; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 17 AAGGAAACACGGACACC 33

RESULT 14
US-09-566-581-20
; Sequence 20, Application US/09566581
; Patent No. 6464972
; GENERAL INFORMATION:
; APPLICANT: Matthias Gromeier and Eckard Wimmer
; TITLE OF INVENTION: RECOMBINANT POLIOVIRUS FOR
; TITLE OF INVENTION: THE TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/566,581
; FILING DATE: May 8, 2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/129,686
; FILING DATE: August 5, 1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
```

REFERENCE/DOCKET NUMBER: 3927-4135US1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 758-4800  
TELEFAX: (212) 751-6849  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 33  
TYPE: nucleotides  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Human Rhinovirus  
STRAIN: Type 2  
POSITION IN GENOME:  
CHROMOSOME/SEGMENT: IRES  
US-09-566-581-20

Query Match 85.0%; Score 17; DB 3; Length 33;  
Best Local Similarity 100.0%; Pred. No. 54;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17  
Db 17 AAGGAACACGGACACC 33

RESULT 15  
US-09-061-273-8  
Sequence 8, Application US/09061273  
Patent No. 6258570  
GENERAL INFORMATION:  
APPLICANT: Glustein, Joseph Z.  
APPLICANT: Ehrlich, Garth D.  
APPLICANT: Zhang, Yingze  
TITLE OF INVENTION: PCR Assay For Bacterial and  
TITLE OF INVENTION: Viral Meningitis  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: University of Pittsburgh  
STREET: Office of Technology Transfer  
CITY: Pittsburgh  
STATE: Pennsylvania  
COUNTRY: USA  
ZIP: 15260  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3-1/2" high density diskette  
COMPUTER: IBM PC or compatibles  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/061,273  
FILING DATE: 17-APR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: No. 6258570 applicable  
FILING DATE: No. 6258570 applicable  
ATTORNEY/AGENT INFORMATION:  
NAME: Mary-Elizabeth Buckles  
REGISTRATION NUMBER: 31,907  
REFERENCE/DOCKET NUMBER: 017917/20132  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/414-9267  
TELEFAX: 202/414/9299  
TELEX: 64711  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 39 nucleotides  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: synthetic DNA  
US-09-061-273-8

Query Match 85.0%; Score 17; DB 3; Length 39;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
Db 1 GAAACACGGACACCCAA 17

RESULT 16  
US-08-221-816B-31/c  
Sequence 31, Application US/08221816B  
Patent No. 5738985  
GENERAL INFORMATION:  
APPLICANT: Miles, Vincent J.  
APPLICANT: Mathews, Michael B.  
APPLICANT: Katze, Michael G.  
APPLICANT: Witherell, Gary  
APPLICANT: Watson, Julia C.  
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
TITLE OF INVENTION: OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
US-08-221-816B-31

Query Match 85.0%; Score 17; DB 2; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
Db 568 GAAACACGGACACCCAA 552

RESULT 17  
US-10-112-547-31/c  
Sequence 31, Application US/10112547  
Patent No. 6579674  
GENERAL INFORMATION:  
APPLICANT: Miles, Vincent J.

Mathews, Michael B.  
Katze, Michael G.  
Witherell, Gary  
Watson, Julia C.  
TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/112,547  
FILING DATE: 28-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-112-547-31  
Query Match 85.0%; Score 17; DB 3; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552  
RESULT 18  
US-10-112-241-31/c  
; Sequence 31, Application US/10112241  
; Patent No. 6623961  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/112,241  
FILING DATE: 28-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-112-241-31  
Query Match 85.0%; Score 17; DB 3; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552  
RESULT 19  
US-10-104-611-31/c  
; Sequence 31, Application US/10104611  
; Patent No. 6667152  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION  
NUMBER OF SEQUENCES: 33  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036/2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/104,611  
FILING DATE: 22-Mar-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/221,816B  
FILING DATE: 01-APR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A

REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7960-030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 31:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 627 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: RNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 31:  
US-10-104-611-31

Query Match 85.0%; Score 17; DB 3; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552

RESULT 20  
US-10-109-368-31/c  
; Sequence 31, Application US/10109368  
; Patent No. 677179  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/109,368  
; FILING DATE: 27-Mar-2002  
; CLASSIFICATION: <unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/221,816  
; FILING DATE: 01-APR-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7960-030  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 627 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-10-109-368-31

Query Match 85.0%; Score 17; DB 3; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552

RESULT 21  
US-09-724-380-31/c  
; Sequence 31, Application US/09724380  
; Patent No. 6824976  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.  
; APPLICANT: Mathews, Michael B.  
; APPLICANT: Katze, Michael G.  
; APPLICANT: Witherell, Gary  
; APPLICANT: Watson, Julia C.  
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
; OF VIRAL REPLICATION  
; NUMBER OF SEQUENCES: 33  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036/2711  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/724,380  
; FILING DATE: 01-APR-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/221,816  
; FILING DATE: 01-APR-1994  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; REFERENCE/DOCKET NUMBER: 7960-030  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212) 790-9090  
; TELEFAX: (212) 869-8864  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 31:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 627 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: RNA  
; US-09-724-380-31

Query Match 85.0%; Score 17; DB 3; Length 627;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552

RESULT 22  
US-09-949-016-78843  
; Sequence 78843, Application US/09949016

RESULT 24  
US-09-949-016-14033  
; Sequence 14033, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN K  
; TITLE OF INVENTION: WITH HUMAN DISEAS

RESULT 26  
US-09-949-016-78842  
; Sequence 78842, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:



```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 78842
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-78842

Query Match      82.0%; Score 16.4; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 1.4e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
Db 288 AAGGAAACACGGACCCCAA 307

RESULT 27
US-09-949-016-194126
; Sequence 194126, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194126
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-194126

Query Match      80.0%; Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAAACACGGACACC 17
Db 450 AGGAAACACGGACACC 465

RESULT 28
US-09-949-016-16963/c
; Sequence 16963, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
```

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16963
; LENGTH: 18568
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16963

Query Match      80.0%; Score 16; DB 3; Length 18568;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACAC 16
Db 17024 AAGGAAACACGGACAC 17009

RESULT 29
US-09-949-016-12196/c
; Sequence 12196, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12196
; LENGTH: 137949
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(137949)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12196

Query Match      80.0%; Score 16; DB 3; Length 137949;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAAACACGGACACC 17
Db 90635 AGGAAACACGGACACC 90620

RESULT 30
US-09-949-016-17260/c
; Sequence 17260, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
```

```

, PRIOR APPLICATION NUMBER: 60/241,755
, PRIOR FILING DATE: 2000-10-20
, PRIOR APPLICATION NUMBER: 60/237,768
, PRIOR FILING DATE: 2000-10-03
, PRIOR APPLICATION NUMBER: 60/231,498
, PRIOR FILING DATE: 2000-09-08
, NUMBER OF SEQ ID NOS: 207012
, SOFTWARE: FASTSEQ for Windows Version 4.0
, SEQ ID NO 17260
, LENGTH: 137956
, TYPE: DNA
, ORGANISM: Human
, FEATURE:
, NAME/KEY: misc_feature
, LOCATION: (1)..(137956)
, OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17260

```

```
Query Match      80.0%; Score 16; DB 3; Length 137956;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 2 AGGAACACGGACACC 17  
|||  
db 90635 AGGAACACGGACACC 90620

RESULT 31  
US-09-949-016-56995  
; Sequence 56995, Application US/09949016  
; Patent NO. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 56995  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
; US-09-949-016-56995

```
Query Match          79.0%; Score 15.8; DB 3; Length 601;
Best Local Similarity 89.5%; Pred. No. 2.8e+02;
Matches 17: Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 AAGGAAACACGGACACCCA 19  
|||  
Dp 303 AAGGAAAGAGGGACACCCA 321

RESULT 32  
US-09-134-000C-1077  
; Sequence 1077, Application US/09134000C  
; Patent No. 6617156  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 032796-032  
; CURRENT APPLICATION NUMBER: US/09/134,000C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/055,778

```

; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1077
; LENGTH: 1560
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-1077

```

```
Query Match      79.0%; Score 15.8; DB 3; Length 1560;
Best Local Similarity 89.5%; Pred. No. 3.1e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

Qy 1 AAGGAAACACGGACACCCA 19  
||| ||| ||| ||| ||| ||| ||| |||  
Dy 1194 AAGTAAACACGGACACCCA 1212

RESULT 33  
US-08-743-637B-1  
; Sequence 1, Application US/08743637B  
; Patent No. 5994066

GENERAL INFORMATION:  
 APPLICANT: BERGERON, Michel G.  
 APPLICANT: PICARD, François J.  
 APPLICANT: OUELLETTE, Marc  
 APPLICANT: ROY, Paul H.

Query Match	79.0%	Score 15.8;	DB 2;	Length 1817;
Best Local Similarity	89.5%	Pred. No. 3.1e+02;		
Matches 17: Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;



;; PRIOR FILING DATE: 2000-10-03  
;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13390  
;; LENGTH: 46626  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-13390

Query Match 79.0%; Score 15.8; DB 3; Length 46626;  
Best Local Similarity 89.5%; Pred. No. 4.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 32280 AAGGAACACGGACACCCA 32262

## RESULT 38

US-09-270-767-247/c  
;; Sequence 247, Application US/09270767  
;; Patent No. 6703491  
;; GENERAL INFORMATION:  
;; APPLICANT: Homburger et al.  
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
;; FILE REFERENCE: File Reference: 7326-094  
;; CURRENT APPLICATION NUMBER: US/09/270,767  
;; CURRENT FILING DATE: 1999-03-17  
;; NUMBER OF SEQ ID NOS: 62517  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 247  
;; LENGTH: 2053  
;; TYPE: DNA  
;; ORGANISM: Drosophila melanogaster  
US-09-270-767-247

Query Match 77.0%; Score 15.4; DB 3; Length 2053;  
Best Local Similarity 94.1%; Pred. No. 4.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGACACCCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1036 GGAACACGGACACCCA 1020

## RESULT 39

US-09-270-767-15529/c  
;; Sequence 15529, Application US/09270767  
;; Patent No. 6703491  
;; GENERAL INFORMATION:  
;; APPLICANT: Homburger et al.  
;; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
;; FILE REFERENCE: File Reference: 7326-094  
;; CURRENT APPLICATION NUMBER: US/09/270,767  
;; CURRENT FILING DATE: 1999-03-17  
;; NUMBER OF SEQ ID NOS: 62517  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 15529  
;; LENGTH: 2053  
;; TYPE: DNA  
;; ORGANISM: Drosophila melanogaster  
US-09-270-767-15529

Query Match 77.0%; Score 15.4; DB 3; Length 2053;  
Best Local Similarity 94.1%; Pred. No. 4.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGACACCCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 1036 GGAACACGGACACCCA 1020

## RESULT 40

US-09-999-833A-514/c  
;; Sequence 514, Application US/0999833A  
;; Patent No. 6916648  
;; GENERAL INFORMATION:  
;; APPLICANT: Ashkenazi, Avi  
;; APPLICANT: Baker Kevin P.  
;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan  
;; APPLICANT: Ferrara, Napoleon  
;; APPLICANT: Filvaroff, Ellen  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gao, Wei-Qiang  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
;; APPLICANT: Gurney, Austin L.  
;; APPLICANT: Hillan, Kenneth J.  
;; APPLICANT: Kijavlin, Ivar J.  
;; APPLICANT: Kuo, Sophia S.  
;; APPLICANT: Napier, Mary A.  
;; APPLICANT: Pan, James  
;; APPLICANT: Paoni, Nicholas F.  
;; APPLICANT: Roy, Margaret Ann  
;; APPLICANT: Shelton, David L.  
;; APPLICANT: Stewart, Timothy A.  
;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2630P1C65  
;; CURRENT APPLICATION NUMBER: US/09/999,833A  
;; CURRENT FILING DATE: 2001-10-24  
;; PRIOR APPLICATION NUMBER: 09/918585  
;; PRIOR FILING DATE: 2001-07-30  
;; PRIOR APPLICATION NUMBER: 60/062250  
;; PRIOR FILING DATE: 1997-10-17  
;; PRIOR APPLICATION NUMBER: 60/064249  
;; PRIOR FILING DATE: 1997-11-03  
;; PRIOR APPLICATION NUMBER: 60/065311  
;; PRIOR FILING DATE: 1997-11-13  
;; PRIOR APPLICATION NUMBER: 60/066364  
;; PRIOR FILING DATE: 1997-11-21  
;; PRIOR APPLICATION NUMBER: 60/077450  
;; PRIOR FILING DATE: 1998-03-10  
;; PRIOR APPLICATION NUMBER: 60/077632  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077641  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077649  
;; PRIOR FILING DATE: 1998-03-11  
;; PRIOR APPLICATION NUMBER: 60/077791  
;; PRIOR FILING DATE: 1998-03-12  
;; PRIOR APPLICATION NUMBER: 60/078004  
;; PRIOR FILING DATE: 1998-03-13  
;; PRIOR APPLICATION NUMBER: 60/078886  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078936  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078910  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/078939  
;; PRIOR FILING DATE: 1998-03-20  
;; PRIOR APPLICATION NUMBER: 60/079294  
;; PRIOR FILING DATE: 1998-03-25  
;; PRIOR APPLICATION NUMBER: 60/079656  
;; PRIOR FILING DATE: 1998-03-26  
;; PRIOR APPLICATION NUMBER: 60/079664

; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079689  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079663  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079728  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079786  
; PRIOR FILING DATE: 1998-03-27  
; PRIOR APPLICATION NUMBER: 60/079920  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/079923  
; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080107  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080165  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080327  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080328  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080333  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/080334  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: 60/081070  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081049  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081071  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081195  
; PRIOR FILING DATE: 1998-04-08  
; PRIOR APPLICATION NUMBER: 60/081203  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081229  
; PRIOR FILING DATE: 1998-04-09  
; PRIOR APPLICATION NUMBER: 60/081955  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081817  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081819  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081952  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/081838  
; PRIOR FILING DATE: 1998-04-15  
; PRIOR APPLICATION NUMBER: 60/082568  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082569  
; PRIOR FILING DATE: 1998-04-21  
; PRIOR APPLICATION NUMBER: 60/082704  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082804  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082700  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082797  
; PRIOR FILING DATE: 1998-04-22  
; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
; PRIOR FILING DATE: 1998-04-29

; PRIOR APPLICATION NUMBER: 60/083496  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083499  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 77.08; Score 15.4; DB 3; Length 2690;  
Best Local Similarity 94.1%; Pred. No. 5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 4 GAAACACGGACCCCAA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 169 GAAACACGGACCCCAA 153

RESULT 41  
US-10-020-445A-514/c  
; Sequence 514, Application US/10020445A  
; Patent No. 6962797  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630PIC74  
CURRENT APPLICATION NUMBER: US/10/020,445A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
PRIOR FILING DATE: 1998-03-10  
PRIOR APPLICATION NUMBER: 60/077632  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077641  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077649  
PRIOR FILING DATE: 1998-03-11  
PRIOR APPLICATION NUMBER: 60/077791  
PRIOR FILING DATE: 1998-03-12  
PRIOR APPLICATION NUMBER: 60/078004  
PRIOR FILING DATE: 1998-03-13  
PRIOR APPLICATION NUMBER: 60/078886  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078936  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/078939  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/079294  
PRIOR FILING DATE: 1998-03-25  
PRIOR APPLICATION NUMBER: 60/079656  
PRIOR FILING DATE: 1998-03-26  
PRIOR APPLICATION NUMBER: 60/079664  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079689  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079663  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079728  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079786  
PRIOR FILING DATE: 1998-03-27  
PRIOR APPLICATION NUMBER: 60/079920  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/079923  
PRIOR FILING DATE: 1998-03-30  
PRIOR APPLICATION NUMBER: 60/080105  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080107  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080165  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080194  
PRIOR FILING DATE: 1998-03-31  
PRIOR APPLICATION NUMBER: 60/080327  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080328  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080333  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/080334  
PRIOR FILING DATE: 1998-04-01  
PRIOR APPLICATION NUMBER: 60/081070  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081049  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081071  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081195  
PRIOR FILING DATE: 1998-04-08  
PRIOR APPLICATION NUMBER: 60/081203  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081229  
PRIOR FILING DATE: 1998-04-09  
PRIOR APPLICATION NUMBER: 60/081955  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081817  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081819  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081952  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/081838  
PRIOR FILING DATE: 1998-04-15  
PRIOR APPLICATION NUMBER: 60/082568  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082569  
PRIOR FILING DATE: 1998-04-21  
PRIOR APPLICATION NUMBER: 60/082704  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082804  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082700  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082797  
PRIOR FILING DATE: 1998-04-22  
PRIOR APPLICATION NUMBER: 60/082796  
PRIOR FILING DATE: 1998-04-23  
PRIOR APPLICATION NUMBER: 60/083336  
PRIOR FILING DATE: 1998-04-27  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/083392  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083495  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083496  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083499  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083545  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083554

; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083742  
; PRIOR FILING DATE: 1998-04-30  
; PRIOR APPLICATION NUMBER: 60/084366  
; PRIOR FILING DATE: 1998-05-05  
; PRIOR APPLICATION NUMBER: 60/084414  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084441  
; PRIOR FILING DATE: 1998-05-06  
; PRIOR APPLICATION NUMBER: 60/084637  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084639  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084640  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084598  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084600  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084627  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/084643  
; PRIOR FILING DATE: 1998-05-07  
; PRIOR APPLICATION NUMBER: 60/085339  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085338  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085323  
; PRIOR FILING DATE: 1998-05-13  
; PRIOR APPLICATION NUMBER: 60/085582  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085700  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085689  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085579  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085580  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085573  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085704  
; PRIOR FILING DATE: 1998-05-15  
; PRIOR APPLICATION NUMBER: 60/085697

Query Match 77.0%; Score 15.4; DB 3; Length 2690;  
Best Local Similarity 94.1%; Pred. No. 5e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGACACCCAA 20  
Db 169 GAAACACGACACCCAA 153

RESULT 42  
US-09-949-016-11868/c  
; Sequence 11868, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11868  
; LENGTH: 300598  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(300598)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-11868

Query Match 77.0%; Score 15.4; DB 3; Length 300598;  
Best Local Similarity 94.1%; Pred. No. 7.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACC 17  
Db 105906 AAGGAACACGACACC 105890

RESULT 43  
US-09-949-016-14588/c  
; Sequence 14588, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14588  
; LENGTH: 302604  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)...(302604)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14588

Query Match 77.0%; Score 15.4; DB 3; Length 302604;  
Best Local Similarity 94.1%; Pred. No. 7.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACC 17  
Db 155912 AAGGAACACGACACC 155896

RESULT 44  
US-09-949-016-14589/c  
; Sequence 14589, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016

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; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14589
; LENGTH: 302604
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(302604)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14589

Query Match 77.0%; Score 15.4; DB 3; Length 302604;
Best Local Similarity 94.1%; Pred. No. 7.7e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 155912 AAGGAAACACGGACAC 155896

RESULT 45
US-09-949-016-17119/c
; Sequence 17119, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17119
; LENGTH: 308362
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(308362)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17119

Query Match 77.0%; Score 15.4; DB 3; Length 308362;
Best Local Similarity 94.1%; Pred. No. 7.8e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACC 17
Db 155728 AAGGAAACACGGACAC 155712

RESULT 46
US-09-107-532A-826
; Sequence 826, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 826:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 507 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...507
; SEQUENCE DESCRIPTION: SEQ ID NO: 826:
US-09-107-532A-826

Query Match 76.0%; Score 15.2; DB 3; Length 507;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACCCAA 20
Db 332 AAGGACACACGGAAACGAA 351

RESULT 47
US-09-949-016-26382/c
; Sequence 26382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26382  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-26382

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
|||||  
DB 333 AAGGAAACACACACACAA 314  
|||||

## RESULT 48

US-09-949-016-26383/c  
; Sequence 26383, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26383  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-26383

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
|||||  
DB 594 AAGGAAACACACACACAA 575  
|||||

## RESULT 49

US-09-949-016-58446/c  
; Sequence 58446, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58446  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human

US-09-949-016-58446

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
|||||  
DB 257 AAGGAGACACAGACACCAA 238  
|||||

## RESULT 50

US-09-949-016-58447/c  
; Sequence 58447, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58447  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-58447

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
|||||  
DB 396 AAGGAGACACAGACACCAA 377  
|||||

## RESULT 51

US-09-949-016-58448/c  
; Sequence 58448, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58448  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-58448

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 412 AAGGAGACACAGACACCAA 393

RESULT 52  
US-09-949-016-58449/c  
; Sequence 58449, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58449  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-58449

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 508 AAGGAGACACAGACACCAA 489

RESULT 53  
US-09-949-016-58450/c  
; Sequence 58450, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 58450  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-58450

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 538 AAGGAGACACAGACACCAA 519

RESULT 54  
US-09-949-016-110157  
; Sequence 110157, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110157  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-110157

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 93 AAGGAAACACAGTACCCAA 112

RESULT 55  
US-09-949-016-110158  
; Sequence 110158, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 110158  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-110158

Query Match 76.0%; Score 15.2; DB 3; Length 601;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 258 AAGGAAACACAGTACCCAA 277

RESULT 56  
US-09-949-016-110159  
; Sequence 110159, Application US/09949016  
; Patent No. 6812339

```
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 110159
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-110159

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 536 AGGGAACACGATCACCACAA 555

RESULT 57
US-09-949-016-138287/c
; Sequence 138287, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138287
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-138287

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 333 AAGGAAACACACACACAA 314

RESULT 58
US-09-949-016-138288/c
; Sequence 138288, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
```

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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138288
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-138288

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 594 AAGGAAACACACACACAA 575

RESULT 59
US-09-949-016-149759
; Sequence 149759, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 149759
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-149759

Query Match          76.0%; Score 15.2; DB 3; Length 601;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   |||||
Db 328 AAGGAAACACGTGACACAA 347

RESULT 60
US-09-533-559-6526
; Sequence 6526, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
```

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; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6526
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Aspergillus oryzae
US-09-533-559-6526

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 675;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 370 ACGGAATAAGGACACCCAA 389

RESULT 61
US-09-248-796A-4726/c
; Sequence 4726, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 4726
; LENGTH: 1455
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-4726

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 3; Length 1455;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 287 AACGAATATGGACACCCAA 268

RESULT 62
US-08-631-200-13/c
; Sequence 13, Application US/08631200
; Patent No. 5646040
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/629,553
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MEDIUM TYPE: DNA (genomic)
US-08-631-200-13

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 2; Length 1622;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 63
US-08-829-553-13/c
; Sequence 13, Application US/08829553
; Patent No. 5817762
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/829,553
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; MEDIUM TYPE: DNA (genomic)
US-08-829-553-13
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; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
US-08-829-553-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 64
US-08-922-267A-13/c
; Sequence 13, Application US/08922267A
; Patent No. 5861239
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 82
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/922,267A
; FILING DATE: 2-SEP-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION NUMBER: US 08/829,553
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/631,200
; FILING DATE: 12-APR-1996
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-085
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-922-267A-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 65
US-08-936-707A-13/c
; Sequence 13, Application US/08936707A
; Patent No. 5871931
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,707A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
US-08-936-707A-13

Query Match          76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 1180 AAGGATAGACAGACCCAA 1161

RESULT 66
US-08-936-706A-13/c
; Sequence 13, Application US/08936706A
; Patent No. 5876919
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/936,706A
; FILING DATE: 24-SEP-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-099
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-936-706A-13

Query Match 76.0%; Score 15.2; DB 2; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 67
US-09-248-203-13/c
; Sequence 13, Application US/09248203
; Patent No. 6043346
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/248,203
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/936,707
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-248-203-13/c

Query Match 76.0%; Score 15.2; DB 3; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 68
US-09-406-071-13/c
; Sequence 13, Application US/09406071
; Patent No. 6207386
; GENERAL INFORMATION:
; APPLICANT: Klevn, Patrick W.
; APPLICANT: Moore, Karen J.
; TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/406,071
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/936,707
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7853-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1622 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-09-406-071-13/c

Query Match 76.0%; Score 15.2; DB 3; Length 1622;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 1180 AAGGATAGACAGACACCCAA 1161

RESULT 69
US-09-814-986-13/c
; Sequence 13, Application US/09814986
; Patent No. 6605437
; GENERAL INFORMATION:
```

APPLICANT: Klevyn, Patrick W.  
Moore, Karen J.  
TITLE OF INVENTION: COMPOSITIONS FOR THE TREATMENT AND  
DIAGNOSIS OF BODY WEIGHT DISORDERS, INCLUDING OBESITY  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Pennie & Edmonds LLP  
STREET: 1155 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 10036-2711  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/814,986  
FILING DATE: 22-Mar-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/936,707  
FILING DATE: 24-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Coruzzi, Laura A.  
REGISTRATION NUMBER: 30,742  
REFERENCE/DOCKET NUMBER: 7853-100  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 790-9090  
TELEFAX: (212) 869-9741/8864  
TELEX: 66141 PENNIE  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1622 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 13:  
US-09-814-986-13  
Query Match 76.0%; Score 15.2; DB 3; Length 1622;  
Best Local Similarity 85.0%; Pred. No. 5.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 AAGGAAACACGGACACCCAA 20  
Db 1180 AAGGATAGACAGACACCCAA 1161  
RESULT 70  
US-08-990-379-1/c  
Sequence 1, Application US/08990379  
Patent No. 5998188  
GENERAL INFORMATION:  
APPLICANT: Stork, Philip J  
APPLICANT: Misra-Press, Anita  
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and  
Their Biologically Active Expression Products  
FILE REFERENCE: 4104-000322USA  
CURRENT APPLICATION NUMBER: US/08/990,379  
CURRENT FILING DATE: 1997-12-15  
EARLIER APPLICATION NUMBER: PCT/US96/10402  
EARLIER FILING DATE: 1996-06-14  
EARLIER APPLICATION NUMBER: 60/000,263  
EARLIER FILING DATE: 1995-06-16  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-08-990-379-1  
Query Match 76.0%; Score 15.2; DB 3; Length 1622;  
Best Local Similarity 85.0%; Pred. No. 5.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 AAGGAAACACGGACACCCAA 20  
Db 1180 AAGGATAGACAGACACCCAA 1161  
RESULT 70  
US-08-990-379-1/c  
Sequence 1, Application US/08990379  
Patent No. 5998188  
GENERAL INFORMATION:  
APPLICANT: Stork, Philip J  
APPLICANT: Misra-Press, Anita  
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and  
Their Biologically Active Expression Products  
FILE REFERENCE: 4104-000322USA  
CURRENT APPLICATION NUMBER: US/08/990,379  
CURRENT FILING DATE: 1997-12-15  
EARLIER APPLICATION NUMBER: PCT/US96/10402  
EARLIER FILING DATE: 1996-06-14  
EARLIER APPLICATION NUMBER: 60/000,263  
EARLIER FILING DATE: 1995-06-16  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 1  
TYPE: DNA  
ORGANISM: Rattus norvegicus

US-08-990-379-1  
Query Match 76.0%; Score 15.2; DB 2; Length 1987;  
Best Local Similarity 85.0%; Pred. No. 6.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 AAGGAAACACGGACACCCAA 20  
Db 1826 AAGGAAACACGGACACCCAA 1807  
RESULT 71  
US-08-990-379-2/c  
Sequence 2, Application US/08990379  
Patent No. 5998188  
GENERAL INFORMATION:  
APPLICANT: Stork, Philip J  
APPLICANT: Misra-Press, Anita  
TITLE OF INVENTION: Mitogen Activated Protein Kinase Phosphatase cDNAs and  
Their Biologically Active Expression Products  
FILE REFERENCE: 4104-000322USA  
CURRENT APPLICATION NUMBER: US/08/990,379  
CURRENT FILING DATE: 1997-12-15  
EARLIER APPLICATION NUMBER: PCT/US96/10402  
EARLIER FILING DATE: 1996-06-14  
EARLIER APPLICATION NUMBER: 60/000,263  
EARLIER FILING DATE: 1995-06-16  
NUMBER OF SEQ ID NOS: 19  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
TYPE: DNA  
ORGANISM: Rattus norvegicus  
US-08-990-379-2  
Query Match 76.0%; Score 15.2; DB 2; Length 1993;  
Best Local Similarity 85.0%; Pred. No. 6.1e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 AAGGAAACACGGACACCCAA 20  
Db 1832 AAGGAAACACGGACACCCAA 1813  
RESULT 72  
US-09-555-820A-1  
Sequence 1, Application US/09555820A  
Patent No. 6680429  
GENERAL INFORMATION:  
APPLICANT: Webster, David  
APPLICANT: Burgess, Diane  
TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of  
Starch  
FILE REFERENCE: SVS3801P0302US  
CURRENT APPLICATION NUMBER: US/09/555,820A  
CURRENT FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 21  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 1  
LENGTH: 2391  
TYPE: DNA  
ORGANISM: Pisum sativum  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1274)..(1350)  
OTHER INFORMATION: N=A or C or G or T/U  
US-09-555-820A-1  
Query Match 76.0%; Score 15.2; DB 3; Length 2391;  
Best Local Similarity 85.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Oy 1 AAGGAAACACGGACACCCAA 20  
Db 1832 AAGGAAACACGGACACCCAA 1813

Db 1947 ACGGAGACACGGACACCAAA 1966

## RESULT 73

US-09-555-820A-2  
; Sequence 2, Application US/09555820A  
; Patent No. 6680429  
; GENERAL INFORMATION:  
; APPLICANT: Webster, David  
; APPLICANT: Burgess, Diane  
; TITLE OF INVENTION: A Starchless Variety of Pisum Sativum Having Elevated Levels of Starch  
; FILE REFERENCE: SVS3801P0302US  
; CURRENT APPLICATION NUMBER: US/09/555,820A  
; CURRENT FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 2  
; LENGTH: 2391  
; TYPE: DNA  
; ORGANISM: Pisum sativum  
US-09-555-820A-2

Query Match 76.0%; Score 15.2; DB 3; Length 2391;  
Best Local Similarity 85.0%; Pred. No. 6.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 1947 ACGGAGACACGGACACCAAA 1966

## RESULT 74

US-09-270-767-12587  
; Sequence 12587, Application US/09270767  
; Patent No. 6703491  
; GENERAL INFORMATION:  
; APPLICANT: Homburger et al.  
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
; FILE REFERENCE: File Reference: 7326-094  
; CURRENT APPLICATION NUMBER: US/09/270,767  
; CURRENT FILING DATE: 1999-03-17  
; NUMBER OF SEQ ID NOS: 62517  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 12587  
; LENGTH: 4983  
; TYPE: DNA  
; ORGANISM: Drosophila melanogaster  
US-09-270-767-12587

Query Match 76.0%; Score 15.2; DB 3; Length 4983;  
Best Local Similarity 85.0%; Pred. No. 6.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 1762 AGGGAACACCGAACCCAA 1781

## RESULT 75

US-09-949-016-13437  
; Sequence 13437, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12838

; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13437  
; LENGTH: 17353  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13437

Query Match 76.0%; Score 15.2; DB 3; Length 17353;  
Best Local Similarity 85.0%; Pred. No. 7.6e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 4679 AAGGAGACACGACCAACCA 4698

## RESULT 76

US-09-949-016-14781/c  
; Sequence 14781, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14781  
; LENGTH: 54463  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14781

Query Match 76.0%; Score 15.2; DB 3; Length 54463;  
Best Local Similarity 85.0%; Pred. No. 8.5e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20

Db 14853 AGGGAACACGATCACCCAA 14834

## RESULT 77

US-09-949-016-12838/c  
; Sequence 12838, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: Venter, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12838



```
; LENGTH: 57178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12838

Query Match          76.0%; Score 15.2; DB 3; Length 57178;
Best Local Similarity 85.0%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 9713 AAGGAAACACACATACACAA 9694

RESULT 78
US-09-949-016-17458/c
; Sequence 17458, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17458
; LENGTH: 57178
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17458

Query Match          76.0%; Score 15.2; DB 3; Length 57178;
Best Local Similarity 85.0%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 9713 AAGGAAACACACATACACAA 9694

RESULT 79
US-09-949-016-15543
; Sequence 15543, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15543
; LENGTH: 75929
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)...(75929)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15543

Query Match          76.0%; Score 15.2; DB 3; Length 75929;
Best Local Similarity 85.0%; Pred. No. 8.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 47908 AAGGAAACACAGACACCTA 47927

RESULT 80
US-09-949-016-15544
; Sequence 15544, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15544
; LENGTH: 75929
; TYPE: DNA
; ORGANISM: Human
; NAME/KEY: misc_feature
; LOCATION: (1)...(75929)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15544

Query Match          76.0%; Score 15.2; DB 3; Length 75929;
Best Local Similarity 85.0%; Pred. No. 8.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20
   ||||| ||||| |||||
DB 47908 AAGGAAACACAGACACCTA 47927

RESULT 81
US-09-949-016-13597/c
; Sequence 13597, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13597
; LENGTH: 98439
; TYPE: DNA
```

```
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(98439)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13597

Query Match          76.0%; Score 15.2; DB 3; Length 98439;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      94040 AGGAAACACGGACACCCCA 94021

RESULT 82
US-09-949-016-15953
; Sequence 15953, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15953
; LENGTH: 105050
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15953

Query Match          76.0%; Score 15.2; DB 3; Length 105050;
Best Local Similarity 85.0%; Pred. No. 9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      93225 AAGGACACACGACACACAA 93244

RESULT 83
US-09-949-016-12080/c
; Sequence 12080, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12080
; LENGTH: 119594
; TYPE: DNA
; ORGANISM: Human

US-09-949-016-12080

Query Match          76.0%; Score 15.2; DB 3; Length 119594;
Best Local Similarity 85.0%; Pred. No. 9.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      13996 AAGAAACACTGACACCCAA 13977

RESULT 84
US-09-949-016-15952/c
; Sequence 15952, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15952
; LENGTH: 119601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15952

Query Match          76.0%; Score 15.2; DB 3; Length 119601;
Best Local Similarity 85.0%; Pred. No. 9.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      13996 AAGAAACACTGACACCCAA 13977

RESULT 85
US-09-949-016-12174
; Sequence 12174, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12174
; LENGTH: 153642
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(153642)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12174
```

```
Query Match          76.0%; Score 15.2; DB 3; Length 153642;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 121010 AAGGAAACACACACACACAA 121029

RESULT 86
US-09-949-016-15635
; Sequence 15635, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15635
; LENGTH: 153643
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(153643)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15635

Query Match          76.0%; Score 15.2; DB 3; Length 153643;
Best Local Similarity 85.0%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 121010 AAGGAAACACACACACACAA 121029

RESULT 87
US-09-949-016-14157/c
; Sequence 14157, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14157
; LENGTH: 455726
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
```

```
; LOCATION: (1)....(455726)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14157

Query Match          76.0%; Score 15.2; DB 3; Length 455726;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 416568 AAGGAAACACACACACACAA 416549

RESULT 88
US-09-949-016-11940/c
; Sequence 11940, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11940
; LENGTH: 481115
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)....(481115)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-11940

Query Match          76.0%; Score 15.2; DB 3; Length 481115;
Best Local Similarity 85.0%; Pred. No. 9.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB 393957 AAGGAAACACACACACACAA 393938

RESULT 89
US-08-361-337-12
; Sequence 12, Application US/08361337
; Patent No. 5728519
; GENERAL INFORMATION:
; APPLICANT: Levenbook, Inessa S.
; APPLICANT: Chumakov, Konstantin M.
; APPLICANT: No. 5728519wood, Laurie P.
; APPLICANT: Roninson, Igor
; TITLE OF INVENTION: ASSAY FOR VIRULENT REVERTANTS OF
; ATTENUATED LIVE VACCINES
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NEEDLE & ROSENBERG, P.C.
; STREET: 127 Peachtree Street, N.E.
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/361.337
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Periyman, David G.
; REGISTRATION NUMBER: 33,438
; REFERENCE/DOCKET NUMBER: 1414.634
; TELEPHONE: (404) 688-0770
; TELEFAX: (404) 688-9880
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-361-337-12

Query Match 75.0%; Score 15; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACACGGACACCCAA 20
Db 1 AACACGGACACCCAA 15

RESULT 90
US-09-396-149-1/c
; Sequence 1, Application US/09396149
; Patent No. 6538176
; GENERAL INFORMATION:
; APPLICANT: Mahajan, Pramod B.
; TITLE OF INVENTION: Maize Replication Protein A and Use
; FILE REFERENCE: 5718-59
; CURRENT APPLICATION NUMBER: US/09/396,149
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2497
; TYPE: DNA
; ORGANISM: Zea Mays
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (157)...(2025)
; OTHER INFORMATION: Coding sequence for the Maize RPA Large Subunit
; OTHER INFORMATION: Homologue-1
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Maize RPA Large subunit Homologue-1
US-09-396-149-1

Query Match 75.0%; Score 15; DB 3; Length 2497;
Best Local Similarity 100.0%; Pred. No. 7.7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 AACACGGACACCCAA 20
Db 1769 AACACGGACACCCAA 1755

RESULT 91
US-09-949-016-12147
; Sequence 12147, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12147
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12147

Query Match 75.0%; Score 15; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACA 15
Db 407477 AAGGAACACGGACA 407491

RESULT 92
US-09-949-016-17361
; Sequence 17361, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17361
; LENGTH: 767677
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(767677)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17361

Query Match 75.0%; Score 15; DB 3; Length 767677;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACA 15
Db 407477 AAGGAACACGGACA 407491

RESULT 93
US-09-621-976-1696/c
; Sequence 1696, Application US/09621976
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## RESULT 97

US-09-107-532A-3518  
; Sequence 3518, Application US/09107532A  
; Patent No. 6583275  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
; NUMBER OF SEQUENCES: 7310  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354

COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: PC  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: ASCII

CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,532A  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/085,598  
; FILING DATE: 14 May 1998  
; APPLICATION NUMBER: 60/051571  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-012  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-8277  
; TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 3518:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1281 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Enterococcus faecium  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8) LOCATION 1...1281  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3518:

US-09-107-532A-3518

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12/c

; Sequence 12, Application US/09722377

; Patent No. 6791007

; GENERAL INFORMATION:  
; APPLICANT: Schulze-Lefert, Paul MJ  
; APPLICANT: Panstruga, Ralph  
; TITLE OF INVENTION: Buschges, Rainer  
; TITLE OF INVENTION: Polynucleotide and its use for modulating a defence  
; FILE REFERENCE: 620-58

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

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Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

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US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCC 18

Db 844 AAGGAACACGACACCC 861

US-09-722-377-12

Query Match 74.0%; Score 14.8; DB 3; Length 1281;

Best Local Similarity 88.9%; Pred. No. 9e+02; Mismatches 0; Indels 0; Gaps 0;

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RESULT 100
US-09-722-377-6/c
; Sequence 6, Application US/09722377
; Patent No. 6791007
; GENERAL INFORMATION:
; APPLICANT: Schulze-Lefert, Paul MJ
; APPLICANT: Panstruga, Ralph
; APPLICANT: Buschges, Rainer
; TITLE OF INVENTION: Polynucleotide and its use for modulating a defence
; TITLE OF INVENTION: response in plants
; FILE REFERENCE: 620-58
; CURRENT APPLICATION NUMBER: US/09/722,377
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: PCT/GB97/02046
; PRIOR FILING DATE: 1997-07-29
; PRIOR APPLICATION NUMBER: GB 9615879.5
; PRIOR FILING DATE: 1996-07-29
; PRIOR APPLICATION NUMBER: GB 9622626.1
; PRIOR FILING DATE: 1996-10-30
; PRIOR APPLICATION NUMBER: GB 9704789.8
; PRIOR FILING DATE: 1997-03-07
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 2281
; TYPE: DNA
; ORGANISM: Hordeum vulgare
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (7, 90, 93, 115, 177, 183, 217, 249, 254, 272, 356, 357)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (364, 1017, 1037, 1041, 1458, 1616, 1641, 1861, 1879)
; OTHER INFORMATION: n is a or g or c or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1923, 2050)
; OTHER INFORMATION: n is a or g or c or t
US-09-722-377-6

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Query Match      74.0%; Score 14.8; DB 3; Length 2281;
Best Local Similarity 88.9%; Pred. NO. 9.6e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      1294 AGGAAACACGGACATCCA 1277

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Search completed: March 8, 2006, 21:07:05  
Job time : 91.9223 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:29:05 ; Search time 435.728 Seconds  
(Without alignments)  
105.905 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacaccaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 7673375 seqs, 115364844 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA New:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq.\*
- 2: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq.\*
- 5: /cgn2\_6/ptodata/2/pubpna/US09\_NEW\_PUB.seq.\*
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- 10: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 11: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 12: /cgn2\_6/ptodata/2/pubpna/US11\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/2/pubpna/US60\_NEW\_PUB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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C 1	18.4	92.0	810	12	US-11-155-478A-137
C 2	17	85.0	415	7	US-10-886-517A-21
C 3	17	85.0	627	12	US-11-195-109-31
C 4	17	85.0	681	12	US-11-155-478A-138
C 5	16.8	84.0	585	6	US-09-925-065A-156382
C 6	16.8	84.0	585	6	US-09-925-065A-156383
C 7	16.8	84.0	147700	8	US-10-857-780-3
C 8	16.6	83.0	25	12	US-11-119-231-48
C 9	16.6	83.0	25	12	US-11-119-231-96
C 10	16.4	82.0	201	8	US-10-995-561-41106
C 11	16.4	82.0	201	12	US-11-124-367A-33200
C 12	16.4	82.0	201	12	US-11-124-367A-33200
C 13	16.4	82.0	578	6	US-09-925-065A-139374
C 14	16.4	82.0	778	8	US-10-750-185-62571
C 15	16.4	82.0	778	8	US-10-750-623-62571
C 16	16.4	82.0	42060	12	US-11-124-367A-5040
C 17	16.4	82.0	1195000	8	US-10-995-561-13286
C 18	15.8	79.0	169	6	US-09-925-065A-187976
C 19	15.8	79.0	449	6	US-09-925-065A-527437
C 20	15.8	79.0	449	6	US-09-925-065A-527438
C 21	15.8	79.0	449	6	US-09-925-065A-527438
C 22	15.8	79.0	449	6	US-09-925-065A-527438
C 23	15.8	79.0	449	6	US-09-925-065A-527438
C 24	15.8	79.0	449	6	US-09-925-065A-527438
C 25	15.8	79.0	449	6	US-09-925-065A-527438
C 26	15.8	79.0	449	6	US-09-925-065A-527438
C 27	15.8	79.0	449	6	US-09-925-065A-527438
C 28	15.8	79.0	449	6	US-09-925-065A-527438
C 29	15.8	79.0	449	6	US-09-925-065A-527438
C 30	15.8	79.0	449	6	US-09-925-065A-527438
C 31	15.8	79.0	449	6	US-09-925-065A-527438
C 32	15.8	79.0	449	6	US-09-925-065A-527438
C 33	15.8	79.0	449	6	US-09-925-065A-527438
C 34	15.8	79.0	449	6	US-09-925-065A-527438
C 35	15.8	79.0	449	6	US-09-925-065A-527438
C 36	15.8	79.0	449	6	US-09-925-065A-527438
C 37	15.8	79.0	449	6	US-09-925-065A-527438
C 38	15.8	79.0	449	6	US-09-925-065A-527438
C 39	15.8	79.0	449	6	US-09-925-065A-527438
C 40	15.8	79.0	449	6	US-09-925-065A-527438
C 41	15.8	79.0	449	6	US-09-925-065A-527438
C 42	15.8	79.0	449	6	US-09-925-065A-527438
C 43	15.8	79.0	449	6	US-09-925-065A-527438
C 44	15.8	79.0	449	6	US-09-925-065A-527438
C 45	15.8	79.0	449	6	US-09-925-065A-527438
C 46	15.8	79.0	449	6	US-09-925-065A-527438
C 47	15.8	79.0	449	6	US-09-925-065A-527438
C 48	15.8	79.0	449	6	US-09-925-065A-527438
C 49	15.8	79.0	449	6	US-09-925-065A-527438
C 50	15.8	79.0	449	6	US-09-925-065A-527438
C 51	15.8	79.0	449	6	US-09-925-065A-527438
C 52	15.8	79.0	449	6	US-09-925-065A-527438
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C 99	15.8	79.0	449	6	US-09-925-065A-527438
C 100	15.8	79.0	449	6	US-09-925-065A-527438

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c 94	15.2	76.0	2828	8	US-10-750-623-54418	Sequence 54418, A	167	14.4	72.0	641	6	US-09-925-065A-481968	Sequence 481968,
c 95	15.2	76.0	23367	7	US-10-330-773-916	Sequence 916, App	c 168	14.4	72.0	654	8	US-10-467-657-8509	Sequence 8509, Ap
c 96	15.2	76.0	123331	7	US-10-330-773-829	Sequence 829, App	c 169	14.4	72.0	658	6	US-09-925-065A-313953	Sequence 313953,
c 97	15.2	76.0	161874	12	US-11-121-086-75	Sequence 75, App	c 170	14.4	72.0	664	6	US-09-925-065A-518152	Sequence 518152,
c 98	15.2	76.0	171423	12	US-11-121-086-85	Sequence 85, App	c 171	14.4	72.0	784	6	US-09-925-065A-953534	Sequence 953534,
c 99	15.2	76.0	1691140	12	US-11-091-018-1	Sequence 1, Appli	c 172	14.4	72.0	784	6	US-09-925-065A-953535	Sequence 953535,
c 100	15	75.0	201	8	US-10-995-561-51045	Sequence 51045, A	c 173	14.4	72.0	842	6	US-09-925-065A-57538	Sequence 57538, A
c 101	15	75.0	537	6	US-09-925-065A-366332	Sequence 366332, A	c 174	14.4	72.0	938	8	US-10-750-185-43041	Sequence 43041, A
c 102	15	75.0	50353	8	US-10-995-561-13305	Sequence 13305, A	c 175	14.4	72.0	942	8	US-10-750-623-43041	Sequence 43041, A
c 103	15	75.0	180531	9	US-11-114-798-57	Sequence 57, Appl	c 176	14.4	72.0	1219	8	US-10-750-185-61348	Sequence 61348, A
c 104	14.8	74.0	20	8	US-10-310-914A-1088291	Sequence 1088291, A	c 177	14.4	72.0	1219	8	US-10-750-623-61348	Sequence 61348, A
c 105	14.8	74.0	25	12	US-11-121-849-93014	Sequence 93014, A	c 178	14.4	72.0	2243	6	US-09-925-065A-548770	Sequence 548770, A
c 106	14.8	74.0	201	8	US-10-995-561-35609	Sequence 35609, A	c 179	14.4	72.0	2595	7	US-10-932-182A-1628	Sequence 1628, Ap
c 107	14.8	74.0	201	8	US-10-995-561-69262	Sequence 69262, A	c 180	14.4	72.0	2595	7	US-10-932-182A-1628	Sequence 1628, Ap
c 108	14.8	74.0	323	6	US-09-925-065A-481041	Sequence 481041, A	c 181	14.4	72.0	27553	7	US-10-922-2328-54	Sequence 54, Appl
c 109	14.8	74.0	491	6	US-09-925-065A-523226	Sequence 523226, A	c 182	14.4	72.0	103665	7	US-10-330-773-680	Sequence 680, App
c 110	14.8	74.0	491	6	US-09-925-065A-523227	Sequence 523227, A	c 183	14.4	72.0	127722	7	US-10-330-773-278	Sequence 278, App
c 111	14.8	74.0	491	6	US-09-925-065A-523228	Sequence 523228, A	c 184	14.4	72.0	171423	12	US-11-121-086-85	Sequence 85, Appl
c 112	14.8	74.0	491	6	US-09-925-065A-429072	Sequence 429072, A	c 185	14.4	72.0	181172	12	US-11-121-086-41	Sequence 41, Appl
c 113	14.8	74.0	551	6	US-09-925-065A-183625	Sequence 183625, A	c 186	14.4	72.0	201309	9	US-11-114-798-51	Sequence 51, Appl
c 114	14.8	74.0	575	6	US-09-925-065A-462434	Sequence 462434, A	c 187	14.4	72.0	21	8	US-10-750-185-11072	Sequence 11072, A
c 115	14.8	74.0	599	6	US-09-925-065A-954034	Sequence 954034, A	c 188	14.4	72.0	21	8	US-10-750-623-11072	Sequence 11072, A
c 116	14.8	74.0	603	6	US-09-925-065A-954559	Sequence 954559, A	c 189	14.2	71.0	21	8	US-10-310-914A-892075	Sequence 892075, A
c 117	14.8	74.0	606	6	US-09-925-065A-324037	Sequence 324037, A	c 190	14.2	71.0	21	8	US-10-310-914A-1006288	Sequence 1006288, A
c 118	14.8	74.0	643	6	US-09-925-065A-312506	Sequence 312506, A	c 191	14.2	71.0	25	7	US-10-932-182A-13878	Sequence 13878, A
c 119	14.8	74.0	647	6	US-09-925-065A-453189	Sequence 453189, A	c 192	14.2	71.0	25	7	US-10-932-182A-13878	Sequence 13878, A
c 120	14.8	74.0	647	6	US-09-925-065A-453190	Sequence 453190, A	c 193	14.2	71.0	33	8	US-10-310-914A-891835	Sequence 891835, A
c 121	14.8	74.0	753	8	US-10-750-185-45627	Sequence 45627, A	c 194	14.2	71.0	201	8	US-10-995-561-18661	Sequence 18661, A
c 122	14.8	74.0	753	8	US-10-750-623-45627	Sequence 45627, A	c 195	14.2	71.0	201	8	US-10-995-561-19907	Sequence 19907, A
c 123	14.8	74.0	886	6	US-09-925-065A-804	Sequence 804, App	c 196	14.2	71.0	201	8	US-10-995-561-30110	Sequence 30110, A
c 124	14.8	74.0	1176	8	US-10-750-185-34939	Sequence 34939, A	c 197	14.2	71.0	201	8	US-10-995-561-30127	Sequence 30127, A
c 125	14.8	74.0	1176	8	US-10-750-623-34939	Sequence 34939, A	c 198	14.2	71.0	201	12	US-11-124-368A-18918	Sequence 18918, A
c 126	14.8	74.0	1233	7	US-10-524-972-123	Sequence 123, App	c 199	14.2	71.0	201	12	US-11-124-368A-18919	Sequence 18919, A
c 127	14.8	74.0	1233	8	US-10-524-647-135	Sequence 135, App	c 200	14.2	71.0	201	12	US-11-124-368A-18920	Sequence 18920, A
c 128	14.8	74.0	1343	6	US-09-925-065A-94518	Sequence 94518, A	c 201	14.2	71.0	201	12	US-11-124-368A-18921	Sequence 18921, A
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c 133	14.8	74.0	1888	5	US-09-978-360A-15	Sequence 15, Appl	c 206	14.2	71.0	287	6	US-09-925-065A-471636	Sequence 471636, A
c 134	14.8	74.0	1896	6	US-09-925-065A-704574	Sequence 704574, A	c 207	14.2	71.0	300	6	US-09-925-065A-521676	Sequence 521676, A
c 135	14.8	74.0	2332	9	US-11-096-568A-33708	Sequence 33708, A	c 208	14.2	71.0	323	6	US-09-925-065A-581746	Sequence 581746, A
c 136	14.8	74.0	4090	12	US-11-183-136-37	Sequence 37, Appl	c 209	14.2	71.0	429	6	US-09-925-065A-615108	Sequence 615108, A
c 137	14.8	74.0	5506	8	US-10-821-234-277	Sequence 277, App	c 210	14.2	71.0	429	6	US-09-925-065A-615109	Sequence 615109, A
c 138	14.8	74.0	5510	12	US-11-150-406-1	Sequence 1, Appli	c 211	14.2	71.0	436	6	US-09-925-065A-208786	Sequence 208786, A
c 139	14.8	74.0	13816	8	US-10-995-561-13409	Sequence 13409, A	c 212	14.2	71.0	436	6	US-09-925-065A-208787	Sequence 208787, A
c 140	14.8	74.0	21728	7	US-10-330-773-362	Sequence 362, App	c 213	14.2	71.0	465	6	US-09-925-065A-763835	Sequence 763835, A
c 141	14.8	74.0	142303	12	US-11-121-086-42	Sequence 42, App	c 214	14.2	71.0	469	6	US-09-925-065A-752751	Sequence 752751, A
c 142	14.8	74.0	149382	8	US-10-995-561-13272	Sequence 13272, A	c 215	14.2	71.0	490	6	US-09-925-065A-512113	Sequence 512113, A
c 143	14.8	74.0	149419	12	US-11-112-908-49	Sequence 49, Appl	c 216	14.2	71.0	490	6	US-09-925-065A-512114	Sequence 512114, A
c 144	14.8	74.0	161726	12	US-11-112-908-48	Sequence 48, Appl	c 217	14.2	71.0	490	6	US-09-925-065A-512115	Sequence 512115, A
c 145	14.8	74.0	161726	12	US-11-112-908-52	Sequence 52, Appl	c 218	14.2	71.0	490	6	US-09-925-065A-818203	Sequence 818203, A
c 146	14.8	74.0	166111	12	US-11-112-908-47	Sequence 47, Appl	c 219	14.2	71.0	496	6	US-09-925-065A-342392	Sequence 342392, A
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c 151	14.4	72.0	318	6	US-09-925-065A-150099	Sequence 150099, A	c 224	14.2	71.0	520	6	US-09-925-065A-497349	Sequence 497349, A
c 152	14.4	72.0	452	6	US-09-925-065A-150402	Sequence 150402, A	c 225	14.2	71.0	522	6	US-09-925-065A-325467	Sequence 325467, A
c 153	14.4	72.0	477	6	US-09-925-065A-137786	Sequence 137786, A	c 226	14.2	71.0	522	6	US-09-925-065A-482451	Sequence 482451, A
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c 155	14.4	72.0	477	6	US-09-925-065A-137788	Sequence 137788, A	c 228	14.2	71.0	532	6	US-09-925-065A-235531	Sequence 235531, A
c 156	14.4	72.0	477	6	US-09-925-065A-137789	Sequence 137789, A	c 229	14.2	71.0	532	6	US-09-925-065A-235532	Sequence 235532, A
c 157	14.4	72.0	559	6	US-09-925-065A-583921	Sequence 583921, A	c 230	14.2	71.0	532	6	US-09-925-065A-235533	Sequence 235533, A
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c 159	14.4	72.0	581	6	US-09-925-065A-515041	Sequence 515041, A	c 232	14.2	71.0	533	6	US-09-925-065A-45824	Sequence 45824, A
c 160	14.4	72.0	581	6	US-09-925-065A-515042	Sequence 515042, A	c 233	14.2	71.0	533	6	US-09-925-065A-45825	Sequence 45825, A
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C 241	14.2	71.0	552	6	US-09-925-065A-921929	Sequence 921929,	C 314	14.2	71.0	621	6	US-09-925-065A-597870	Sequence 597870,
C 242	14.2	71.0	552	6	US-09-925-065A-921930	Sequence 921930,	C 315	14.2	71.0	622	6	US-09-925-065A-233258	Sequence 233258,
C 243	14.2	71.0	553	6	US-09-925-065A-11710	Sequence 11710, A	C 316	14.2	71.0	623	6	US-09-925-065A-499562	Sequence 499562,
C 244	14.2	71.0	553	6	US-09-925-065A-143226	Sequence 143226,	C 317	14.2	71.0	623	6	US-09-925-065A-499563	Sequence 499563,
C 245	14.2	71.0	553	6	US-09-925-065A-143227	Sequence 143227,	C 318	14.2	71.0	629	6	US-09-925-065A-4144	Sequence 4144, Ap
C 246	14.2	71.0	554	6	US-09-925-065A-354533	Sequence 354533,	C 319	14.2	71.0	629	6	US-09-925-065A-8386	Sequence 8386, Ap
C 247	14.2	71.0	555	6	US-09-925-065A-249844	Sequence 249844,	C 320	14.2	71.0	629	6	US-09-925-065A-8387	Sequence 8387, Ap
C 248	14.2	71.0	555	7	US-10-932-182A-723	Sequence 723, App	C 321	14.2	71.0	630	6	US-09-925-065A-389147	Sequence 389147,
C 249	14.2	71.0	555	7	US-10-932-182A-723	Sequence 723, App	C 322	14.2	71.0	630	6	US-09-925-065A-696244	Sequence 696244,
C 250	14.2	71.0	557	6	US-09-925-065A-404002	Sequence 404002,	C 323	14.2	71.0	630	6	US-09-925-065A-589336	Sequence 589336,
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C 252	14.2	71.0	559	6	US-09-925-065A-175503	Sequence 175503,	C 325	14.2	71.0	634	6	US-09-925-065A-748571	Sequence 748571,
C 253	14.2	71.0	559	6	US-09-925-065A-175504	Sequence 175504,	C 326	14.2	71.0	636	6	US-09-925-065A-105150	Sequence 105150,
C 254	14.2	71.0	559	6	US-09-925-065A-175505	Sequence 175505,	C 327	14.2	71.0	636	6	US-09-925-065A-105151	Sequence 105151,
C 255	14.2	71.0	561	6	US-09-925-065A-477325	Sequence 477325,	C 328	14.2	71.0	636	6	US-09-925-065A-430366	Sequence 430366,
C 256	14.2	71.0	564	6	US-09-925-065A-619215	Sequence 619215,	C 329	14.2	71.0	636	6	US-09-925-065A-430366	Sequence 430366,
C 257	14.2	71.0	564	6	US-09-925-065A-882569	Sequence 882569,	C 330	14.2	71.0	636	6	US-09-925-065A-445981	Sequence 445981,
C 258	14.2	71.0	566	6	US-09-925-065A-559996	Sequence 559996,	C 331	14.2	71.0	636	6	US-09-925-065A-445982	Sequence 445982,
C 259	14.2	71.0	567	6	US-09-925-065A-236566	Sequence 236566,	C 332	14.2	71.0	636	6	US-09-925-065A-445983	Sequence 445983,
C 260	14.2	71.0	567	6	US-09-925-065A-236567	Sequence 236567,	C 333	14.2	71.0	636	6	US-09-925-065A-799253	Sequence 799253,
C 261	14.2	71.0	569	6	US-09-925-065A-248722	Sequence 248722,	C 334	14.2	71.0	636	6	US-09-925-065A-799254	Sequence 799254,
C 262	14.2	71.0	573	6	US-09-925-065A-713915	Sequence 713915,	C 335	14.2	71.0	636	6	US-09-925-065A-936168	Sequence 936168,
C 263	14.2	71.0	573	6	US-09-925-065A-713916	Sequence 713916,	C 336	14.2	71.0	638	6	US-09-925-065A-807900	Sequence 807900,
C 264	14.2	71.0	573	6	US-09-925-065A-713917	Sequence 713917,	C 337	14.2	71.0	638	6	US-09-925-065A-807901	Sequence 807901,
C 265	14.2	71.0	573	6	US-09-925-065A-713918	Sequence 713918,	C 338	14.2	71.0	640	6	US-09-925-065A-135368	Sequence 135368,
C 266	14.2	71.0	573	6	US-09-925-065A-713919	Sequence 713919,	C 339	14.2	71.0	640	6	US-09-925-065A-135369	Sequence 135369,
C 267	14.2	71.0	576	6	US-09-925-065A-730016	Sequence 730016,	C 340	14.2	71.0	640	6	US-09-925-065A-135370	Sequence 135370,
C 268	14.2	71.0	576	6	US-09-925-065A-356603	Sequence 356603,	C 341	14.2	71.0	643	6	US-09-925-065A-44116	Sequence 44116, A
C 269	14.2	71.0	576	6	US-09-925-065A-744905	Sequence 744905,	C 342	14.2	71.0	643	6	US-09-925-065A-805622	Sequence 805622,
C 270	14.2	71.0	576	6	US-09-925-065A-789822	Sequence 789822,	C 343	14.2	71.0	643	6	US-09-925-065A-805623	Sequence 805623,
C 271	14.2	71.0	577	6	US-09-925-065A-516079	Sequence 516079,	C 344	14.2	71.0	644	6	US-09-925-065A-790768	Sequence 790768,
C 272	14.2	71.0	577	6	US-09-925-065A-516079	Sequence 516079,	C 345	14.2	71.0	644	6	US-09-925-065A-790769	Sequence 790769,
C 273	14.2	71.0	578	6	US-09-925-065A-607936	Sequence 607936,	C 346	14.2	71.0	644	6	US-09-925-065A-151158	Sequence 151158,
C 274	14.2	71.0	581	6	US-09-925-065A-889420	Sequence 889420,	C 347	14.2	71.0	652	6	US-09-925-065A-822532	Sequence 822532,
C 275	14.2	71.0	581	6	US-09-925-065A-889421	Sequence 889421,	C 348	14.2	71.0	652	6	US-09-925-065A-910807	Sequence 910807,
C 276	14.2	71.0	582	6	US-09-925-065A-321250	Sequence 321250,	C 349	14.2	71.0	675	12	US-11-112-908-263	Sequence 263, App
C 277	14.2	71.0	582	6	US-09-925-065A-882978	Sequence 882978,	C 350	14.2	71.0	684	6	US-09-925-065A-852893	Sequence 852893,
C 278	14.2	71.0	582	6	US-09-925-065A-882979	Sequence 882979,	C 351	14.2	71.0	684	6	US-09-925-065A-852894	Sequence 852894,
C 279	14.2	71.0	584	6	US-09-925-065A-235529	Sequence 235529,	C 352	14.2	71.0	684	6	US-09-925-065A-852895	Sequence 852895,
C 280	14.2	71.0	584	6	US-09-925-065A-235530	Sequence 235530,	C 353	14.2	71.0	689	6	US-09-925-065A-60905	Sequence 60905, A
C 281	14.2	71.0	584	6	US-09-925-065A-882609	Sequence 882609,	C 354	14.2	71.0	689	6	US-09-925-065A-60907	Sequence 60907, A
C 282	14.2	71.0	586	6	US-09-925-065A-274346	Sequence 274346,	C 355	14.2	71.0	689	6	US-09-925-065A-60908	Sequence 60908, A
C 283	14.2	71.0	590	6	US-09-925-065A-296988	Sequence 296988,	C 356	14.2	71.0	710	8	US-10-750-185-64550	Sequence 64550, A
C 284	14.2	71.0	590	6	US-09-925-065A-296989	Sequence 296989,	C 357	14.2	71.0	710	8	US-10-750-623-64550	Sequence 64550, A
C 285	14.2	71.0	591	6	US-09-925-065A-830156	Sequence 830156,	C 358	14.2	71.0	737	6	US-09-925-065A-7201	Sequence 7201, Ap
C 286	14.2	71.0	593	6	US-09-925-065A-126190	Sequence 126190,	C 359	14.2	71.0	737	6	US-09-925-065A-756781	Sequence 756781,
C 287	14.2	71.0	593	6	US-09-925-065A-208471	Sequence 208471,	C 360	14.2	71.0	737	6	US-09-925-065A-756782	Sequence 756782,
C 288	14.2	71.0	593	6	US-09-925-065A-899051	Sequence 899051,	C 361	14.2	71.0	738	6	US-09-925-065A-766996	Sequence 766996,
C 289	14.2	71.0	595	6	US-09-925-065A-715182	Sequence 715182,	C 362	14.2	71.0	738	6	US-09-925-065A-766997	Sequence 766997,
C 290	14.2	71.0	596	6	US-09-925-065A-227365	Sequence 227365,	C 363	14.2	71.0	744	6	US-09-925-065A-55140	Sequence 55140, A
C 291	14.2	71.0	597	6	US-09-925-065A-829916	Sequence 829916,	C 364	14.2	71.0	756	7	US-10-932-182A-166571	Sequence 166571,
C 292	14.2	71.0	597	6	US-09-925-065A-829916	Sequence 829916,	C 365	14.2	71.0	756	7	US-10-932-182A-166571	Sequence 166571,
C 293	14.2	71.0	599	6	US-09-925-065A-922050	Sequence 922050,	C 366	14.2	71.0	810	6	US-09-925-065A-945311	Sequence 945311,
C 294	14.2	71.0	600	8	US-10-750-185-799	Sequence 194548,	C 367	14.2	71.0	823	6	US-09-925-065A-6486	Sequence 6486, Ap
C 295	14.2	71.0	600	8	US-10-750-185-799	Sequence 799, App	C 368	14.2	71.0	839	6	US-09-925-065A-82977	Sequence 82977, A
C 296	14.2	71.0	600	8	US-10-750-185-1336	Sequence 1336, Ap	C 369	14.2	71.0	839	6	US-09-925-065A-82978	Sequence 82978, A
C 297	14.2	71.0	600	8	US-10-750-185-19785	Sequence 19785, A	C 370	14.2	71.0	870	8	US-10-750-185-45333	Sequence 45333, A
C 298	14.2	71.0	600	8	US-10-750-623-1336	Sequence 1336, Ap	C 371	14.2	71.0	870	8	US-10-750-623-45333	Sequence 45333, A
C 299	14.2	71.0	600	8	US-10-750-623-1336	Sequence 1336, Ap	C 372	14.2	71.0	1006	6	US-09-925-065A-73399	Sequence 73399, A
C 300	14.2	71.0	604	6	US-09-925-065A-405672	Sequence 405672,	C 373	14.2	71.0	1006	6	US-09-925-065A-73400	Sequence 73400, A
C 301	14.2	71.0	604	6	US-09-925-065A-405673	Sequence 405673,	C 374	14.2	71.0	1007	6	US-09-925-065A-31699	Sequence 31699, A
C 302	14.2	71.0	607	6	US-09-925-065A-852892	Sequence 852892,	C 375	14.2	71.0	1007	6	US-09-925-065A-31699	Sequence 31699, A
C 303	14.2	71.0	610	6	US-09-925-065A-543749	Sequence 543749,	C 376	14.2	71.0	1007	6	US-09-925-065A-31700	Sequence 31700, A
C 304	14.2	71.0	610	6	US-09-925-065A-543750	Sequence 543750,	C 377	14.2	71.0	1007	6	US-09-925-065A-31701	Sequence 31701, A
C 305	14.2	71.0	611	6	US-09-925-065A-249762	Sequence 249762,	C 378	14.2	71.0	1007	6	US-09-925-065A-31702	Sequence 31702, A
C 306	14.2	71.0	611	6	US-09-925-065A-459592	Sequence 459592,	C 379	14.2	71.0	1031	8	US-10-750-185-57459	Sequence 57459, A
C 307	14.2	71.0	613	12	US-11-055-822-207	Sequence 207, App	C 380	14.2	71.0	1031	8	US-10-750-623-57459	Sequence 57459, A
C 308	14.2	71.0	613	12	US-11-055-822-207	Sequence 207, App	C 381	14.2	71.0	1041	8	US-10-689-742-22	Sequence 22, Appl
C 309	14.2	71.0	617	6	US-09-925-065A-107890	Sequence 107890,	C 382	14.2	71.0	1059	8	US-10-750-185-42014	Sequence 42014, A
C 310	14.2	71.0	617	6	US-09-925-065A-443856	Sequence 443856,	C 383	14.2	71.0	1059	8	US-10-750-623-42014	Sequence 42014, A
C 311	14.2	71.0	619	6	US-09-925-065A-243730	Sequence 243730,	C 384	14.2	71.0	1104	6	US-09-925-065A-49527	Sequence 49527, A
C 312	14.2	71.0	620	6	US-09-925-065A-682927	Sequence 682927,	C 385	14.2	71.0	1107	11	US-11-033-764-61	Sequence 61, Appl



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; LOCATION: (1)....(810)
; OTHER INFORMATION: human Enterovirus
; OTHER INFORMATION: strain Coxsackievirus B1
; OTHER INFORMATION: accession number ml6560
US-11-155-478A-137

Query Match          92.0%; Score 18.4; DB 12; Length 810;
Best Local Similarity 95.0%; Pred. No. 14;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
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Db 118 AATGAACACGGACACCCAA 99

RESULT 2
US-10-886-517A-21/c
; Sequence 21, Application US/10886517A
; Publication No. US2006000810A1
; GENERAL INFORMATION:
; APPLICANT: LEE, MING-CHOU
; APPLICANT: KONG, LILLY
; APPLICANT: GROEN, JAN
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING
; TITLE OF INVENTION: RHINOVIRUSES
; FILE REFERENCE: F003-003
; CURRENT APPLICATION NUMBER: US/10/886,517A
; CURRENT FILING DATE: 2004-07-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 415
; TYPE: DNA
; ORGANISM: human rhinovirus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1, 23, 24, 25, 26, 27, 28, 29, 31, 32, 33, 34, 35, 44, 60,
; LOCATION: 61, 135, 136, 137, 138, 139, 167, 203, 224, 225, 231, 232,
; LOCATION: 284, 346, 390
; OTHER INFORMATION: n = A,T,C or G
US-10-886-517A-21

Query Match          85.0%; Score 17; DB 7; Length 415;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
   |||||
Db 415 GAAACACGGACACCCAA 399

RESULT 3
US-11-195-109-31/c
; Sequence 31, Application US/11195109
; Publication No. US20050265975A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; APPLICANT: Mathews, Michael B.
; APPLICANT: Katze, Michael G.
; APPLICANT: Witherell, Gary
; APPLICANT: Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; TITLE OF INVENTION: OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette

Query Match          85.0%; Score 17; DB 12; Length 681;
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; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/11/195,109
; FILING DATE: 01-Aug-2005
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/867,798
; FILING DATE: 14-Jun-2004
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
US-11-195-109-31

Query Match          85.0%; Score 17; DB 12; Length 627;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
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Db 568 GAAACACGGACACCCAA 552

RESULT 4
US-11-155-478A-138/c
; Sequence 138, Application US/11155478A
; Publication No. US20060014140A1
; GENERAL INFORMATION:
; APPLICANT: Boivin, Guy
; APPLICANT: UNIVERSITE LAVAL
; TITLE OF INVENTION: MOLECULES METHODS AND COMPOSITIONS FOR DETECTING AND QUANTIFYING
; TITLE OF INVENTION: RESPIRATORY VIRUSES
; FILE REFERENCE: 6013-148US
; CURRENT APPLICATION NUMBER: US/11/155,478A
; CURRENT FILING DATE: 2005-06-20
; PRIOR APPLICATION NUMBER: CA 2,411,264
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: CA 2,418,004
; PRIOR FILING DATE: 2003-01-24
; PRIOR APPLICATION NUMBER: PCT/CA2003/001994
; PRIOR FILING DATE: 2003-12-19
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 681
; TYPE: DNA
; ORGANISM: human Rhinovirus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1)...(681)
; OTHER INFORMATION: human Rhinovirus
; OTHER INFORMATION: strain 14
; OTHER INFORMATION: accession number k02121
US-11-155-478A-138
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Best Local Similarity 100.0%; Pred. No. 68;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
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Db 92 GAAACACGGACACCCAA 76

## RESULT 5

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US-09-925-065A-156382
; Sequence 156382, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 156382
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-156382

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Query Match      84.0%; Score 16.8; DB 6; Length 585;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AAGGAAACACGGACACCCAA 20  
85 AAGGAAACACGGACACCCAA 104

## RESULT 6

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US-09-925-065A-156383
; Sequence 156383, Application US/09925065A
; Publication No. US20040191048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 156383
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens

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US-09-925-065A-156383

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Query Match      84.0%; Score 16.8; DB 6; Length 585;
Best Local Similarity 90.0%; Pred. No. 83;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Qy 1 AAGGAAACAGGACACCCAA 20  
85 AAGGAAACAGGACACCCAA 104

Db

## RESULT 7

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US-10-857-780-3/c
; Sequence 3, Application US/10857780
; Publication No. US20050272043A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: REYNOLDS, RICHARD HENRY
; APPLICANT: ROYAL-WRIGHTSON, CAROLYN R.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/857,780
; CURRENT FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/723,681
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: 60/490,234
; PRIOR FILING DATE: 2003-07-24
; PRIOR APPLICATION NUMBER: 60/525,239
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 4962
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 147700
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51510)..(51510)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (51526)..(51526)
; OTHER INFORMATION: n is a, c, g, or t
; US-10-857-780-3

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Query Match	84.0%	Score 16.8;	DB 8;	Length 147700;
Best Local Similarity	90.0%;	Pred. No. 1.9e+02;		
Matches 18: Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

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1 AAGGAAACACGGACACCCAA 20  
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Db 50345 ATGGAAACACGGGCACCCAA 50326

## RESULTS

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RESUB. 0
US-11-119-231-48
; Sequence 48, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briesse
; TITLE OF INVENTION: Mass tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 48

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; LENGTH: 25
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS
US-11-119-231-48

Query Match      83.0%; Score 16.6; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAACACGGACGCCCAA 20
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Db 1 GAAACACGGACGCCCAA 17

RESULT 9
US-11-119-231-96
; Sequence 96, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 25
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS
US-11-119-231-96

Query Match      83.0%; Score 16.6; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAACACGGACGCCCAA 20
   |||||:|||||
Db 1 GAAACACGGACGCCCAA 17

RESULT 10
US-10-995-561-41106
; Sequence 41106, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41106
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-41106

Query Match      82.0%; Score 16.4; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACGCCCAA 20
   |||||:|||||
Db 1 AAGGAACACGGACGCCCAA 20

US-11-119-231-96
; Sequence 96, Application US/11119231
; Publication No. US20060003352A1
; GENERAL INFORMATION:
; APPLICANT: Lipkin, W. Ian
; APPLICANT: Jingyue, Ju
; APPLICANT: Thomas, Briese
; TITLE OF INVENTION: Mass Tag PCR For Multiplex Diagnostics
; FILE REFERENCE: 0575/71310-A
; CURRENT APPLICATION NUMBER: US/11/119,231
; CURRENT FILING DATE: 2005-04-28
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 96
; LENGTH: 25
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: REVERSE PRIMER FOR ENTEROVIRUS
US-11-119-231-96

Query Match      83.0%; Score 16.6; DB 12; Length 25;
Best Local Similarity 94.1%; Pred. No. 66;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GAAACACGGACGCCCAA 20
   |||||:|||||
Db 1 GAAACACGGACGCCCAA 17

RESULT 10
US-10-995-561-41106
; Sequence 41106, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 41106
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-41106

Query Match      82.0%; Score 16.4; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACGCCCAA 20
   |||||:|||||
Db 1 AAGGAACACGGACGCCCAA 20

US-11-124-367A-15797/c
; Sequence 15797, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Hongjin Huang
; APPLICANT: Michele Cargill
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15797
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-15797

Query Match      82.0%; Score 16.4; DB 12; Length 201;
Best Local Similarity 94.4%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 AGGAACACGGACGCCCAA 19
   |||||:|||||
Db 185 AGGAACACGGACGCCCAA 168

RESULT 12
US-11-124-367A-33200
; Sequence 33200, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Fibrosis Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
; PRIOR FILING DATE: 2004-08-09
; NUMBER OF SEQ ID NOS: 34460
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33200
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-367A-33200

Query Match      82.0%; Score 16.4; DB 12; Length 201;
Best Local Similarity 85.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACGCCCAA 20
   |||||:|||||
Db 88 AAGGAACACGGACGCCCAA 107
```

RESULT 13  
US-09-925-065A-319374  
; Sequence 319374, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827,135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 319374  
; LENGTH: 578  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-319374

Query Match 82.0%; Score 16.4; DB 6; Length 578;  
Best Local Similarity 94.4%; Pred. No. 1.3e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 3 GGAACACGACACCCAA 20  
|||||  
Db 89 GGAACACGACACCCAA 106

RESULT 14  
US-10-750-185-62571  
; Sequence 62571, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750,185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62571  
; LENGTH: 778  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-750-185-62571

Query Match 82.0%; Score 16.4; DB 8; Length 778;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 AAGAAACACGACACCC 18  
|||||  
Db 300 AAGAAACACGTACACCC 317

RESULT 15  
US-10-750-623-62571  
; Sequence 62571, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 62571  
; LENGTH: 778  
; TYPE: DNA  
; ORGANISM: Bovine 19866881638593  
US-10-750-623-62571

Query Match 82.0%; Score 16.4; DB 8; Length 778;  
Best Local Similarity 94.4%; Pred. No. 1.4e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 1 AAGAAACACGACACCC 18  
|||||  
Db 300 AAGAAACACGTACACCC 317

RESULT 16  
US-11-124-367A-5040/c  
; Sequence 5040, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: CL001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; CURRENT FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5040  
; LENGTH: 42060  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-5040

Query Match 82.0%; Score 16.4; DB 12; Length 42060;  
Best Local Similarity 94.4%; Pred. No. 2.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
  
Qy 2 AGGAAACACGACACCCA 19  
|||||  
Db 28555 AGGAAACACGACACCCA 28538

RESULT 17  
US-10-995-561-13286  
; Sequence 13286, Application US/10995561





; Sequence 287845, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 287845  
; LENGTH: 500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-287845

Query Match 79.0%; Score 15.8; DB 6; Length 500;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 19  
||| ||||| ||||| ||||| |||||  
Db 26 AAGCAACACGTGACACCCA 8

RESULT 22  
US-09-925-065A-216395/c  
; Sequence 216395, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 216395  
; LENGTH: 532  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-216395

Query Match 79.0%; Score 15.8; DB 6; Length 532;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCCA 20  
||| ||||| ||||| ||||| |||||  
Db 299 AGGAACACGACACCCCA 281

RESULT 23  
US-09-925-065A-187867  
; Sequence 187867, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 187867  
; LENGTH: 560  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-187867

Query Match 79.0%; Score 15.8; DB 6; Length 560;  
Best Local Similarity 89.5%; Pred. No. 2.6e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCCA 20  
||| ||||| ||||| ||||| |||||  
Db 273 AGGAACGTGACACCCA 291

RESULT 24  
US-09-925-065A-708503  
; Sequence 708503, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 708503  
; LENGTH: 632  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-708503

Query Match 79.0%; Score 15.8; DB 6; Length 632;  
Best Local Similarity 89.5%; Pred. No. 2.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCA 19

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Db      85 AAGGAAACAGCTCACCCA 103
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RESULT 25
US-09-925-065A-136278
; Sequence 136278, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136278
; LENGTH: 634
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-136278

Query Match          79.0%; Score 15.8; DB 6; Length 634;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 AGGAAACACGGACACCCA 20
    ||| ||| ||| ||| ||| ||| |||
DB  155 AGGAAACACGGACACCCA 173

RESULT 26
US-09-925-065A-879054
; Sequence 879054, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 879054
; LENGTH: 647
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-879054

Query Match          79.0%; Score 15.8; DB 6; Length 647;
Best Local Similarity 89.5%; Pred. No. 2.7e+02;

```

Query Match 79.0%; Score 15.8; DB 6; Length 1463;  
Best Local Similarity 89.5%; Pred. No. 3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19  
Db 246 AAGGAACACGGACACTCA 228

RESULT 29  
US-10-750-185-47447/c  
; Sequence 47447, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-2  
; CURRENT APPLICATION NUMBER: US/10/750.185  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 47447  
; LENGTH: 3908  
; TYPE: DNA  
; ORGANISM: Bovine 19866880584558  
US-10-750-185-47447

Query Match 79.0%; Score 15.8; DB 8; Length 3908;  
Best Local Similarity 89.5%; Pred. No. 3.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19  
Db 2887 AAGGACACGGACACCCA 2869

RESULT 30  
US-10-623-47447/c  
; Sequence 47447, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMI GENOMICS, INC.  
; APPLICANT: DENISE, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750.623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patent in version 3.1  
; SEQ ID NO 47447  
; LENGTH: 3908  
; TYPE: DNA  
; ORGANISM: Bovine 19866880584558  
US-10-750-623-47447

Query Match 79.0%; Score 15.8; DB 8; Length 3908;  
Best Local Similarity 89.5%; Pred. No. 3.5e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AAGGAACACGGACACCCA 19  
Db 2887 AAGGACACGGACACCCA 2869

RESULT 31  
US-10-330-773-896  
; Sequence 896, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 896  
; LENGTH: 98638  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(98638)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-330-773-896

Query Match 79.0%; Score 15.8; DB 7; Length 98638;  
Best Local Similarity 89.5%; Pred. No. 5.5e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCA 19  
Db 59276 AAGGAGTCACGGACACCCA 59294

RESULT 32  
US-10-330-773-365/c  
; Sequence 365, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 365  
; LENGTH: 137454  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-330-773-365

Query Match 79.0%; Score 15.8; DB 7; Length 137454;  
Best Local Similarity 89.5%; Pred. No. 5.7e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAGGAACACGGACACCCA 20  
Db 34447 AGGAAGCCCGACACCCA 34429

RESULT 33  
US-10-330-773-937/c  
; Sequence 937, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris

; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 937  
; LENGTH: 390183  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; NAME/KEY: misc feature  
; LOCATION: (1)...((390183))  
; OTHER INFORMATION: n = A,T,C or G  
US-10-330-773-937

Query Match 79.0%; Score 15.8; DB 7; Length 390183;  
Best Local Similarity 89.5%; Pred. No. 6.4e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20  
Db 228440 AGGAAACCGGACACTCAA 228422

## RESULT 34

US-11-175-859-2211  
; Sequence 2211, Application US/11175859  
; Publication No. US20060024715A1  
; GENERAL INFORMATION:  
; APPLICANT: Affymetrix, Inc.  
; APPLICANT: Liu, Guoying et al.  
; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
; FILE REFERENCE: 3690.1  
; CURRENT APPLICATION NUMBER: US/11/175,859  
; CURRENT FILING DATE: 2005-07-05  
; PRIOR APPLICATION NUMBER: US 60/585,352  
; PRIOR FILING DATE: 2004-07-02  
; NUMBER OF SEQ ID NOS: 116251  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 2211  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: homo sapien  
US-11-175-859-2211

Query Match 77.0%; Score 15.4; DB 12; Length 50;  
Best Local Similarity 94.1%; Pred. No. 2.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCC 18  
Db 33 AGGAAACACGGACACCC 49

## RESULT 35

US-09-925-065A-366331/c  
; Sequence 366331, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 366331  
; LENGTH: 537  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-366331

Query Match 77.0%; Score 15.4; DB 6; Length 537;  
Best Local Similarity 94.1%; Pred. No. 4.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17  
Db 345 AAGGAACACGGACACC 329

## RESULT 36

US-09-925-065A-366333/c  
; Sequence 366333, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 366333  
; LENGTH: 537  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-366333

Query Match 77.0%; Score 15.4; DB 6; Length 537;  
Best Local Similarity 94.1%; Pred. No. 4.1e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17  
Db 345 AAGGAACACGGACACC 329

## RESULT 37

US-09-925-065A-544937/c  
; Sequence 544937, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 544937  
; LENGTH: 620  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-544937

Query Match 77.0%; Score 15.4; DB 6; Length 620;  
Best Local Similarity 94.1%; Pred. No. 4.2e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGACACCCA 19  
Db 190 GGAACACGACACCCA 174

## RESULT 38

US-11-136-527-1862/c  
; Sequence 1862, Application US/11136527  
; Publication No. US20050287570A1  
; GENERAL INFORMATION:  
; APPLICANT: Wyeth  
; APPLICANT: Mounts, William M  
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes  
; FILE REFERENCE: 031898-041000 (AM101086)  
; CURRENT APPLICATION NUMBER: US/11/136,527  
; PRIOR FILING DATE: 2005-05-25  
; PRIOR APPLICATION NUMBER: US 60/574,294  
; PRIOR FILING DATE: 2005-05-26  
; NUMBER OF SEQ ID NOS: 362830  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1862  
; LENGTH: 4562  
; TYPE: DNA  
; ORGANISM: Rattus norvegicus  
US-11-136-527-1862

Query Match 77.0%; Score 15.4; DB 12; Length 4562;  
Best Local Similarity 94.1%; Pred. No. 5.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17  
Db 1532 ATGGAACACGGACACC 1516

## RESULT 39

US-11-124-368A-2902/c  
; Sequence 2902, Application US/11124368A  
; Publication No. US20050287559A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: James J. Devlin  
; APPLICANT: May Luke  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: CL001524  
; CURRENT APPLICATION NUMBER: US/11/124,368A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,845  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/625,936  
; PRIOR FILING DATE: 2004-11-09  
; NUMBER OF SEQ ID NOS: 21112  
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2902  
; LENGTH: 94035  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-368A-2902

Query Match 77.0%; Score 15.4; DB 12; Length 94035;  
Best Local Similarity 94.1%; Pred. No. 8.6e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACC 17  
Db 30098 AAGGAACACGACACC 30082

## RESULT 40

US-11-114-798-49/c  
; Sequence 49, Application US/11114798  
; Publication No. US20060035246A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, RINA  
; APPLICANT: MARQUEZ, ABBEY  
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND  
; FILE REFERENCE: 0618.011.0004  
; CURRENT APPLICATION NUMBER: US/11/114,798  
; CURRENT FILING DATE: 2005-04-26  
; PRIOR APPLICATION NUMBER: 10/173,525  
; PRIOR FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: 09/952,851  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 49  
; LENGTH: 121736  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: nucleotide sequence  
US-11-114-798-49

Query Match 77.0%; Score 15.4; DB 9; Length 121736;  
Best Local Similarity 94.1%; Pred. No. 8.9e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
Db 71690 GAAACACGACACCCAA 71674

## RESULT 41

US-11-114-798-58/c  
; Sequence 58, Application US/11114798  
; Publication No. US20060035246A1  
; GENERAL INFORMATION:  
; APPLICANT: WU, RINA  
; APPLICANT: MARQUEZ, ABBEY  
; TITLE OF INVENTION: CHROMOGENIC IN SITU HYBRIDIZATION METHODS, KITS, AND  
; FILE REFERENCE: 0618.011.0004  
; CURRENT APPLICATION NUMBER: US/11/114,798  
; CURRENT FILING DATE: 2005-04-26  
; PRIOR APPLICATION NUMBER: 10/173,525  
; PRIOR FILING DATE: 2002-06-17  
; PRIOR APPLICATION NUMBER: 09/952,851  
; PRIOR FILING DATE: 2001-09-14  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn Ver. 3.3  
; SEQ ID NO 58  
; LENGTH: 318488  
; TYPE: DNA  
; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: nucleotide sequence  
US-11-114-798-58

Query Match 77.0%; Score 15.4; DB 9; Length 318488;  
Best Local Similarity 94.1%; Pred. No. 9.7e+02;  
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGACGCCAA 20  
|||||  
Db 33125 GAAACACACGCCAA 33109

## RESULT 42

US-10-857-780-1527/c  
; Sequence 1527, Application US/10857780  
; Publication No. US20050272043A1

## GENERAL INFORMATION:

; APPLICANT: ROTH, RICHARD B.  
; APPLICANT: BRAUN, ANDREAS  
; APPLICANT: KAMMERER, STEFAN M.  
; APPLICANT: NELSON, MATTHEW ROBERTS  
; APPLICANT: RENELAND, RIKARD HENRY  
; APPLICANT: HOVAL-WRIGHTSON, CAROLYN R.  
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS  
; FILE OF INVENTION: THEREOF  
; FILE REFERENCE: SEQ-4069-CP  
; CURRENT APPLICATION NUMBER: US/10/857,780  
; CURRENT FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: 10/723,681  
; PRIOR FILING DATE: 2003-11-25  
; PRIOR APPLICATION NUMBER: 60/490,234  
; PRIOR FILING DATE: 2003-07-24  
; PRIOR APPLICATION NUMBER: 60/525,239  
; PRIOR FILING DATE: 2003-11-25  
; NUMBER OF SEQ ID NOS: 4962  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 1527  
; LENGTH: 30  
; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Synthetic primer  
US-10-857-780-1527

Query Match 76.0%; Score 15.2; DB 8; Length 30;  
Best Local Similarity 85.0%; Pred. No. 3.4e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20  
|||||  
Db 23 AAGCAACACCGACATCAA 4

## RESULT 43

US-10-500-831-260  
; Sequence 260, Application US/10500831  
; Publication No. US20050244813A1

## GENERAL INFORMATION:

; APPLICANT: FRANK KARLSEN  
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS B6 mRNA  
; FILE REFERENCE: B0192.70052U800  
; CURRENT APPLICATION NUMBER: US/10/500,831  
; CURRENT FILING DATE: 2004-07-07  
; PRIOR APPLICATION NUMBER: GB 0200258.2  
; PRIOR FILING DATE: 2002-01-07  
; PRIOR APPLICATION NUMBER: GB 0214124.0  
; PRIOR FILING DATE: 2002-06-19  
; NUMBER OF SEQ ID NOS: 387  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 260  
; LENGTH: 55

; TYPE: DNA  
; ORGANISM: Human papillomavirus type 45  
US-10-500-831-260

Query Match 76.0%; Score 15.2; DB 8; Length 55;  
Best Local Similarity 85.0%; Pred. No. 3.7e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20  
|||||  
Db 28 AAGCACCACGACACCAA 47

## RESULT 44

US-10-310-914A-143  
; Sequence 143, Application US/10310914A  
; Publication No. US20060003322A1

## GENERAL INFORMATION:

; APPLICANT: Bentwich, Isaac  
; APPLICANT: Shiler, Kvuzat  
; TITLE OF INVENTION: Bioinformatically detectable group of novel regulatory genes and  
; FILE OF INVENTION: uses thereof  
; FILE REFERENCE: 06087.0200.CPUS01  
; CURRENT APPLICATION NUMBER: US/10/310,914A  
; CURRENT FILING DATE: 2002-12-06  
; NUMBER OF SEQ ID NOS: 1388402  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 143  
; LENGTH: 61  
; TYPE: RNA  
; ORGANISM: Human  
US-10-310-914A-143

Query Match 76.0%; Score 15.2; DB 8; Length 61;  
Best Local Similarity 85.0%; Pred. No. 3.8e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20  
|||||  
Db 26 AAGGAUACACAGACACCUAA 45

## RESULT 45

US-10-775-169-361/c  
; Sequence 361, Application US/10775169  
; Publication No. US20050287532A9

## GENERAL INFORMATION:

; APPLICANT: Wyeth  
; APPLICANT: Burczynski, Michael  
; APPLICANT: Twine, Natalie  
; APPLICANT: Dörner, Andrew  
; APPLICANT: Trepicchio, William  
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo  
; FILE REFERENCE: AM101080 (031896-013000)  
; CURRENT APPLICATION NUMBER: US/10/775,169  
; CURRENT FILING DATE: 2004-02-11  
; NUMBER OF SEQ ID NOS: 5278  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 361  
; LENGTH: 81  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-775-169-361

Query Match 76.0%; Score 15.2; DB 8; Length 81;  
Best Local Similarity 85.0%; Pred. No. 3.9e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCAA 20  
|||||  
Db 66 AAGGAACACGACACTCCAA 47

```
RESULT 46
US-10-995-561-35611/c
; Sequence 35611, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35611
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-35611

Query Match      76.0%; Score 15.2; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      122 AAGGAGACGGACACGCTA 103

RESULT 47
US-10-995-561-69264/c
; Sequence 69264, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995.561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 69264
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-69264

Query Match      76.0%; Score 15.2; DB 8; Length 201;
Best Local Similarity 85.0%; Pred. No. 4.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      122 AAGGAGACGGACACGCTA 103

RESULT 48
US-09-925-065A-102175
; Sequence 102175, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252.147
; PRIOR FILING DATE: 2000-11-20
```

```
; PRIOR APPLICATION NUMBER: US 60/250.092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261.766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289.846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102175
; LENGTH: 440
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-102175

Query Match      76.0%; Score 15.2; DB 6; Length 440;
Best Local Similarity 85.0%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      201 AAGCAATATACAGACCCAA 220

RESULT 49
US-09-925-065A-192787
; Sequence 192787, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252.147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250.092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261.766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289.846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192787
; LENGTH: 542
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192787

Query Match      76.0%; Score 15.2; DB 6; Length 542;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      406 AAGGAAACACGGACACTGAA 425

RESULT 50
US-09-925-065A-20386
; Sequence 20386, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925.065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243.096
```



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; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20386
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-20386

Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
DB 130 AAGGAAACACGGACCTAA 149

RESULT 51
US-09-925-065A-482407
; Sequence 482407, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482407
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-482407

Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
DB 136 AAGGAAACACTGTCCACCAA 155

RESULT 52
US-09-925-065A-482408
; Sequence 482408, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
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; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 482408
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-482408

Query Match          76.0%; Score 15.2; DB 6; Length 550;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
DB 136 AAGGAAACACTGTCCACCAA 155

RESULT 53
US-09-925-065A-138729
; Sequence 138729, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138729
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-138729

Query Match          76.0%; Score 15.2; DB 6; Length 560;
Best Local Similarity 85.0%; Pred. No. 5.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACCCCAA 20
DB 487 AAGGAAACACTGTCCACCAA 506

RESULT 54
US-09-925-065A-99970/c
; Sequence 99970, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 99970  
; LENGTH: 580  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-99970

Query Match 76.0%; Score 15.2; DB 6; Length 580;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 256 AAGGAAACACGGACACCCAA 237

## RESULT 55

US-09-925-065A-412774  
; Sequence 412774, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 412774  
; LENGTH: 580  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-412774

Query Match 76.0%; Score 15.2; DB 6; Length 580;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 11 AAGGAAACACACACACAA 30

## RESULT 56

US-09-925-065A-794043/c  
; Sequence 794043, Application US/09925065A

; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 794043  
; LENGTH: 585  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-794043

Query Match 76.0%; Score 15.2; DB 6; Length 585;  
Best Local Similarity 85.0%; Pred. No. 5.2e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 221 AAGGAGACGGACACCCGAA 202

## RESULT 57

US-09-925-065A-436621  
; Sequence 436621, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 436621  
; LENGTH: 597  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-436621

Query Match 76.0%; Score 15.2; DB 6; Length 597;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 564 AAGGAAACACGGACACCCCA 583

RESULT 58  
US-09-925-065A-436622  
; Sequence 436622, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 436622  
; LENGTH: 597  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-436622

Query Match 76.0%; Score 15.2; DB 6; Length 597;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 564 AAGGAAACACGACACCCAA 583

RESULT 59  
US-09-925-065A-919663  
; Sequence 919663, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 919663  
; LENGTH: 614  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-919663

Query Match 76.0%; Score 15.2; DB 6; Length 614;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||

Db 574 ATGGAACACGACACCCAA 593  
RESULT 60  
US-09-925-065A-919664  
; Sequence 919664, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 919664  
; LENGTH: 614  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-919664

Query Match 76.0%; Score 15.2; DB 6; Length 614;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||||  
Db 574 ATGGAACACGACACCCAA 593

RESULT 61  
US-09-925-065A-692481  
; Sequence 692481, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692481  
; LENGTH: 623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-692481

Query Match 76.0%; Score 15.2; DB 6; Length 623;  
Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 423 AAGGAACACATACACAA 442

RESULT 62  
 US-09-925-065A-820980  
 ; Sequence 820980, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US 09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 820980  
 ; LENGTH: 625  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-820980

Query Match 76.0%; Score 15.2; DB 6; Length 625;  
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 300 AAGGAACACGGACACAA 319

RESULT 63  
 US-09-925-065A-783213/c  
 ; Sequence 783213, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US 09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 783213  
 ; LENGTH: 633  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-783213

Query Match 76.0%; Score 15.2; DB 6; Length 633;  
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 365 AAGGAACACGGACACAA 346

RESULT 64  
 US-09-925-065A-214200/c  
 ; Sequence 214200, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US 09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 214200  
 ; LENGTH: 650  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-065A-214200

Query Match 76.0%; Score 15.2; DB 6; Length 650;  
 Best Local Similarity 85.0%; Pred. No. 5.3e+02;  
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 641 AAGGAACACGGACACAA 622

RESULT 65  
 US-09-925-065A-529196  
 ; Sequence 529196, Application US/09925065A  
 ; Publication No. US20040181048A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Wang, David G.  
 ; TITLE OF INVENTION: Identification and Mapping of Single  
 ; Nucleotide Polymorphisms in the Human Genome  
 ; FILE REFERENCE: 108827.135  
 ; CURRENT APPLICATION NUMBER: US 09/925,065A  
 ; PRIOR FILING DATE: 2001-08-08  
 ; PRIOR APPLICATION NUMBER: US 60/243,096  
 ; PRIOR FILING DATE: 2000-10-24  
 ; PRIOR APPLICATION NUMBER: US 60/252,147  
 ; PRIOR FILING DATE: 2000-11-20  
 ; PRIOR APPLICATION NUMBER: US 60/250,092  
 ; PRIOR FILING DATE: 2000-11-30  
 ; PRIOR APPLICATION NUMBER: US 60/261,766  
 ; PRIOR FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US 60/289,846  
 ; PRIOR FILING DATE: 2001-05-09  
 ; NUMBER OF SEQ ID NOS: 957086  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 529196  
 ; LENGTH: 654  
 ; TYPE: DNA

```
; ORGANISM: Homo sapiens
; US-09-925-065A-529196

Query Match      76.0%; Score 15.2; DB 6; Length 654;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    ||||| ||||| ||||| ||||| |||||
Db 133 AAGGAGACACGGAAACTCAA 152

RESULT 66
US-09-925-065A-529197
; Sequence 529197, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 529197
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-529197

Query Match      76.0%; Score 15.2; DB 6; Length 654;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    ||||| ||||| ||||| ||||| |||||
Db 133 AAGGAGACACGGAAACTCAA 152

RESULT 67
US-09-925-065A-192788
; Sequence 192788, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192788
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192788

Query Match      76.0%; Score 15.2; DB 6; Length 674;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    ||||| ||||| ||||| ||||| |||||
Db 186 AAGGAAACACGGACACTGAA 205

RESULT 68
US-09-925-065A-192789
; Sequence 192789, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192789
; LENGTH: 674
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192789

Query Match      76.0%; Score 15.2; DB 6; Length 674;
Best Local Similarity 85.0%; Pred. No. 5.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    ||||| ||||| ||||| ||||| |||||
Db 186 AAGGAAACACGGACACTGAA 205

RESULT 69
US-09-925-065A-6885
; Sequence 6885, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6885
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-6885
```

```
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6885
; LENGTH: 766
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-6885

Query Match          76.0%; Score 15.2; DB 6; Length 766;
Best Local Similarity 85.0%; Pred. No. 5.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 222 AAGGAACACTCACCCAA 241

RESULT 70
US-10-750-185-27789/c
; Sequence 27789, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27789
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866881436091
US-10-750-185-27789

Query Match          76.0%; Score 15.2; DB 8; Length 877;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 258 AAGGAACAGTTACCCAA 239

RESULT 71
US-10-750-623-27789/c
; Sequence 27789, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 27789
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866881436091
US-10-750-185-27789

Query Match          76.0%; Score 15.2; DB 8; Length 877;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 258 AAGGAACAGTTACCCAA 239

RESULT 72
US-10-750-185-61482/c
; Sequence 61482, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-185-61482

Query Match          76.0%; Score 15.2; DB 8; Length 878;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 658 AGGAGACACGAGCTCCAA 639

RESULT 73
US-10-750-623-61482/c
; Sequence 61482, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-185-61482
```

```
; SEQ ID NO 27789
; LENGTH: 877
; TYPE: DNA
; ORGANISM: Bovine 19866881436091
US-10-750-623-27789

Query Match          76.0%; Score 15.2; DB 8; Length 877;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 258 AAGGAACAGTTACCCAA 239

RESULT 72
US-10-750-185-61482/c
; Sequence 61482, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-185-61482

Query Match          76.0%; Score 15.2; DB 8; Length 878;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
   ||||| ||||| ||||| |||||
Db 658 AGGAGACACGAGCTCCAA 639

RESULT 73
US-10-750-623-61482/c
; Sequence 61482, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 61482
; LENGTH: 878
; TYPE: DNA
; ORGANISM: Bovine 19866880980307
US-10-750-185-61482
```

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; ORGANISM: Bovine 19866880980307
US-10-750-623-61482

Query Match          76.0%; Score 15.2; DB 8; Length 878;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 658 AGGGAGACACGCGACTCCCAA 639

RESULT 74
US-09-925-065A-710787/c
; Sequence 710787, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710787
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710787

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 229 AAGGACACACACACCCAA 210

RESULT 75
US-09-925-065A-710788/c
; Sequence 710788, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710788
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710788

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 229 AAGGACACACACACCCAA 210

RESULT 76
US-09-925-065A-710789/c
; Sequence 710789, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 710789
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-710789

Query Match          76.0%; Score 15.2; DB 6; Length 925;
Best Local Similarity 85.0%; Pred. No. 5.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 229 AAGGACACACACACCCAA 210

RESULT 77
US-09-925-065A-717601/c
; Sequence 717601, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717601
; LENGTH: 925
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717601
```

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; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717601
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717601

Query Match          76.0%; Score 15.2; DB 6; Length 1125;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 619 AAGGAAACATTACACCAA 600

RESULT 78
US-09-925-065A-717602/c
; Sequence 717602, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 717602
; LENGTH: 1125
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-717602

Query Match          76.0%; Score 15.2; DB 6; Length 1125;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 619 AAGGAAACATTACACCAA 600

RESULT 79
US-10-750-185-59220/c
; Sequence 59220, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
```

```
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59220
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Bovine 19866881082830
US-10-750-185-59220

Query Match          76.0%; Score 15.2; DB 8; Length 1139;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 966 AAGGAAACAGACACACAA 947

RESULT 80
US-10-750-623-59220/c
; Sequence 59220, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59220
; LENGTH: 1139
; TYPE: DNA
; ORGANISM: Bovine 19866881082830
US-10-750-623-59220

Query Match          76.0%; Score 15.2; DB 8; Length 1139;
Best Local Similarity 85.0%; Pred. No. 5.8e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 966 AAGGAAACAGACACACAA 947

RESULT 81
US-10-932-182A-76110
; Sequence 76110, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 76110
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
```



```
US-10-932-182A-76110
Query Match      76.0%; Score 15.2; DB 7; Length 1371;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 154 AATGAATACGGACACCTAA 173

RESULT 82
US-10-932-182A-76110
; Sequence 76110, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORTIHA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 76110
; LENGTH: 1371
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-76110

Query Match      76.0%; Score 15.2; DB 7; Length 1371;
Best Local Similarity 85.0%; Pred. No. 5.9e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 154 AATGAATACGGACACCTAA 173

RESULT 83
US-10-185-25747
; Sequence 25747, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25747
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Bovine 19866880936728
US-10-185-25747

Query Match      76.0%; Score 15.2; DB 8; Length 1619;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 1497 AAGGAAACACGGACACCCAA 1478

RESULT 84
US-10-750-623-25747
; Sequence 25747, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 25747
; LENGTH: 1619
; TYPE: DNA
; ORGANISM: Bovine 19866880936728
US-10-750-623-25747

Query Match      76.0%; Score 15.2; DB 8; Length 1619;
Best Local Similarity 85.0%; Pred. No. 6.1e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 702 AAGAAACTCTGACACCCAA 721

RESULT 85
US-10-185-33198/C
; Sequence 33198, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 33198
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Bovine 19866880641575
US-10-185-33198

Query Match      76.0%; Score 15.2; DB 8; Length 1816;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 1497 AAGGAAACACGGACACCCAA 1478
```

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RESULT 86
US-10-750-623-33198/c
; Sequence 33198, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33198
; LENGTH: 1816
; TYPE: DNA
; ORGANISM: Bovine 19866880641575
US-10-750-623-33198

Query Match      76.0%; Score 15.2; DB 8; Length 1816;
Best Local Similarity 85.0%; Pred. No. 6.2e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCAA 20
      ||||| ||||| ||||| |||||
Db      1497 AAGGAAACACGACACCCAA 1478

RESULT 87
US-10-750-185-31642
; Sequence 31642, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31642
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-185-31642

Query Match      76.0%; Score 15.2; DB 8; Length 2168;
Best Local Similarity 85.0%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCAA 20
      ||||| ||||| ||||| |||||
Db      265 AAGGAAACACGACACCCAA 284

RESULT 88
US-10-750-623-31642
; Sequence 31642, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31642
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-623-31642

Query Match      76.0%; Score 15.2; DB 8; Length 2168;
Best Local Similarity 85.0%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCAA 20
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Db      265 AAGGAAACACGACACCCAA 284
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; Sequence 31642, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31642
; LENGTH: 2168
; TYPE: DNA
; ORGANISM: Bovine 19866880775685
US-10-750-623-31642

Query Match      76.0%; Score 15.2; DB 8; Length 2168;
Best Local Similarity 85.0%; Pred. No. 6.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCAA 20
      ||||| ||||| ||||| |||||
Db      265 AAGGAAACACGACACCCAA 284

RESULT 89
US-10-932-182A-1309/c
; Sequence 1309, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1309
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1309

Query Match      76.0%; Score 15.2; DB 7; Length 2406;
Best Local Similarity 85.0%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGACACCCAA 20
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Db      892 AAGGAAACCGGACCCAA 873

RESULT 90
US-10-932-182A-1309/c
; Sequence 1309, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
```

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; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1309
; LENGTH: 2406
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-1309

Query Match          76.0%; Score 15.2; DB 7; Length 2406;
Best Local Similarity 85.0%; Pred. No. 6.4e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 892 AAGGAAACCGGACCCAA 873

RESULT 91
US-09-925-065A-697075/c
; Sequence 697075, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697075
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697075

Query Match          76.0%; Score 15.2; DB 6; Length 2590;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 2581 AAGGAAACACGACATTCAA 2562

RESULT 92
US-09-925-065A-697076/c
; Sequence 697076, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 697076
; LENGTH: 2590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-697076

Query Match          76.0%; Score 15.2; DB 6; Length 2590;
Best Local Similarity 85.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 2581 AAGGAAACACGACATTCAA 2562

RESULT 93
US-10-750-185-54418/c
; Sequence 54418, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54418
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-54418

Query Match          76.0%; Score 15.2; DB 8; Length 2828;
Best Local Similarity 85.0%; Pred. No. 6.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 245 AAGGAAACATGCGACCCAA 226

RESULT 94
US-10-750-623-54418/c
; Sequence 54418, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
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; FILE REFERENCE: MM11100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54418
; LENGTH: 2828
; TYPE: DNA
; ORGANISM: Bovine 1986880791558
US-10-750-623-54418

Query Match      76.0%; Score 15.2; DB 8; Length 2828;
Best Local Similarity 85.0%; Pred. No. 6.e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 245 AAGGAACACTGCCACCAA 226

RESULT 95
US-10-330-773-916/c
; Sequence 916, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 916
; LENGTH: 23367
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23367)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-916

Query Match      76.0%; Score 15.2; DB 7; Length 23367;
Best Local Similarity 85.0%; Pred. No. 9.e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 12303 AAGGAACACGGACAGACAA 12284

RESULT 96
US-10-330-773-829/c
; Sequence 829, Application US/10330773
; Publication No. US20060040262A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001300
; CURRENT APPLICATION NUMBER: US/10/330,773
; CURRENT FILING DATE: 2002-12-27
; NUMBER OF SEQ ID NOS: 981
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 829
; LENGTH: 123331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature

; LOCATION: (1)...(123331)
; OTHER INFORMATION: n = A,T,C or G
US-10-330-773-829

Query Match      76.0%; Score 15.2; DB 7; Length 123331;
Best Local Similarity 85.0%; Pred. No. 1.1.e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 32548 AAGGAATATGGACACCAA 32529

RESULT 97
US-11-121-086-75
; Sequence 75, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 75
; LENGTH: 161874
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-75

Query Match      76.0%; Score 15.2; DB 12; Length 161874;
Best Local Similarity 85.0%; Pred. No. 1.1.e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 51954 AAGGAACACGTCACAGCAA 51973

RESULT 98
US-11-121-086-85
; Sequence 85, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 85
; LENGTH: 171423
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-85

Query Match      76.0%; Score 15.2; DB 12; Length 171423;
Best Local Similarity 85.0%; Pred. No. 1.1.e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 36823 AAGGAACACTGCAGACAA 36842
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Search completed: March 9, 2006, 01:19:05  
Job time : 448.728 secs

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RESULT 99
US-11-091-018-1/c
; Sequence 1, Application US/11091018
; Publication No. US20050287551A1
; GENERAL INFORMATION:
; APPLICANT: Greta Sottir, Solveig
; APPLICANT: Thorleifsson, Gudmar
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: SUSCEPTIBILITY GENE FOR HUMAN STROKE;
; FILE REFERENCE: 2345.2010-016
; CURRENT APPLICATION NUMBER: US/11/091,018
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: PCT/US03/29906
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 10/255,120
; PRIOR FILING DATE: 2002-09-25
; PRIOR APPLICATION NUMBER: 10/419,723
; PRIOR FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: 10/650,120
; PRIOR FILING DATE: 2003-08-27
; PRIOR APPLICATION NUMBER: 10/067,514
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 09/811,352
; PRIOR FILING DATE: 2001-03-19
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1691140
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; LOCATION: (1)...(1691140)
; OTHER INFORMATION: n=A,T,C or G
US-11-091-018-1

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Query Match 76.0%; Score 15.2; DB 12; Length 1691140;
Best Local Similarity 85.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20
Db 1440757 AAGGAACACCCACCCCAA 1440738

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RESULT 100
US-10-995-561-51045/c
; Sequence 51045, Application US/10995561
; Publication No. US20050272054A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51045
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-995-561-51045

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Query Match 75.0%; Score 15; DB 8; Length 201;
Best Local Similarity 88.2%; Pred. No. 5.6e+02;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 GAAACACGACCCCAA 20
Db 108 GAAACACCCACCCCAA 92

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
285.056 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacacccaa 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications NA Main.\*

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq.\*
- 2: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq.\*
- 6: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq.\*
- 7: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq.\*
- 8: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq.\*
- 9: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq.\*
- 10: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	20	100.0	20	9	US-10-829-474-2
2	20	100.0	21	9	US-10-829-474-25
3	20	100.0	21	9	US-10-829-474-26
4	20	100.0	26	9	US-10-829-474-27
5	20	100.0	107	9	US-10-760-048-53
6	20	100.0	110	9	US-10-760-048-52
7	20	100.0	126	9	US-10-760-048-18
8	20	100.0	236	9	US-10-760-048-55
9	20	100.0	237	9	US-10-760-048-21
10	20	100.0	237	9	US-10-760-048-44
11	20	100.0	237	9	US-10-760-048-45
12	20	100.0	237	9	US-10-760-048-56
13	20	100.0	237	9	US-10-760-048-57
14	20	100.0	237	9	US-10-760-048-59
15	20	100.0	237	9	US-10-760-048-60
16	20	100.0	237	9	US-10-760-048-63
17	20	100.0	237	9	US-10-760-048-64
18	20	100.0	237	9	US-10-760-048-66
19	20	100.0	238	9	US-10-760-048-15
20	20	100.0	238	9	US-10-760-048-30
21	20	100.0	238	9	US-10-760-048-31
22	20	100.0	238	9	US-10-760-048-33
23	20	100.0	238	9	US-10-760-048-33

c 24	20	100.0	238	9	US-10-760-048-38	Sequence 38, Appl
c 25	20	100.0	238	9	US-10-760-048-42	Sequence 42, Appl
c 26	20	100.0	238	9	US-10-760-048-43	Sequence 43, Appl
c 27	20	100.0	238	9	US-10-760-048-46	Sequence 46, Appl
c 28	20	100.0	238	9	US-10-760-048-47	Sequence 47, Appl
c 29	20	100.0	238	9	US-10-760-048-48	Sequence 48, Appl
c 30	20	100.0	238	9	US-10-760-048-58	Sequence 58, Appl
c 31	20	100.0	238	9	US-10-760-048-61	Sequence 61, Appl
c 32	20	100.0	238	9	US-10-760-048-65	Sequence 65, Appl
c 33	20	100.0	709	9	US-10-614-283-1	Sequence 1, Appl
c 34	20	100.0	743	8	US-10-839-729-21	Sequence 21, Appl
c 35	20	100.0	745	8	US-10-489-136-10	Sequence 10, Appl
c 36	20	100.0	2076	3	US-09-884-586A-3	Sequence 3, Appl
c 37	20	100.0	10448	6	US-10-408-456-4	Sequence 4, Appl
c 38	20	100.0	11058	6	US-10-408-456-5	Sequence 5, Appl
c 39	20	100.0	11622	6	US-10-408-456-34	Sequence 34, Appl
c 40	20	100.0	11622	8	US-10-873-573-7	Sequence 7, Appl
c 41	19.6	100.0	62	6	US-10-366-823-5	Sequence 5, Appl
c 42	19.2	100.0	53	6	US-10-408-519-3	Sequence 3, Appl
c 43	19	95.0	19	9	US-10-829-474-21	Sequence 21, Appl
c 44	19	95.0	19	9	US-10-829-474-22	Sequence 22, Appl
c 45	19	95.0	238	9	US-10-760-048-34	Sequence 34, Appl
c 46	19	95.0	238	9	US-10-760-048-35	Sequence 35, Appl
c 47	19	95.0	238	9	US-10-760-048-36	Sequence 36, Appl
c 48	19	95.0	238	9	US-10-760-048-62	Sequence 62, Appl
c 49	18.4	92.0	521	7	US-10-332-123-53	Sequence 53, Appl
c 50	18.4	92.0	235	9	US-10-760-048-41	Sequence 41, Appl
c 51	18.4	92.0	236	9	US-10-760-048-37	Sequence 37, Appl
c 52	18.4	92.0	237	9	US-10-760-048-16	Sequence 16, Appl
c 53	18.4	92.0	237	9	US-10-760-048-52	Sequence 52, Appl
c 54	18.4	92.0	238	9	US-10-760-048-14	Sequence 14, Appl
c 55	18.4	92.0	238	9	US-10-760-048-19	Sequence 19, Appl
c 56	18.4	92.0	238	9	US-10-760-048-23	Sequence 23, Appl
c 57	18.4	92.0	238	9	US-10-760-048-25	Sequence 25, Appl
c 58	18.4	92.0	238	9	US-10-760-048-26	Sequence 26, Appl
c 59	18.4	92.0	238	9	US-10-760-048-27	Sequence 27, Appl
c 60	18.4	92.0	238	9	US-10-760-048-28	Sequence 28, Appl
c 61	18.4	92.0	238	9	US-10-760-048-29	Sequence 29, Appl
c 62	18.4	92.0	520	7	US-10-332-123-54	Sequence 54, Appl
c 63	18.4	92.0	7399	6	US-10-136-819-7	Sequence 7, Appl
c 64	18	90.0	18	9	US-10-829-474-17	Sequence 17, Appl
c 65	18	90.0	18	9	US-10-829-474-18	Sequence 18, Appl
c 66	18	90.0	18	9	US-10-829-474-20	Sequence 20, Appl
c 67	18	90.0	225734	7	US-10-322-696-13	Sequence 13, Appl
c 68	17.8	89.0	40	9	US-10-760-048-10	Sequence 10, Appl
c 69	17	85.0	17	9	US-10-829-474-23	Sequence 23, Appl
c 70	17	85.0	17	9	US-10-829-474-24	Sequence 24, Appl
c 71	17	85.0	20	8	US-10-938-005-4	Sequence 4, Appl
c 72	17	85.0	21	6	US-10-179-082A-3	Sequence 3, Appl
c 73	17	85.0	21	8	US-10-938-005-3	Sequence 3, Appl
c 74	17	85.0	33	6	US-10-175-247-20	Sequence 20, Appl
c 75	17	85.0	40	9	US-10-760-048-9	Sequence 9, Appl
c 76	17	85.0	92	8	US-10-938-005-9	Sequence 9, Appl
c 77	17	85.0	117	9	US-10-760-048-39	Sequence 39, Appl
c 78	17	85.0	117	9	US-10-760-048-40	Sequence 40, Appl
c 79	17	85.0	627	5	US-10-104-611-31	Sequence 31, Appl
c 80	17	85.0	627	5	US-10-112-547-31	Sequence 31, Appl
c 81	17	85.0	627	5	US-10-112-241-31	Sequence 31, Appl
c 82	17	85.0	627	6	US-10-109-368-31	Sequence 31, Appl
c 83	17	85.0	627	8	US-10-867-798-31	Sequence 31, Appl
c 84	16.8	84.0	230	8	US-10-425-115-173501	Sequence 173501, Appl
c 85	16.8	84.0	238	9	US-10-760-048-22	Sequence 22, Appl
c 86	16.8	84.0	238	9	US-10-760-048-24	Sequence 24, Appl
c 87	16.8	84.0	238	9	US-10-760-048-24	Sequence 24, Appl
c 88	16.8	84.0	370	9	US-10-950-009-1102	Sequence 1102, Appl
c 89	16.8	84.0	585	4	US-09-925-065A-156382	Sequence 156382, Appl
c 90	16.8	84.0	585	4	US-09-925-065A-156383	Sequence 156383, Appl
c 91	16.8	84.0	660	9	US-10-760-048-67	Sequence 67, Appl
c 92	16.8	84.0	906	8	US-10-363-345A-23361	Sequence 23361, A
c 93	16.8	84.0	906	8	US-10-363-345A-23362	Sequence 23362, A
c 94	16.8	84.0	906	9	US-10-363-483A-23361	Sequence 23361, A
c 95	16.8	84.0	906	9	US-10-363-483A-23362	Sequence 23362, A
c 96	16.8	84.0	147300	9	US-10-723-681-3	Sequence 3, Appl

97	16.4	82.0	578	4	US-09-925-065A-319374	Sequence 319374,	c 170	15.4	77.0	2690	3	US-09-978-192A-514	Sequence 514, App
c 98	16.4	82.0	47493	7	US-10-052-482-55	Sequence 55, Appl	c 171	15.4	77.0	2690	3	US-09-999-832A-514	Sequence 514, App
99	16	80.0	16	9	US-10-829-474-19	Sequence 19, Appl	c 172	15.4	77.0	2690	3	US-09-978-189-514	Sequence 514, App
100	16	80.0	484	8	US-10-425-115-83354	Sequence 83354, A	c 173	15.4	77.0	2690	3	US-09-978-608A-514	Sequence 514, App
c 101	15.8	79.0	169	4	US-09-925-065A-187976	Sequence 187976,	c 174	15.4	77.0	2690	3	US-09-978-581A-514	Sequence 514, App
c 102	15.8	79.0	201	8	US-10-719-993-25361	Sequence 25361, A	c 175	15.4	77.0	2690	3	US-09-978-191A-514	Sequence 514, App
c 103	15.8	79.0	201	8	US-10-719-993-40170	Sequence 40170, A	c 176	15.4	77.0	2690	3	US-09-978-403A-514	Sequence 514, App
c 104	15.8	79.0	212	7	US-10-437-963-46575	Sequence 46575, A	c 177	15.4	77.0	2690	3	US-09-978-564A-514	Sequence 514, App
c 105	15.8	79.0	357	8	US-10-425-115-50529	Sequence 50529, A	c 178	15.4	77.0	2690	3	US-09-999-833A-514	Sequence 514, App
c 106	15.8	79.0	377	7	US-10-424-599-63366	Sequence 63366, A	c 179	15.4	77.0	2690	3	US-09-981-915A-514	Sequence 514, App
c 107	15.8	79.0	385	7	US-10-437-963-71490	Sequence 71490, A	c 180	15.4	77.0	2690	3	US-09-978-824-514	Sequence 514, App
c 108	15.8	79.0	385	8	US-10-425-115-108968	Sequence 108968,	c 181	15.4	77.0	2690	3	US-09-918-585A-514	Sequence 514, App
c 109	15.8	79.0	449	4	US-09-925-065A-527437	Sequence 527437,	c 182	15.4	77.0	2690	3	US-09-999-834A-514	Sequence 514, App
c 110	15.8	79.0	449	4	US-09-925-065A-527438	Sequence 527438,	c 183	15.4	77.0	2690	3	US-09-978-423A-514	Sequence 514, App
c 111	15.8	79.0	470	9	US-10-972-079-92721	Sequence 92721, A	c 184	15.4	77.0	2690	3	US-09-978-193A-514	Sequence 514, App
c 112	15.8	79.0	500	4	US-09-925-065A-287845	Sequence 287845,	c 185	15.4	77.0	2690	3	US-09-999-830A-514	Sequence 514, App
c 113	15.8	79.0	532	4	US-09-925-065A-216395	Sequence 216395,	c 186	15.4	77.0	2690	3	US-09-978-757A-514	Sequence 514, App
c 114	15.8	79.0	532	6	US-10-029-386-10669	Sequence 10669, A	c 187	15.4	77.0	2690	3	US-09-978-187B-514	Sequence 514, App
c 115	15.8	79.0	560	4	US-09-925-065A-187867	Sequence 187867,	c 188	15.4	77.0	2690	3	US-09-978-643A-514	Sequence 514, App
c 116	15.8	79.0	595	5	US-10-027-632-285012	Sequence 285012,	c 189	15.4	77.0	2690	3	US-09-978-375A-514	Sequence 514, App
c 117	15.8	79.0	595	6	US-10-027-632-285012	Sequence 285012,	c 190	15.4	77.0	2690	3	US-09-978-298A-514	Sequence 514, App
c 118	15.8	79.0	612	5	US-10-027-632-230060	Sequence 230060,	c 191	15.4	77.0	2690	3	US-09-978-188A-514	Sequence 514, App
c 119	15.8	79.0	612	6	US-10-027-632-230060	Sequence 230060,	c 192	15.4	77.0	2690	3	US-09-978-681A-514	Sequence 514, App
c 120	15.8	79.0	632	4	US-09-925-065A-708503	Sequence 708503,	c 193	15.4	77.0	2690	3	US-09-978-194A-514	Sequence 514, App
c 121	15.8	79.0	634	4	US-09-925-065A-136278	Sequence 136278,	c 194	15.4	77.0	2690	3	US-09-999-829A-514	Sequence 514, App
c 122	15.8	79.0	647	4	US-09-925-065A-879054	Sequence 879054,	c 195	15.4	77.0	2690	3	US-09-978-299A-514	Sequence 514, App
c 123	15.8	79.0	660	3	US-09-778-320-224	Sequence 224, App	c 196	15.4	77.0	2690	3	US-09-978-544A-514	Sequence 514, App
c 124	15.8	79.0	660	3	US-09-910-689-224	Sequence 224, App	c 197	15.4	77.0	2690	3	US-09-978-665A-514	Sequence 514, App
c 125	15.8	79.0	660	5	US-10-010-742-224	Sequence 224, App	c 198	15.4	77.0	2690	3	US-09-978-802A-514	Sequence 514, App
c 126	15.8	79.0	660	7	US-10-714-389-224	Sequence 224, App	c 199	15.4	77.0	2690	3	US-09-999-831A-514	Sequence 514, App
c 127	15.8	79.0	660	7	US-10-717-296-224	Sequence 224, App	c 200	15.4	77.0	2690	3	US-09-978-824-514	Sequence 514, App
c 128	15.8	79.0	807	7	US-10-424-599-94135	Sequence 94135, A	c 201	15.4	77.0	2690	5	US-10-052-586-35	Sequence 35, Appl
c 129	15.8	79.0	963	4	US-09-925-065A-722637	Sequence 722637,	c 202	15.4	77.0	2690	5	US-10-174-590-35	Sequence 35, Appl
c 130	15.8	79.0	1013	7	US-10-437-963-38704	Sequence 38704, A	c 203	15.4	77.0	2690	5	US-10-176-758-35	Sequence 35, Appl
c 131	15.8	79.0	1463	4	US-09-925-065A-659377	Sequence 659377, A	c 204	15.4	77.0	2690	5	US-10-175-737-35	Sequence 35, Appl
c 132	15.8	79.0	1616	7	US-10-437-963-986627	Sequence 986627, A	c 205	15.4	77.0	2690	5	US-10-174-581-35	Sequence 35, Appl
c 133	15.8	79.0	1817	3	US-09-452-599-1	Sequence 1, Appl	c 206	15.4	77.0	2690	5	US-10-176-483-35	Sequence 35, Appl
c 134	15.8	79.0	1817	6	US-10-121-120-1	Sequence 1, Appl	c 207	15.4	77.0	2690	5	US-10-176-749-35	Sequence 35, Appl
c 135	15.8	79.0	1817	8	US-10-121-120-1	Sequence 1, Appl	c 208	15.4	77.0	2690	5	US-10-176-914-35	Sequence 35, Appl
c 136	15.8	79.0	1936	8	US-10-739-930-4243	Sequence 4243, Ap	c 209	15.4	77.0	2690	5	US-10-176-915-35	Sequence 35, Appl
c 137	15.8	79.0	2328	7	US-10-437-963-48056	Sequence 48056, A	c 210	15.4	77.0	2690	5	US-10-173-706-35	Sequence 35, Appl
c 138	15.8	79.0	2364	10	US-11-097-143-42710	Sequence 42710, A	c 211	15.4	77.0	2690	5	US-10-175-738-35	Sequence 35, Appl
c 139	15.8	79.0	4670	10	US-11-097-143-42709	Sequence 42709, A	c 212	15.4	77.0	2690	5	US-10-175-752-35	Sequence 35, Appl
c 140	15.8	79.0	4951	3	US-09-070-927A-261	Sequence 261, App	c 213	15.4	77.0	2690	5	US-10-176-482-35	Sequence 35, Appl
c 141	15.8	79.0	12590	8	US-10-719-993-6975	Sequence 6975, Ap	c 214	15.4	77.0	2690	5	US-10-176-757-35	Sequence 35, Appl
c 142	15.8	79.0	70780	8	US-10-719-993-6819	Sequence 6819, Ap	c 215	15.4	77.0	2690	5	US-10-176-913-35	Sequence 35, Appl
c 143	15.8	79.0	175590	3	US-09-911-077A-13	Sequence 13, Appl	c 216	15.4	77.0	2690	5	US-10-180-552-35	Sequence 35, Appl
c 144	15.8	79.0	204621	5	US-10-724-806-13	Sequence 80613, A	c 217	15.4	77.0	2690	5	US-10-180-557-35	Sequence 35, Appl
c 145	15.8	79.0	204621	5	US-10-087-192-958	Sequence 958, App	c 218	15.4	77.0	2690	5	US-10-173-700-35	Sequence 35, Appl
c 146	15.8	79.0	290367	8	US-10-719-993-6887	Sequence 6887, Ap	c 219	15.4	77.0	2690	5	US-10-174-572-35	Sequence 35, Appl
c 147	15.8	79.0	374849	8	US-10-087-192-1627	Sequence 1627, Ap	c 220	15.4	77.0	2690	5	US-10-174-579-35	Sequence 35, Appl
c 148	15.4	77.0	236	9	US-10-760-048-49	Sequence 49, Appl	c 221	15.4	77.0	2690	5	US-10-174-582-35	Sequence 35, Appl
c 149	15.4	77.0	236	9	US-10-760-048-50	Sequence 50, Appl	c 222	15.4	77.0	2690	5	US-10-174-588-35	Sequence 35, Appl
c 150	15.4	77.0	236	9	US-10-760-048-51	Sequence 51, Appl	c 223	15.4	77.0	2690	5	US-10-175-739-35	Sequence 35, Appl
c 151	15.4	77.0	355	7	US-10-424-599-70907	Sequence 70907, A	c 224	15.4	77.0	2690	5	US-10-175-740-35	Sequence 35, Appl
c 152	15.4	77.0	372	7	US-10-424-599-124060	Sequence 124060,	c 225	15.4	77.0	2690	5	US-10-175-743-35	Sequence 35, Appl
c 153	15.4	77.0	478	8	US-10-425-115-5826	Sequence 5826, Ap	c 226	15.4	77.0	2690	5	US-10-176-488-35	Sequence 35, Appl
c 154	15.4	77.0	525	7	US-09-332-123-55	Sequence 55, Appl	c 227	15.4	77.0	2690	5	US-10-176-492-35	Sequence 35, Appl
c 155	15.4	77.0	537	4	US-09-925-065A-366331	Sequence 366331,	c 228	15.4	77.0	2690	5	US-10-176-747-35	Sequence 35, Appl
c 156	15.4	77.0	537	4	US-09-925-065A-366333	Sequence 366333,	c 229	15.4	77.0	2690	5	US-10-176-750-35	Sequence 35, Appl
c 157	15.4	77.0	620	4	US-09-925-065A-544937	Sequence 544937,	c 230	15.4	77.0	2690	5	US-10-176-985-35	Sequence 35, Appl
c 158	15.4	77.0	632	8	US-10-363-345A-27321	Sequence 27321, A	c 231	15.4	77.0	2690	5	US-10-176-987-35	Sequence 35, Appl
c 159	15.4	77.0	632	8	US-10-363-345A-27322	Sequence 27322, A	c 232	15.4	77.0	2690	5	US-10-176-992-35	Sequence 35, Appl
c 160	15.4	77.0	632	9	US-10-363-483A-27321	Sequence 27321, A	c 233	15.4	77.0	2690	5	US-10-176-993-35	Sequence 35, Appl
c 161	15.4	77.0	632	9	US-10-363-483A-27322	Sequence 27322, A	c 234	15.4	77.0	2690	5	US-10-184-658-35	Sequence 35, Appl
c 162	15.4	77.0	657	5	US-10-027-632-25021	Sequence 25021, A	c 235	15.4	77.0	2690	5	US-10-176-991-35	Sequence 35, Appl
c 163	15.4	77.0	657	6	US-10-027-632-25021	Sequence 25021, A	c 236	15.4	77.0	2690	5	US-10-173-695-35	Sequence 35, Appl
c 164	15.4	77.0	1663	7	US-10-437-963-643	Sequence 643, App	c 237	15.4	77.0	2690	5	US-10-173-697-35	Sequence 35, Appl
c 165	15.4	77.0	1781	9	US-10-487-078-141	Sequence 141, App	c 238	15.4	77.0	2690	5	US-10-173-705-35	Sequence 35, Appl
c 166	15.4	77.0	2667	9	US-10-643-795A-50	Sequence 50, Appl	c 239	15.4	77.0	2690	5	US-10-174-576-35	Sequence 35, Appl
c 167	15.4	77.0	2667	9	US-10-948-518-50	Sequence 50, Appl	c 240	15.4	77.0	2690	5	US-10-174-585-35	Sequence 35, Appl
c 168	15.4	77.0	2690	3	US-09-978-295A-514	Sequence 514, App	c 241	15.4	77.0	2690	5	US-10-174-586-35	Sequence 35, Appl
c 169	15.4	77.0	2690	3	US-09-978-697-514	Sequence 514, App	c 242	15.4	77.0	2690	5	US-10-175-747-35	Sequence 35, Appl



C 243	15.4	77.0	2690	5	US-10-176-481-35	Sequence 35, Appl	Sequence 35, Appl	C 316	15.4	77.0	2690	5	US-10-188-767-35	Sequence 35, Appl
C 244	15.4	77.0	2690	5	US-10-176-487-35	Sequence 35, Appl	Sequence 35, Appl	C 317	15.4	77.0	2690	5	US-10-188-769-35	Sequence 35, Appl
C 245	15.4	77.0	2690	5	US-10-176-485-35	Sequence 35, Appl	Sequence 35, Appl	C 318	15.4	77.0	2690	5	US-10-188-770-35	Sequence 35, Appl
C 246	15.4	77.0	2690	5	US-10-176-493-35	Sequence 35, Appl	Sequence 35, Appl	C 319	15.4	77.0	2690	5	US-10-188-773-35	Sequence 35, Appl
C 247	15.4	77.0	2690	5	US-10-176-756-35	Sequence 35, Appl	Sequence 35, Appl	C 320	15.4	77.0	2690	5	US-10-188-781-35	Sequence 35, Appl
C 248	15.4	77.0	2690	5	US-10-176-911-35	Sequence 35, Appl	Sequence 35, Appl	C 321	15.4	77.0	2690	5	US-10-194-361-35	Sequence 35, Appl
C 249	15.4	77.0	2690	5	US-10-176-919-35	Sequence 35, Appl	Sequence 35, Appl	C 322	15.4	77.0	2690	5	US-10-194-423-35	Sequence 35, Appl
C 250	15.4	77.0	2690	5	US-10-176-925-35	Sequence 35, Appl	Sequence 35, Appl	C 323	15.4	77.0	2690	5	US-10-195-897-35	Sequence 35, Appl
C 251	15.4	77.0	2690	5	US-10-176-978-35	Sequence 35, Appl	Sequence 35, Appl	C 324	15.4	77.0	2690	5	US-10-195-901-35	Sequence 35, Appl
C 252	15.4	77.0	2690	5	US-10-179-510-35	Sequence 35, Appl	Sequence 35, Appl	C 325	15.4	77.0	2690	5	US-10-195-903-35	Sequence 35, Appl
C 253	15.4	77.0	2690	5	US-10-180-543-35	Sequence 35, Appl	Sequence 35, Appl	C 326	15.4	77.0	2690	5	US-10-196-743-35	Sequence 35, Appl
C 254	15.4	77.0	2690	5	US-10-180-544-35	Sequence 35, Appl	Sequence 35, Appl	C 327	15.4	77.0	2690	5	US-10-196-760-35	Sequence 35, Appl
C 255	15.4	77.0	2690	5	US-10-180-546-35	Sequence 35, Appl	Sequence 35, Appl	C 328	15.4	77.0	2690	5	US-10-196-760-35	Sequence 35, Appl
C 256	15.4	77.0	2690	5	US-10-180-547-35	Sequence 35, Appl	Sequence 35, Appl	C 329	15.4	77.0	2690	5	US-10-173-708-35	Sequence 35, Appl
C 257	15.4	77.0	2690	5	US-10-180-549-35	Sequence 35, Appl	Sequence 35, Appl	C 330	15.4	77.0	2690	5	US-10-176-479-35	Sequence 35, Appl
C 258	15.4	77.0	2690	5	US-10-180-555-35	Sequence 35, Appl	Sequence 35, Appl	C 331	15.4	77.0	2690	5	US-10-176-748-35	Sequence 35, Appl
C 259	15.4	77.0	2690	5	US-10-180-559-35	Sequence 35, Appl	Sequence 35, Appl	C 332	15.4	77.0	2690	5	US-10-176-916-35	Sequence 35, Appl
C 260	15.4	77.0	2690	5	US-10-181-000-35	Sequence 35, Appl	Sequence 35, Appl	C 333	15.4	77.0	2690	5	US-10-179-507-35	Sequence 35, Appl
C 261	15.4	77.0	2690	5	US-10-183-010-35	Sequence 35, Appl	Sequence 35, Appl	C 334	15.4	77.0	2690	5	US-10-179-516-35	Sequence 35, Appl
C 262	15.4	77.0	2690	5	US-10-183-012-35	Sequence 35, Appl	Sequence 35, Appl	C 335	15.4	77.0	2690	5	US-10-179-519-35	Sequence 35, Appl
C 263	15.4	77.0	2690	5	US-10-184-614-35	Sequence 35, Appl	Sequence 35, Appl	C 336	15.4	77.0	2690	5	US-10-179-525-35	Sequence 35, Appl
C 264	15.4	77.0	2690	5	US-10-184-623-35	Sequence 35, Appl	Sequence 35, Appl	C 337	15.4	77.0	2690	5	US-10-180-540-35	Sequence 35, Appl
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Sequence 514, Appl	US-11-129-762-514

# ALIGNMENTS

RESULT 1  
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 ; Sequence 2, Application US/10829474  
 ; Publication No. US20050239055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GENETICS & IVF  
 ; APPLICANT: MARIANI, Brian D.  
 ; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
 ; FILE REFERENCE: 043956-0121  
 ; CURRENT APPLICATION NUMBER: US/10/829,474  
 ; CURRENT FILING DATE: 2004-04-22  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 2  
 ; LENGTH: 20  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
 ; OTHER INFORMATION: RNA  
 US-10-829-474-2

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; Sequence 25, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 25
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
US-10-829-474-25

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Best Local Similarity 100.0%; Pred. No. 6.8;
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; Sequence 26, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
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; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
US-10-829-474-26

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; Sequence 27, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
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; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
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; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral
US-10-829-474-27

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Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 5
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; Sequence 53, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
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; LENGTH: 107
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-53

Query Match      100.0%; Score 20; DB 9; Length 107;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 20
    |||||
Db 102 AAGGAACACGACACCCCA 83

RESULT 6
US-10-760-048-52/c
; Sequence 52, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 52
; LENGTH: 110
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
```

1 AAGGAAACACGGACACCCAA 20

RESULT 11  
US-10-760-048-45/c  
; Sequence 45, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 45  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-45

Query Match 100.0%; Score 20; DB 9; Length 237;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
DB 105 AAGGAAACACGGACACCCAA 86

## RESULT 12

US-10-760-048-56/c  
; Sequence 56, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 56  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-56

Query Match 100.0%; Score 20; DB 9; Length 237;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
DB 105 AAGGAAACACGGACACCCAA 86

## RESULT 13

US-10-760-048-57/c  
; Sequence 57, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2

; SEQ ID NO 57  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-57

Query Match 100.0%; Score 20; DB 9; Length 237;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
DB 105 AAGGAAACACGGACACCCAA 86

## RESULT 14

US-10-760-048-59/c  
; Sequence 59, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 59  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-59

Query Match 100.0%; Score 20; DB 9; Length 237;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
DB 105 AAGGAAACACGGACACCCAA 86

## RESULT 15

US-10-760-048-60/c  
; Sequence 60, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 60  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-60

```
Query Match      100.0%; Score 20; DB 9; Length 237;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 16  
 US-10-760-048-63/c  
 ; Sequence 63, Application US/10760048  
 ; Publication No. US20050158710A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSANG, SHIRLEY  
 ; APPLICANT: PRICE, JAMES A.  
 ; APPLICANT: HELLYER, TOBIN J.  
 ; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
 ; FILE REFERENCE: 020187.0187PTUS  
 ; CURRENT APPLICATION NUMBER: US/10/760,048  
 ; CURRENT FILING DATE: 2004-01-16  
 ; NUMBER OF SEQ ID NOS: 67  
 ; SOFTWARE: Patent in Ver. 3.2  
 ; SEQ ID NO 63  
 ; LENGTH: 237  
 ; TYPE: DNA  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Viru  
 ; OTHER INFORMATION: 5'untranslated polynucleotide sequenc  
 US-10-760-048-63

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGGAAACACGGACACCCAA 86

```

RESULT 17
US-10-760-048-64/c
; Sequence 64, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in Ver. 3.2
; SEQ ID NO 64
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viru
; OTHER INFORMATION: 5'untranslated polynucleotide sequenc
US-10-760-048-64

```

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGGAAACACGGACACCCAA 86

```

RESULT 18
US-10-760-048-66/c
; Sequence 66, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 66
; LENGTH: 237
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-66

```

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 105 AAGGAAACACGGACACCCAA 86

```

RESULT 19
US-10-760-048-13/c
; Sequence 13, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-13

```

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 20  
US-10-760-048-15/c  
; Sequence 15, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGGAAACACGGACACCCAA 86

FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 15  
LENGTH: 238  
TYPE: DNA  
ORGANISM: Unknown Organism

FEATURE:  
OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-15

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 21

US-10-760-048-30/c  
Sequence 30, Application US/10760048  
Publication No. US20050158710A1  
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY  
APPLICANT: PRICE, JAMES A.  
APPLICANT: HELLYER, TOBIN J.  
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 30

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral  
OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-30

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 22

US-10-760-048-31/c  
Sequence 31, Application US/10760048  
Publication No. US20050158710A1  
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY  
APPLICANT: PRICE, JAMES A.  
APPLICANT: HELLYER, TOBIN J.  
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 31

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral  
OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-38

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral  
OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-31

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 23

US-10-760-048-33/c  
Sequence 33, Application US/10760048  
Publication No. US20050158710A1  
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY  
APPLICANT: PRICE, JAMES A.  
APPLICANT: HELLYER, TOBIN J.  
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 33

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral  
OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-33

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 24

US-10-760-048-38/c  
Sequence 38, Application US/10760048  
Publication No. US20050158710A1  
GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY  
APPLICANT: PRICE, JAMES A.  
APPLICANT: HELLYER, TOBIN J.  
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 38

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral  
OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-38

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
| | | | | | | | | | | | | | | | | |  
Db 105 AAGGAAACACGGACACCCAA 86

## RESULT 25

US-10-760-048-42/c  
; Sequence 42, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 42  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-42

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
| | | | | | | | | | | | | | | | | |  
Db 105 AAGGAAACACGGACACCCAA 86

## RESULT 26

US-10-760-048-43/c  
; Sequence 43, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 43  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-43

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
| | | | | | | | | | | | | | | | | |  
Db 105 AAGGAAACACGGACACCCAA 86

## RESULT 27

US-10-760-048-46/c  
; Sequence 46, Application US/10760048  
; Publication No. US20050158710A1

; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 46  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-46

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
| | | | | | | | | | | | | | | | | |  
Db 105 AAGGAAACACGGACACCCAA 86

## RESULT 28

US-10-760-048-47/c  
; Sequence 47, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 47  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-47

Query Match 100.0%; Score 20; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
| | | | | | | | | | | | | | | | | |  
Db 105 AAGGAAACACGGACACCCAA 86

## RESULT 29

US-10-760-048-48/c  
; Sequence 48, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67



SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 48

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence

US-10-760-048-48

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 238;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20

DB 105 AAGGAAACACGGACACCCAA 86

RESULT 30

US-10-760-048-58/c

Sequence 58, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 58

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence

US-10-760-048-58

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 238;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20

DB 106 AAGGAAACACGGACACCCAA 87

RESULT 31

US-10-760-048-61/c

Sequence 61, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 61

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence

US-10-760-048-61

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 238;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20

DB 105 AAGGAAACACGGACACCCAA 86

RESULT 32

US-10-760-048-65/c

Sequence 65, Application US/10760048

Publication No. US20050158710A1

GENERAL INFORMATION:

APPLICANT: TSANG, SHIRLEY

APPLICANT: PRICE, JAMES A.

APPLICANT: HELLYER, TOBIN J.

TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID

FILE REFERENCE: 020187.0187PTUS

CURRENT APPLICATION NUMBER: US/10/760,048

CURRENT FILING DATE: 2004-01-16

NUMBER OF SEQ ID NOS: 67

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 65

LENGTH: 238

TYPE: DNA

ORGANISM: Unknown Organism

FEATURE:

OTHER INFORMATION: Description of Unknown Organism: Viral

OTHER INFORMATION: 5'untranslated polynucleotide sequence

US-10-760-048-65

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 238;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20

DB 105 AAGGAAACACGGACACCCAA 86

RESULT 33

US-10-614-283-1/c

Sequence 1, Application US/10614283

Publication No. US20050112095A1

GENERAL INFORMATION:

APPLICANT: HSU, TSUNG-YUAN

APPLICANT: WU, TZONG-YUAN

APPLICANT: LEE, JIN-CHING

TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN

FILE REFERENCE: 08842.0002-00000

CURRENT APPLICATION NUMBER: US/10/614,283

CURRENT FILING DATE: 2003-07-08

PRIOR APPLICATION NUMBER: 60/394,269

PRIOR FILING DATE: 2002-07-09

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 1

LENGTH: 709

TYPE: DNA

ORGANISM: Enterovirus 71

US-10-614-283-1

Query Match

Best Local Similarity 100.0%; Score 20; DB 9; Length 709;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20

DB 534 AAGGAAACACGGACACCCAA 515

```
RESULT 34
US-10-839-729-21/c
; Sequence 21, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: Jens Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; FILE REFERENCE: BIOBANK.013A
; CURRENT APPLICATION NUMBER: US/10/839,729
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR FILING DATE: 2003-05-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 743
; TYPE: DNA
; ORGANISM: Mahoney Strain Poliovirus Type I
US-10-839-729-21

Query Match      100.0%; Score 20; DB 8; Length 743;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 563 AAGGAAACACGGACACCCAA 544

RESULT 35
US-10-489-136-10/c
; Sequence 10, Application US/10489136
; Publication No. US20050014150A1
; GENERAL INFORMATION:
; APPLICANT: Atabekov, Joseph
; APPLICANT: Dorokhov, Yuri
; APPLICANT: Skulachev, Maxim
; APPLICANT: Ivanov, Peter
; APPLICANT: Gleba, Yuri
; TITLE OF INVENTION: IDENTIFICATION OF EUKARYOTIC INTERNAL RIBOSOME ENTRY SITE (IRES)
; FILE REFERENCE: 9286.30
; CURRENT APPLICATION NUMBER: US/10/489,136
; CURRENT FILING DATE: 2004-03-02
; PRIOR APPLICATION NUMBER: PCT/EP02/09844
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: DE 101 43 238.0
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Poliovirus
US-10-489-136-10

Query Match      100.0%; Score 20; DB 8; Length 745;
Best Local Similarity 100.0%; Pred. No. 7.3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 568 AAGGAAACACGGACACCCAA 549

RESULT 36
US-09-884-586A-3/c
; Sequence 3, Application US/09884586A
; Publication No. US20030046716A1
; GENERAL INFORMATION:
; APPLICANT: Echelard, Yann
```

```
; APPLICANT: Meade, Harry M.
; APPLICANT: Eichner, Wolfram
; APPLICANT: Sommermeyer, Klaus
; TITLE OF INVENTION: TRANSGENICALLY PRODUCED PLATELET DERIVED
; FILE REFERENCE: GROWTH FACTOR
; FILE REFERENCE: 10275-120001
; CURRENT APPLICATION NUMBER: US/09/884,586A
; CURRENT FILING DATE: 2001-06-19
; PRIOR APPLICATION NUMBER: 60/212,406
; PRIOR FILING DATE: 2000-06-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-884-586A-3

Query Match      100.0%; Score 20; DB 3; Length 2076;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 1317 AAGGAAACACGGACACCCAA 1298

RESULT 37
US-10-408-456-4/c
; Sequence 4, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: KINGSMAN, et al., Alan John
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 10448
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-4

Query Match      100.0%; Score 20; DB 6; Length 10448;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 1541 AAGGAAACACGGACACCCAA 1522

RESULT 38
US-10-408-456-5/c
; Sequence 5, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: KINGSMAN, et al., Alan John
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
```

```
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 11058
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-5

Query Match      100.0%; Score 20; DB 6; Length 11058;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCCAA 20
   |||||
DB 3813 AAGGAAACACGACACCCCAA 3794

RESULT 39
US-10-408-456-34/c
; Sequence 34, Application US/10408456
; Publication No. US20040013648A1
; GENERAL INFORMATION:
; APPLICANT: KINGSMAN, et al., Alan John
; APPLICANT: Oxford Biomedica (UK) Limited
; TITLE OF INVENTION: Vector System
; FILE REFERENCE: 674523-2016
; CURRENT APPLICATION NUMBER: US/10/408,456
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 34
; LENGTH: 11622
; TYPE: DNA
; ORGANISM: Equine Infectious Anemia Virus
US-10-408-456-34

Query Match      100.0%; Score 20; DB 6; Length 11622;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCCAA 20
   |||||
DB 7244 AAGGAAACACGACACCCCAA 7225

RESULT 40
US-10-873-573-7/c
; Sequence 7, Application US/10873573
; Publication No. US20050002907A1
; GENERAL INFORMATION:
; APPLICANT: MITRAPHANOUS, KYRI
; APPLICANT: ROHL, JONATHAN
; APPLICANT: MISKIN, JAMES
; APPLICANT: KINGSMAN, SUSAN MARIE
; TITLE OF INVENTION: VECTOR SYSTEM
; FILE REFERENCE: 674523-2016.1
; CURRENT APPLICATION NUMBER: US/10/873,573
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 10/408,456
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: PCT/GB01/04433
; PRIOR FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: GB 0024550.6
; PRIOR FILING DATE: 2000-10-06
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 11622

; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-573-7

Query Match      100.0%; Score 20; DB 8; Length 11622;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCCAA 20
   |||||
DB 7244 AAGGAAACACGACACCCCAA 7225

RESULT 41
US-10-366-823-5/c
; Sequence 5, Application US/10366823
; Publication No. US20030211526A1
; GENERAL INFORMATION:
; APPLICANT: Juang, Jyh-Lyh
; APPLICANT: Hsiung, Chao Agnes
; APPLICANT: Lin, Chung-Yen
; TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES
; FILE REFERENCE: 12563-006001
; CURRENT APPLICATION NUMBER: US/10/366,823
; CURRENT FILING DATE: 2003-02-14
; PRIOR APPLICATION NUMBER: US 60/357,541
; PRIOR FILING DATE: 2002-02-15
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 62
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-10-366-823-5

Query Match      100.0%; Score 20; DB 6; Length 62;
Best Local Similarity 95.0%; Pred. No. 11;
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCCAA 20
   |||||
DB 57 AAGGAAACACGACACCCCAA 38

RESULT 42
US-10-408-519-3/c
; Sequence 3, Application US/10408519
; Publication No. US20030228683A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Kan-Hung
; APPLICANT: Shih, Yu-Hau
; APPLICANT: Tsai, Chuan-Wei
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Hsiao, Hsiung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Wang, Shin-Hwan
; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES
; FILE REFERENCE: 12674-002002
; CURRENT APPLICATION NUMBER: US/10/408,519
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: US 09/522,417
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
```

; FEATURE:  
; OTHER INFORMATION: Probe from 5' ends of enterovirus genes  
US-10-408-519-3

Query Match 100.0%; Score 20; DB 6; Length 53;  
Best Local Similarity 95.0%; Pred. No. 17;  
Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
||:|||||  
Db 49 AAGGAACACGACACCCAA 30

RESULT 43

US-10-829-474-21  
; Sequence 21, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 21  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
US-10-829-474-21

Query Match 95.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20  
|||||  
Db 1 AGGAACACGACACCCAA 19

RESULT 44

US-10-829-474-22  
; Sequence 22, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 22  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
US-10-829-474-22

Query Match 95.0%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCCA 19  
|||||  
Db 1 AAGGAACACGACACCCCA 19

RESULT 45

US-10-760-048-34/c  
; Sequence 34, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 34  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-34

Query Match 95.0%; Score 19; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20  
|||||  
Db 104 AGGAACACGACACCCAA 86

RESULT 46

US-10-760-048-35/c  
; Sequence 35, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 35  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-35

Query Match 95.0%; Score 19; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGACACCCAA 20  
|||||  
Db 104 AGGAACACGACACCCAA 86

RESULT 47

US-10-760-048-36/c  
; Sequence 36, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.

; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; PRIOR FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-36

Query Match 95.0%; Score 19; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20  
|||||  
Db 104 AGGAAACACGGACACCCAA 86

RESULT 48  
US-10-760-048-62/c  
; Sequence 62, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 62  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-62

Query Match 95.0%; Score 19; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20  
|||||  
Db 104 AGGAAACACGGACACCCAA 86

RESULT 49  
US-10-332-123-53/c  
; Sequence 53, Application US/10332123  
; Publication No. US20040072239A1  
; GENERAL INFORMATION:  
; APPLICANT: RENAUD, Patricia  
; APPLICANT: GUILLLOT, Emmanuelle  
; APPLICANT: MABILAT, Claude  
; APPLICANT: VACHON, Carole  
; APPLICANT: LACROIX, Bruno  
; APPLICANT: VERNET, Guy  
; APPLICANT: ARMAND, Marie-Astrid  
; APPLICANT: LARFAIRE, Philippe  
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
; TITLE OF INVENTION: MEDIUM AND KIT THEREFOR  
; FILE REFERENCE: 114502

; CURRENT APPLICATION NUMBER: US/10/332,123  
; CURRENT FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: FR00-08839  
; PRIOR FILING DATE: 2000-07-06  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 53  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Poliovirus (X00595)  
US-10-332-123-53

Query Match 95.0%; Score 19; DB 7; Length 521;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAAACACGGACACCCAA 20  
|||||  
Db 500 AGGAAACACGGACACCCAA 482

RESULT 50  
US-10-760-048-41/c  
; Sequence 41, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 41  
; LENGTH: 235  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-41

Query Match 92.0%; Score 18.4; DB 9; Length 235;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 105 ATGGAACACGGACACCCAA 86

RESULT 51  
US-10-760-048-37/c  
; Sequence 37, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 236  
; TYPE: DNA  
; ORGANISM: Unknown Organism

; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-37

Query Match 92.0%; Score 18.4; DB 9; Length 236;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 ATGGAACACGGACACCCAA 86  
|||

## RESULT 52

US-10-760-048-16/c  
; Sequence 16, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 16  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-16

Query Match 92.0%; Score 18.4; DB 9; Length 237;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AGGGAACACGGACACCCAA 86  
|||

## RESULT 53

US-10-760-048-32/c  
; Sequence 32, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 32  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-32

Query Match 92.0%; Score 18.4; DB 9; Length 237;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGAAACACGGACACCCAA 86  
|||

## RESULT 54

US-10-760-048-14/c  
; Sequence 14, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 14  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-14

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AAGAAACACGGACACCCAA 86  
|||

## RESULT 55

US-10-760-048-19/c  
; Sequence 19, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 19  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-19

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
|||  
Db 105 AATGAAACACGGACACCCAA 86  
|||

## RESULT 56

US-10-760-048-23/c  
; Sequence 23, Application US/10760048  
; Publication No. US20050158710A1

;; GENERAL INFORMATION:  
;; APPLICANT: TSANG, SHIRLEY  
;; APPLICANT: PRICE, JAMES A.  
;; APPLICANT: HELLYER, TOBIN J.  
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
;; FILE REFERENCE: 020187.0187PTUS  
;; CURRENT APPLICATION NUMBER: US/10/760,048  
;; CURRENT FILING DATE: 2004-01-16  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 23  
;; LENGTH: 238  
;; TYPE: DNA  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Viral  
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-23

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||  
Db 105 AATGAAACACGACACCCAA 86

RESULT 57  
US-10-760-048-25/c  
;; Sequence 25, Application US/10760048  
;; Publication No. US20050158710A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TSANG, SHIRLEY  
;; APPLICANT: PRICE, JAMES A.  
;; APPLICANT: HELLYER, TOBIN J.  
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
;; FILE REFERENCE: 020187.0187PTUS  
;; CURRENT APPLICATION NUMBER: US/10/760,048  
;; CURRENT FILING DATE: 2004-01-16  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 25  
;; LENGTH: 238  
;; TYPE: DNA  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Viral  
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-25

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||  
Db 105 AATGAAACACGACACCCAA 86

RESULT 58  
US-10-760-048-26/c  
;; Sequence 26, Application US/10760048  
;; Publication No. US20050158710A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TSANG, SHIRLEY  
;; APPLICANT: PRICE, JAMES A.  
;; APPLICANT: HELLYER, TOBIN J.  
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
;; FILE REFERENCE: 020187.0187PTUS  
;; CURRENT APPLICATION NUMBER: US/10/760,048  
;; CURRENT FILING DATE: 2004-01-16  
;; NUMBER OF SEQ ID NOS: 67

;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 26  
;; LENGTH: 238  
;; TYPE: DNA  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Viral  
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-26

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||  
Db 105 AATGAAACACGACACCCAA 86

RESULT 59  
US-10-760-048-27/c  
;; Sequence 27, Application US/10760048  
;; Publication No. US20050158710A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TSANG, SHIRLEY  
;; APPLICANT: PRICE, JAMES A.  
;; APPLICANT: HELLYER, TOBIN J.  
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
;; FILE REFERENCE: 020187.0187PTUS  
;; CURRENT APPLICATION NUMBER: US/10/760,048  
;; CURRENT FILING DATE: 2004-01-16  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 27  
;; LENGTH: 238  
;; TYPE: DNA  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Viral  
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-27

Query Match 92.0%; Score 18.4; DB 9; Length 238;  
Best Local Similarity 95.0%; Pred. No. 43;  
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
|||  
Db 105 AATGAAACACGACACCCAA 86

RESULT 60  
US-10-760-048-28/c  
;; Sequence 28, Application US/10760048  
;; Publication No. US20050158710A1  
;; GENERAL INFORMATION:  
;; APPLICANT: TSANG, SHIRLEY  
;; APPLICANT: PRICE, JAMES A.  
;; APPLICANT: HELLYER, TOBIN J.  
;; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
;; FILE REFERENCE: 020187.0187PTUS  
;; CURRENT APPLICATION NUMBER: US/10/760,048  
;; CURRENT FILING DATE: 2004-01-16  
;; NUMBER OF SEQ ID NOS: 67  
;; SOFTWARE: PatentIn Ver. 3.2  
;; SEQ ID NO 28  
;; LENGTH: 238  
;; TYPE: DNA  
;; ORGANISM: Unknown Organism  
;; FEATURE:  
;; OTHER INFORMATION: Description of Unknown Organism: Viral  
;; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-28

Query Match 92.0%; Score 18.4; DB 7; Length 520;



;; GENERAL INFORMATION:  
;; APPLICANT: Genetics & IVF  
;; APPLICANT: MARIANI, Brian D.  
;; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
;; FILE REFERENCE: 043956-0121  
;; CURRENT APPLICATION NUMBER: US/10/829,474  
;; CURRENT FILING DATE: 2004-04-22  
;; NUMBER OF SEQ ID NOS: 57  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 18  
;; LENGTH: 18  
;; TYPE: DNA  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
;; OTHER INFORMATION: RNA  
US-10-829-474-18

Query Match 90.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACACGCGACACCCAA 20  
|||||  
DB 1 GGAACACGCGACACCCAA 18

RESULT 66  
US-10-829-474-20  
; Sequence 20, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 20  
; LENGTH: 18  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-20

Query Match 90.0%; Score 18; DB 9; Length 18;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAACACGCGACACCCCA 19  
|||||  
DB 1 AGGAACACGCGACACCCCA 18

RESULT 67  
US-10-322-696-13  
; Sequence 13, Application US/10322696  
; Publication No. US20040166490A1  
; GENERAL INFORMATION:  
; APPLICANT: Malandro, Marc  
; APPLICANT: Morris, David W.  
; TITLE OF INVENTION: NOVEL THERAPEUTIC TARGETS IN CANCER  
; FILE REFERENCE: 529452001200  
; CURRENT APPLICATION NUMBER: US/10/322,696  
; CURRENT FILING DATE: 2003-10-17  
; NUMBER OF SEQ ID NOS: 186  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 225734

;; TYPE: DNA  
;; ORGANISM: Mus musculus  
;; FEATURE:  
;; NAME/KEY: misc feature  
;; LOCATION: (1)...(225734)  
;; OTHER INFORMATION: n = A,T,C or G  
US-10-322-696-13

Query Match 90.0%; Score 18; DB 7; Length 225734;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACACGCGACACCCAA 20  
|||||  
DB 57400 GGAACACGCGACACCCAA 57417

RESULT 68  
US-10-760-048-10  
; Sequence 10, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 10  
; LENGTH: 40  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Primer  
US-10-760-048-10

Query Match 89.0%; Score 17.8; DB 9; Length 40;  
Best Local Similarity 89.5%; Pred. No. 81;  
Matches 17; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGCGACACCCCA 19  
|||||  
DB 22 AADRAACACGCGACACCCCA 40

RESULT 69  
US-10-829-474-23  
; Sequence 23, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 23  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-23

Query Match 85.0%; Score 17; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGAACACGGACACCCA 19  
Db 1 GGAACACGGACACCCA 17

## RESULT 70

US-10-829-474-24  
; Sequence 24, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 24  
; LENGTH: 17  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-24

Query Match 85.0%; Score 17; DB 9; Length 17;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 AGGAACACGGACACCC 18  
Db 1 AGGAACACGGACACCC 17

## RESULT 71

US-10-938-005-4/c  
; Sequence 4, Application US/10938005  
; Publication No. US20050048475A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul, John H.  
; APPLICANT: Casper, Erica T.  
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus  
; FILE REFERENCE: USF-114XC621  
; CURRENT APPLICATION NUMBER: US/10/938,005  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: 10/857,109  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 4  
; LENGTH: 20  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer Ent P3  
US-10-938-005-4

Query Match 85.0%; Score 17; DB 8; Length 20;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCC 17  
Db 17 AAGGAACACGGACACCC 1

## RESULT 72

US-10-179-082A-3/c  
; Sequence 3, Application US/10179082A  
; Publication No. US20030186222A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul, John H.  
; TITLE OF INVENTION: RAPID DETECTION OF ENTEROVIRUSES IN ENVIRONMENTAL SAMPLES BY NASBA  
; FILE REFERENCE: USF-114XC6  
; CURRENT APPLICATION NUMBER: US/10/179,082A  
; CURRENT FILING DATE: 2002-11-04  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Poliovirus sp.  
US-10-179-082A-3

Query Match 85.0%; Score 17; DB 6; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
Db 21 GAAACACGGACACCCAA 5

## RESULT 73

US-10-938-005-3/c  
; Sequence 3, Application US/10938005  
; Publication No. US20050048475A1  
; GENERAL INFORMATION:  
; APPLICANT: Paul, John H.  
; APPLICANT: Casper, Erica T.  
; APPLICANT: Patterson, Stacey S.  
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus  
; FILE REFERENCE: USF-114XC621  
; CURRENT APPLICATION NUMBER: US/10/938,005  
; CURRENT FILING DATE: 2004-09-10  
; PRIOR APPLICATION NUMBER: 10/857,109  
; PRIOR FILING DATE: 2004-05-28  
; PRIOR APPLICATION NUMBER: 10/179,082  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: 60/301,218  
; PRIOR FILING DATE: 2001-06-27  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 3  
; LENGTH: 21  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: probe for poliovirus  
US-10-938-005-3

Query Match 85.0%; Score 17; DB 8; Length 21;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
Db 21 GAAACACGGACACCCAA 5

## RESULT 74

US-10-175-247-20  
; Sequence 20, Application US/10175247  
; Publication No. US20030165466A1  
; GENERAL INFORMATION:  
; APPLICANT: Gromeier PHD, Matthias  
; APPLICANT: Wimmer Prof, Eckard  
; TITLE OF INVENTION: Recombinant Poliovirus For The Treatment of Cancer

```
; FILE REFERENCE: Recomb Poliovirus for Cancer Treatment
; CURRENT APPLICATION NUMBER: US/10/175,247
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: US/09/129,686
; PRIOR FILING DATE: 1998-08-05
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Human rhinovirus 2
US-10-175-247-20

Query Match      85.0%; Score 17; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACC 17
      |||||
Db      17 AAGGAAACACGGACACC 33

RESULT 75
US-10-760-048-9/c
; Sequence 9, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 9
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-760-048-9

Query Match      85.0%; Score 17; DB 9; Length 40;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAAACACGGACACCCAA 20
      |||||
Db      40 GAAACACGGACACCCAA 24

RESULT 76
US-10-938-005-9/c
; Sequence 9, Application US/10938005
; Publication No. US20050048475A1
; GENERAL INFORMATION:
; APPLICANT: Paul, John H.
; APPLICANT: Casper, Erica T.
; APPLICANT: Patterson, Stacey S.
; TITLE OF INVENTION: Materials and Methods for Detection of Enterovirus and Norovirus
; FILE REFERENCE: USF-114XC621
; CURRENT APPLICATION NUMBER: US/10/938,005
; CURRENT FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: 10/857,109
; PRIOR FILING DATE: 2004-05-28
; PRIOR APPLICATION NUMBER: 10/179,082
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: 60/301,218
; PRIOR FILING DATE: 2001-06-27
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
```

```
; SEQ ID NO 9
; LENGTH: 92
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Enteroviral Internal Control
US-10-938-005-9

Query Match      85.0%; Score 17; DB 8; Length 92;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACC 17
      |||||
Db      17 AAGGAAACACGGACACC 1

RESULT 77
US-10-760-048-39/c
; Sequence 39, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 39
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-39

Query Match      85.0%; Score 17; DB 9; Length 117;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 GAAACACGGACACCCAA 20
      |||||
Db      102 GAAACACGGACACCCAA 86

RESULT 78
US-10-760-048-40/c
; Sequence 40, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 40
; LENGTH: 117
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-40

Query Match      85.0%; Score 17; DB 9; Length 117;
```

Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
|||||  
Db 102 GAAACACGGACACCCAA 86

## RESULT 79

US-10-104-611-31/c  
; Sequence 31, Application US/10104611  
; Publication No. US20020160976A1  
; GENERAL INFORMATION:  
; APPLICANT: Miles, Vincent J.

; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/104,611

FILING DATE: 22-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,816B

FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 627 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-10-104-611-31

Query Match 85.0%; Score 17; DB 5; Length 627;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552

## RESULT 80

US-10-112-547-31/c  
; Sequence 31, Application US/10112547  
; Publication No. US20020160977A1  
; GENERAL INFORMATION:

; APPLICANT: Miles, Vincent J.

; Mathews, Michael B.  
; Katze, Michael G.  
; Witherell, Gary  
; Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/112,547

FILING DATE: 28-Mar-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/221,816B

FILING DATE: 01-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7960-030

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 31:

SEQUENCE CHARACTERISTICS:

LENGTH: 627 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

SEQUENCE DESCRIPTION: SEQ ID NO: 31:

US-10-112-547-31

Query Match 85.0%; Score 17; DB 5; Length 627;  
Best Local Similarity 100.0%; Pred. No. 2.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20  
|||||  
Db 568 GAAACACGGACACCCAA 552

## RESULT 81

US-10-112-241-31/c

; Sequence 31, Application US/10112241

; Publication No. US20020165194A1

; GENERAL INFORMATION:

; APPLICANT: Miles, Vincent J.

; Mathews, Michael B.

; Katze, Michael G.

; Witherell, Gary

; Watson, Julia C.

TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION  
OF VIRAL REPLICATION

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036/2711

```
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSEQ Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/10/112,241
;; FILING DATE: 28-Mar-2002
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/221,816B
;; FILING DATE: 01-APR-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7960-030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 627 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-112-241-31
Query Match      85.0%; Score 17; DB 5; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  GAAACACGGACACCCAA 20
Db      568 GAAACACGGACACCCAA 552

RESULT 82
US-10-109-368-31/c
; Sequence 31, Application US/10109368
; Publication No. US2003014226A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
```

```
;;
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 7960-030
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 31:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 627 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-109-368-31
Query Match      85.0%; Score 17; DB 6; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4  GAAACACGGACACCCAA 20
Db      568 GAAACACGGACACCCAA 552

RESULT 83
US-10-867-798-31/c
; Sequence 31, Application US/10867798
; Publication No. US20040254140A1
; GENERAL INFORMATION:
; APPLICANT: Miles, Vincent J.
; Mathews, Michael B.
; Katze, Michael G.
; Witherell, Gary
; Watson, Julia C.
; TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
; OF VIRAL REPLICATION
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036/2711
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/867,798
; FILING DATE: 14-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/10/109,368
; FILING DATE: 27-Mar-2002
; APPLICATION NUMBER: US/08/221,816
; FILING DATE: 01-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7960-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 627 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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```
; MOLECULE TYPE: RNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 31:
US-10-867-798-31

Query Match      85.0%; Score 17; DB 8; Length 627;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCAA 20
Db 568 GAAACACGGACACCCAA 552
|||||
|

RESULT 84
US-10-425-115-173501
; Sequence 173501, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 173501
; LENGTH: 230
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89813C.1
US-10-425-115-173501

Query Match      84.0%; Score 16.8; DB 8; Length 230;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 53 AGGGAACACGGAAACCCAA 72
|||||
|

RESULT 85
US-10-760-048-17/c
; Sequence 17, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 17
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-17

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGTACCCAA 86
|||||
|

RESULT 86
US-10-760-048-22/c
; Sequence 22, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 22
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-22

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAAGAAACACGGTACCCAA 86
|||||
|

RESULT 87
US-10-760-048-24/c
; Sequence 24, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 24
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-24

Query Match      84.0%; Score 16.8; DB 9; Length 238;
Best Local Similarity 90.0%; Pred. No. 2.6e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAAGAAACACGGTACCCAA 86
|||||
|

RESULT 88
US-10-950-009-1102/c
; Sequence 1102, Application US/10950009
; Publication No. US20050069934A1
; GENERAL INFORMATION:
```

APPLICANT: BERKA, Randy  
APPLICANT: BASHKIROVA, Elena  
APPLICANT: REY, Michael  
TITLE OF INVENTION: Methods For Monitoring Gene Expression  
FILE REFERENCE: 10541.200-US  
CURRENT APPLICATION NUMBER: US/10/950,009  
CURRENT FILING DATE: 2004-09-24  
PRIOR APPLICATION NUMBER: 60/506,140  
PRIOR FILING DATE: 2003-09-25  
NUMBER OF SEQ ID NOS: 1190  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1102  
LENGTH: 370  
TYPE: DNA  
ORGANISM: Trichoderma reesei  
US-10-950-009-1102

Query Match 84.0%; Score 16.8; DB 9; Length 370;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 262 AAGGAAACACGGACACCCAA 243

RESULT 89  
US-09-925-065A-156382  
Sequence 156382, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 156382  
LENGTH: 585  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-156382

Query Match 84.0%; Score 16.8; DB 4; Length 585;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 85 AAGGAAACACGGACACCCAA 104

RESULT 90  
US-09-925-065A-156383  
Sequence 156383, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 156383  
LENGTH: 585  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-156383

Query Match 84.0%; Score 16.8; DB 4; Length 585;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 85 AAGGAAACACGGACACCCAA 104

RESULT 91  
US-10-760-048-67/c  
Sequence 67, Application US/10760048  
Publication No. US20050158710A1  
GENERAL INFORMATION:  
APPLICANT: TSANG, SHIRLEY  
APPLICANT: PRICE, JAMES A.  
APPLICANT: HELLYER, TOBIN J.  
TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
FILE REFERENCE: 020187.0187PTUS  
CURRENT APPLICATION NUMBER: US/10/760,048  
CURRENT FILING DATE: 2004-01-16  
NUMBER OF SEQ ID NOS: 67  
SOFTWARE: PatentIn Ver. 3.2  
SEQ ID NO 67  
LENGTH: 660  
TYPE: DNA  
ORGANISM: Coxsackievirus B3  
US-10-760-048-67

Query Match 84.0%; Score 16.8; DB 9; Length 660;  
Best Local Similarity 90.0%; Pred. No. 2.6e+02;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 1 AAGGAAACACGGACACCCAA 20  
|||||  
Db 487 AAGGAAACACGGACACCCAA 468

RESULT 92  
US-10-363-345A-23361/c  
Sequence 23361, Application US/10363345A  
Publication No. US20040234960A1  
GENERAL INFORMATION:  
APPLICANT: Alexander Olek  
APPLICANT: Christian Piepenbrock  
TITLE OF INVENTION: Method for determining the degree of methylation of defined  
FILE REFERENCE: E01/1227  
CURRENT APPLICATION NUMBER: US/10/363,345A  
CURRENT FILING DATE: 2003-03-03  
NUMBER OF SEQ ID NOS: 40712  
SEQ ID NO 23361

```

; LENGTH: 906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23361
US-10-363-345A-23361

Query Match      84.0%; Score 16.8; DB 8; Length 906;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      291 AACGAAACACGAAACCCAA 272

RESULT 93
US-10-363-345A-23362
; Sequence 23362, Application US/10363345A
; Publication No. US20040234960A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Method for determining the degree of methylation of defined
; TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3
; FILE REFERENCE: E01/1227
; CURRENT APPLICATION NUMBER: US/10/363,345A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23362
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23362
US-10-363-345A-23362

Query Match      84.0%; Score 16.8; DB 8; Length 906;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      616 AACGAAACACGAAACCCAA 635

RESULT 94
US-10-363-483A-23361/c
; Sequence 23361, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23361
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23361
US-10-363-483A-23361

Query Match      84.0%; Score 16.8; DB 9; Length 906;

```

```

Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      291 AACGAAACACGAAACCCAA 272

RESULT 95
US-10-363-483A-23362
; Sequence 23362, Application US/10363483A
; Publication No. US20050064401A1
; GENERAL INFORMATION:
; APPLICANT: Alexander Olek
; APPLICANT: Christian Piepenbrock
; APPLICANT: Kurt Berlin
; TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
; TITLE OF INVENTION: illnesses
; FILE REFERENCE: 82011
; CURRENT APPLICATION NUMBER: US/10/363,483A
; CURRENT FILING DATE: 2003-03-03
; NUMBER OF SEQ ID NOS: 40712
; SEQ ID NO 23362
; LENGTH: 906
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; OTHER INFORMATION: CpG-island No: 23362
US-10-363-483A-23362

Query Match      84.0%; Score 16.8; DB 9; Length 906;
Best Local Similarity 90.0%; Pred. No. 2.7e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20
Db      616 AACGAAACACGAAACCCAA 635

RESULT 96
US-10-723-681-3/c
; Sequence 3, Application US/10723681
; Publication No. US2005019239A1
; GENERAL INFORMATION:
; APPLICANT: ROTH, RICHARD B.
; APPLICANT: NELSON, MATTHEW ROBERTS
; APPLICANT: BRAUN, ANDREAS
; APPLICANT: KAMMERER, STEFAN M.
; APPLICANT: RENEKAND, RIKARD
; TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND
; TITLE OF INVENTION: TREATMENTS THEREOF
; FILE REFERENCE: SEQ-4069-CP
; CURRENT APPLICATION NUMBER: US/10/723,681
; CURRENT FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: US 60/429,136
; PRIOR FILING DATE: 2002-11-25
; PRIOR APPLICATION NUMBER: US 60/490,234
; PRIOR FILING DATE: 2003-07-24
; NUMBER OF SEQ ID NOS: 835
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 147300
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-723-681-3

Query Match      84.0%; Score 16.8; DB 9; Length 147300;
Best Local Similarity 90.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 AAGGAAACACGGACACCCAA 20

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Db 50059 ATGGAACACGGGACCCAA 50040

## RESULT 97

US-09-925-065A-319374  
; Sequence 319374, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 319374  
; LENGTH: 578  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-319374

Query Match 82.0%; Score 16.4; DB 4; Length 578;  
Best Local Similarity 94.4%; Pred. No. 4.1e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGAACACGGGACCCAA 20

Db 89 GGAACACGGGACCCAA 106

## RESULT 98

US-10-052-482-55/c  
; Sequence 55, Application US/10052482  
; Publication No. US20040072264A1  
; GENERAL INFORMATION:  
; APPLICANT: Engelhard, Eric  
; APPLICANT: Morris, David  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER  
; FILE REFERENCE: A-71087/RMS/DCF  
; CURRENT APPLICATION NUMBER: US/10/052,482  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02  
; NUMBER OF SEQ ID NOS: 241  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 47493  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1241)..(1975)  
; OTHER INFORMATION: "n" at positions 1241 to 1975 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (13629)..(13648)  
; OTHER INFORMATION: "n" at positions 13629 to 13648 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15882)..(16151)

; OTHER INFORMATION: "n" at positions 15882 to 16151 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (22065)..(22084)  
; OTHER INFORMATION: "n" at positions 22065 to 22084 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (26226)..(26285)  
; OTHER INFORMATION: "n" at positions 26226 to 26285 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (30454)..(30473)  
; OTHER INFORMATION: "n" at positions 30454 to 30473 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (31687)..(32259)  
; OTHER INFORMATION: "n" at positions 31687 to 32259 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (40899)..(41095)  
; OTHER INFORMATION: "n" at positions 40899 to 41095 can be any base  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (42909)..(43118)  
; OTHER INFORMATION: "n" at positions 42909 to 43118 can be any base  
US-10-052-482-55

Query Match 82.0%; Score 16.4; DB 7; Length 47493;  
Best Local Similarity 94.4%; Pred. No. 4.5e+02;  
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAACACGGGACCCCA 19

Db 11461 AGGAACACGGGACCCCA 11444

## RESULT 99

US-10-829-474-19  
; Sequence 19, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 19  
; LENGTH: 16  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized reverse primer for amplifying enteroviral  
; OTHER INFORMATION: RNA  
US-10-829-474-19

Query Match 80.0%; Score 16; DB 9; Length 16;  
Best Local Similarity 100.0%; Pred. No. 6e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGAACACGGGACCC 18

Db 1 GGAACACGGGACCC 16

## RESULT 100

US-10-425-115-83354  
; Sequence 83354, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.

; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425,115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 83354  
; LENGTH: 484  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MET4577\_176031C.1  
US-10-425-115-83354

Query Match 80.0%; Score 16; DB 8; Length 484;  
Best Local Similarity 100.0%; Pred. No. 6.4e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GAAACACGGACACCCA 19  
| | | | | | | | | | | | | | | | | | | | | |  
Db 29 GAAACACGGACACCCA 44

Search completed: March 9, 2006, 08:33:39  
Job time : 588.194 secs

GenCore version 5.1.7

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 200.388 Seconds  
(without alignments)  
665.178 Million cell updates/sec

Title: US-10-829-474-2

Perfect score: 20

Sequence: 1 aaggaacacggacaccaa 20

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 100%

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database :

N\_Geneseq\_21.\*

1: Geneseqn1980s.\*

2: Geneseqn1990s.\*

3: Geneseqn2000s.\*

4: Geneseqn2001as.\*

5: Geneseqn2001bs.\*

6: Geneseqn2002as.\*

7: Geneseqn2002bs.\*

8: Geneseqn2003as.\*

9: Geneseqn2003bs.\*

10: Geneseqn2003cs.\*

11: Geneseqn2003ds.\*

12: Geneseqn2004as.\*

13: Geneseqn2004bs.\*

14: Geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	20	100.0	105	14	ABE56869 Human ech
C 2	20	100.0	106	14	ABE56868 Human ech
C 3	20	100.0	107	14	ABE56814 Viral 5'
C 4	20	100.0	110	14	ABE56813 Viral 5'
C 5	20	100.0	126	14	ABE56779 Viral 5'
C 6	20	100.0	176	3	Az58488 Recombina
C 7	20	100.0	180	14	ABE56834 Human cox
C 8	20	100.0	195	10	Abz69931 Polioviru
C 9	20	100.0	198	14	ABE56860 Human ech
C 10	20	100.0	198	14	ABE56858 Human ech
C 11	20	100.0	198	14	ABE56863 Human ech
C 12	20	100.0	198	14	ABE56854 Human ech
C 13	20	100.0	236	14	ABE56816 Viral 5'
C 14	20	100.0	237	14	ABE56837 Human cox
C 15	20	100.0	237	14	ABE56862 Human ech
C 16	20	100.0	237	14	ABE56879 Human pol
C 17	20	100.0	237	14	ABE56881 Human pol
C 18	20	100.0	237	14	ABE56827 Viral 5'
C 19	20	100.0	237	14	ABE56875 Human pol

C 20	20	100.0	237	14	ABE56876
C 21	20	100.0	237	14	ABE56880
C 22	20	100.0	237	14	ABE56825 Viral 5'
C 23	20	100.0	237	14	ABE56805
C 24	20	100.0	237	14	ABE56818 Viral 5'
C 25	20	100.0	237	14	ABE56873
C 26	20	100.0	237	14	ABE56806
C 27	20	100.0	237	14	ABE56861
C 28	20	100.0	237	14	ABE56817 Viral 5'
C 29	20	100.0	237	14	ABE56820 Viral 5'
C 30	20	100.0	237	14	ABE56871 Human ent
C 31	20	100.0	237	14	ABE56821 Viral 5'
C 32	20	100.0	237	14	ABE56872
C 33	20	100.0	237	14	ABE56782 Viral 5'
C 34	20	100.0	237	14	ABE56824 Viral 5'
C 35	20	100.0	238	14	ABE56791 Viral 5'
C 36	20	100.0	238	14	ABE56826 Viral 5'
C 37	20	100.0	238	14	ABE56849
C 38	20	100.0	238	14	ABE56846
C 39	20	100.0	238	14	ABE56847 Human cox
C 40	20	100.0	238	14	ABE56819 Viral 5'
C 41	20	100.0	238	14	ABE56807 Viral 5'
C 42	20	100.0	238	14	ABE56822 Viral 5'
C 43	20	100.0	238	14	ABE56799 Viral 5'
C 44	20	100.0	238	14	ABE56874
C 45	20	100.0	238	14	ABE56803
C 46	20	100.0	238	14	ABE56829 Consensus
C 47	20	100.0	238	14	ABE56774 Viral 5'
C 48	20	100.0	238	14	ABE56792 Viral 5'
C 49	20	100.0	238	14	ABE56864
C 50	20	100.0	238	14	ABE56877
C 51	20	100.0	238	14	ABE56794 Viral 5'
C 52	20	100.0	238	14	ABE56859 Human ech
C 53	20	100.0	238	14	ABE56776 Viral 5'
C 54	20	100.0	238	14	ABE56809 Viral 5'
C 55	20	100.0	238	14	ABE56831
C 56	20	100.0	238	14	ABE56808
C 57	20	100.0	238	14	ABE56882
C 58	20	100.0	238	14	ABE56804 Viral 5'
C 59	20	100.0	514	3	AAZ58487
C 60	20	100.0	628	2	AAQ58715
C 61	20	100.0	628	2	AAQ58726
C 62	20	100.0	632	13	ADP74707
C 63	20	100.0	682	13	ADU77356
C 64	20	100.0	709	14	AEA00424
C 65	20	100.0	743	14	ADM37919
C 66	20	100.0	745	8	ACC48197
C 67	20	100.0	2076	6	ABK14791
C 68	20	100.0	4148	5	AAH20890
C 69	20	100.0	5252	12	ADO07652
C 70	20	100.0	7185	12	ADP74699
C 71	20	100.0	7185	12	ADP74701
C 72	20	100.0	7235	12	ADP74714
C 73	20	100.0	7235	12	ADP74715
C 74	20	100.0	7235	12	ADP74700
C 75	20	100.0	7235	12	ADP74713
C 76	20	100.0	7392	8	ABX12440
C 77	20	100.0	7400	3	AAZ98719
C 78	20	100.0	7400	3	AAZ98717
C 79	20	100.0	7400	3	AAZ98718
C 80	20	100.0	7400	3	AAA29863
C 81	20	100.0	7421	3	AAZ98720
C 82	20	100.0	7431	2	AAQ30148
C 83	20	100.0	7432	2	AAQ22965
C 84	20	100.0	7440	1	AAH20042
C 85	20	100.0	7441	2	AAH26152
C 86	20	100.0	7873	8	ACC43138
C 87	20	100.0	7925	12	ADP74702
C 88	20	100.0	7943	8	ACC43139
C 89	20	100.0	8298	2	AAV18096
C 90	20	100.0	10448	6	ABK86535
C 91	20	100.0	10633	12	ADO07660
C 92	20	100.0	11058	6	ABK86536

C 93	20	100.0	11326	2	AAV12373	Aav12373 Chimexic	C 166	17	85.0	608	5	AAC93057	Aac93057 Human rhi
C 94	20	100.0	11746	12	ADO07659	Ado07659 Viral vec	C 167	17	85.0	610	1	AAH1398	Aan81398 Sequence
C 95	20	100.0	38246	12	ADO07662	Ado07662 Viral vec	C 168	17	85.0	627	8	ABX11923	Abx11923 Human rhi
C 96	19.6	100.0		62	ADK66744	Adk66744 Picornavi	C 169	17	85.0	627	8	ABX11971	Abx11971 Human rhi
C 97	19.6	100.0	62	14	AEC07516	Aec07516 Picornavi	C 170	17	85.0	627	10	ADB84230	Adb84230 Rhinoviru
C 98	19.2	100.0	28	8	ACD26711	Acd26711 Enterovir	C 171	17	85.0	627	10	ADA15642	Ada15642 Human rhi
C 99	19.2	100.0	28	13	ADU47464	Adu47464 p3 probe	C 172	17	85.0	627	14	ADV78854	Adv78854 Novel ant
C 100	19	95.0	70	14	ADM75017	Adm75017 Human rhi	C 173	17	85.0	627	14	ADW71616	Adw71616 Human rhi
C 101	19	95.0	238	14	AEBS6850	Aeb56850 Human cox	C 174	17	85.0	681	12	ADP82874	Adp82874 Human rhi
C 102	19	95.0	238	14	AEBS6878	Aeb56878 Human pol	C 175	17	85.0	7100	2	AAQ03360	Aaq03360 Complete
C 103	19	95.0	238	14	AEBS6797	Aeb56797 Viral 5'	C 176	17	85.0	7100	2	AAQ03418	Aaq03418 Complete
C 104	19	95.0	238	14	AEBS6851	Aeb56851 Human cox	C 177	17	85.0	7102	1	AAN60044	Aan60044 Sequence
C 105	19	95.0	238	14	AEBS6852	Aeb56852 Human cox	C 178	17	85.0	7102	1	AAN81393	Aan81393 Rhinoviru
C 106	19	95.0	238	14	AEBS6795	Aeb56795 Viral 5'	C 179	17	85.0	7227	1	AAN60194	Aan60194 Sequence
C 107	19	95.0	238	14	AEBS6796	Aeb56796 Viral 5'	C 180	16.8	84.0	41	14	ADZ76557	Adz76557 Enterovir
C 108	19	95.0	238	14	AEBS6823	Aeb56823 Viral 5'	C 181	16.8	84.0	238	14	AEBS6840	Aeb56840 Human cox
C 109	19	95.0	521	6	ABL53111	Ab153111 Micro-org	C 182	16.8	84.0	238	14	AEBS6838	Aeb56838 Human cox
C 110	19	95.0	618	1	AAN81397	Aan81397 Sequence	C 183	16.8	84.0	238	14	AEBS6785	Aeb56785 Viral 5'
C 111	19	95.0	7152	1	AAN81390	Aan81390 Sequence	C 184	16.8	84.0	238	14	AEBS6783	Aeb56783 Viral 5'
C 112	19	95.0	7152	1	AAN80153	Aan80153 Human Rhi	C 185	16.8	84.0	238	14	AEBS6833	Aeb56833 Human cox
C 113	18.4	92.0	198	14	AEBS6853	Aeb56853 Human ech	C 186	16.8	84.0	238	14	AEBS6778	Aeb56778 Viral 5'
C 114	18.4	92.0	235	14	AEBS6802	Aeb56802 Viral 5'	C 187	16.8	84.0	238	14	ADY99748	Ady99748 T. reesei
C 115	18.4	92.0	236	14	AEBS6798	Aeb56798 Viral 5'	C 188	16.8	84.0	660	4	AAC85174	Aac85174 Cxsackie
C 116	18.4	92.0	237	14	AEBS6848	Aeb56848 Human cox	C 189	16.8	84.0	660	14	AEBS6828	Aeb56828 Cxsackie
C 117	18.4	92.0	237	14	AEBS6777	Aeb56777 Viral 5'	C 190	16.8	84.0	750	2	AAQ21315	Aaq21315 DNA encod
C 118	18.4	92.0	237	14	AEBS6793	Aeb56793 Viral 5'	C 191	16.8	84.0	906	6	ABQ36770	Abq36770 Oligonucl
C 119	18.4	92.0	237	14	AEBS6857	Aeb56857 Human ech	C 192	16.8	84.0	906	6	ABQ36771	Abq36771 Oligonucl
C 120	18.4	92.0	238	14	AEBS6839	Aeb56839 Human cox	C 193	16.8	84.0	147300	12	ADP45593	Adp45593 Human Rho
C 121	18.4	92.0	238	14	AEBS6789	Aeb56789 Viral 5'	C 194	16.8	84.0	147700	14	ADX98570	Adx98570 Human gua
C 122	18.4	92.0	238	14	AEBS6775	Aeb56775 Viral 5'	C 195	16.4	82.0	47493	9	ADA02549	Ada02549 Mouse Wnt
C 123	18.4	92.0	238	14	AEBS6842	Aeb56842 Human cox	C 196	16.4	82.0	47493	10	ADB72287	Adb72287 Mouse Wnt
C 124	18.4	92.0	238	14	AEBS6832	Aeb56832 Human cox	C 197	16.4	82.0	47493	10	ADP95797	Adp95797 Mouse Wnt
C 125	18.4	92.0	238	14	AEBS6835	Aeb56835 Human cox	C 198	16.4	82.0	63079	14	ADZ12509	Adz12509 Murine ca
C 126	18.4	92.0	238	14	AEBS6780	Aeb56780 Viral 5'	C 199	16	80.0	20	10	ABZ79843	Abz79843 Exemplary
C 127	18.4	92.0	238	14	AEBS6784	Aeb56784 Viral 5'	C 200	15.8	79.0	532	12	ACH77474	Ach77474 Human gen
C 128	18.4	92.0	238	14	AEBS6843	Aeb56843 Human cox	C 201	15.8	79.0	568	4	AAH13480	Aah13480 Human CDN
C 129	18.4	92.0	238	14	AEBS6845	Aeb56845 Human cox	C 202	15.8	79.0	660	4	AAH55696	Aah55696 Human bre
C 130	18.4	92.0	238	14	AEBS6788	Aeb56788 Viral 5'	C 203	15.8	79.0	660	7	ADU01443	Adu01443 Breast ca
C 131	18.4	92.0	238	14	AEBS6786	Aeb56786 Viral 5'	C 204	15.8	79.0	660	7	ADZ41707	Adz41707 Human bre
C 132	18.4	92.0	238	14	AEBS6787	Aeb56787 Viral 5'	C 205	15.8	79.0	660	12	ADN40469	Adn40469 Human bre
C 133	18.4	92.0	238	14	AEBS6830	Aeb56830 Human cox	C 206	15.8	79.0	1530	14	ADV16700	Adv16700 E. faecal
C 134	18.4	92.0	238	14	AEBS6790	Aeb56790 Viral 5'	C 207	15.8	79.0	1560	10	ADH83192	Adh83192 Enterococ
C 135	18.4	92.0	238	14	AEBS6841	Aeb56841 Human cox	C 208	15.8	79.0	1817	2	AAT28545	Aat28545 E. faecal
C 136	18.4	92.0	238	14	AEBS6844	Aeb56844 Human cox	C 209	15.8	79.0	1817	2	ABA76825	Aba76825 Enterococ
C 137	18.4	92.0	497	8	ABX12446	Abx12446 Cxsackie	C 210	15.8	79.0	1936	13	ADT18917	Adt18917 Plant CDN
C 138	18.4	92.0	502	8	ABX12451	Abx12451 Cxsackie	C 211	15.8	79.0	2008	4	AAH16730	Aah16730 Human CDN
C 139	18.4	92.0	520	6	ABL53112	Ab153112 Micro-org	C 212	15.8	79.0	2364	4	ABL30313	Ab130313 Drosophil
C 140	18.4	92.0	556	8	ABX12449	Abx12449 Cxsackie	C 213	15.8	79.0	2378	4	AAH23696	Aah23696 Human tum
C 141	18.4	92.0	654	4	AAC85173	Aac85173 Cxsackie	C 214	15.8	79.0	4670	4	ABL30312	Ab130312 Drosophil
C 142	18.4	92.0	745	4	AAC85152	Aac85152 Cxsackie	C 215	15.8	79.0	4951	2	AAH13198	Aah13198 Enterococ
C 143	18.4	92.0	810	12	ADP82873	Adp82873 Human cox	C 216	15.8	79.0	4951	6	ABS98993	Abs98993 Enterococ
C 144	18.4	92.0	1560	13	ADU47469	Adu47469 Enterovir	C 217	15.8	79.0	13294	4	AAK85255	Aak85255 Human imm
C 145	18.4	92.0	7399	2	AAQ11816	Aaq11816 RNA encod	C 218	15.8	79.0	28906	4	AAH23705	Aah23705 Human tum
C 146	18.4	92.0	7399	10	ABV76134	Abv76134 Cxsackie	C 219	15.8	79.0	98638	12	ADQ97919	Adq97919 Mouse can
C 147	18	90.0	225734	12	ADQ93777	Adq93777 Human can	C 220	15.8	79.0	110000	11	ACN44932	1 ACN44932
C 148	18	90.0	225734	14	ADZ13617	Adz13617 Murine ca	C 221	15.8	79.0	110000	12	ADQ97960	2 ADQ97960
C 149	17.8	89.0	40	14	AEBS6771	Aeb56771 Enterovir	C 222	15.8	79.0	110000	13	ABQ32921	5 ABQ32921
C 150	17	85.0	21	14	ADY39814	Ady39814 Enterovir	C 223	15.8	79.0	137454	12	ADQ97388	ADQ97388
C 151	17	85.0	21	2	AAQ06252	Aaq06252 Probe for	C 224	15.8	79.0	175590	10	ADP50650	ADP50650
C 152	17	85.0	21	3	AAV65062	Aav65062 Enterovir	C 225	15.8	79.0	175590	14	ADV77908	Adv77908 Human BAC
C 153	17	85.0	21	3	AAH14164	Aah14164 Enterovir	C 226	15.8	79.0	204621	11	ACN44486	Acn44486 Human gen
C 154	17	85.0	21	10	ADP37351	Adp37351 Polioviru	C 227	15.8	79.0	209613	14	ADY25743	Ady25743 Uridine p
C 155	17	85.0	21	14	ADY39813	Ady39813 Polioviru	C 228	15.4	77.0	235	6	ABK12649	Abk12649 P. patens
C 156	17	85.0	21	14	ADZ68662	Adz68662 Enterovir	C 229	15.4	77.0	198	14	AEBS6865	Aeb56865 Human ech
C 157	17	85.0	25	2	AAT37522	Aat37522 Enterovir	C 230	15.4	77.0	236	14	AEBS6811	Aeb56811 Viral 5'
C 158	17	85.0	33	3	AZ59478	Aaz59478 Polioviru	C 231	15.4	77.0	236	14	AEBS6810	Aeb56810 Viral 5'
C 159	17	85.0	39	4	AA09940	Aa09940 Probe EVP	C 232	15.4	77.0	236	14	AEBS6812	Aeb56812 Viral 5'
C 160	17	85.0	40	14	AEBS6770	Aeb56770 Enterovir	C 233	15.4	77.0	238	14	AEBS6867	Aeb56867 Human ech
C 161	17	85.0	92	14	ADY39819	Ady39819 Enterovir	C 234	15.4	77.0	238	14	AEBS6866	Aeb56866 Human ech
C 162	17	85.0	117	14	AEBS6800	Aeb56800 Viral 5'	C 235	15.4	77.0	525	6	ABL53113	Ab153113 Micro-org
C 163	17	85.0	117	14	AEBS6801	Aeb56801 Viral 5'	C 236	15.4	77.0	632	6	ABQ40730	Abq40730 Oligonucl
C 164	17	85.0	173	14	AEBS6856	Aeb56856 Human ech	C 237	15.4	77.0	632	6	ABQ40731	Abq40731 Oligonucl
C 165	17	85.0	173	14	AEBS6855	Aeb56855 Human ech	C 238	15.4	77.0	646	4	AAC85153	Aac85153 Echo viru

C 239	15.4	77.0	1596	14	ADM16475	Adw16475 Eucalyptu	C 312	15.4	77.0	2690	8	ACC81149	Acc81149 Human sec
C 240	15.4	77.0	1781	10	ACC79086	Acc79086 Human sec	C 313	15.4	77.0	2690	8	ACA95473	ACA95473 Novel hum
C 241	15.4	77.0	2000	8	ADA72841	Ada72841 Rice gene	C 314	15.4	77.0	2690	8	ACA66430	ACA66430 Human cDN
C 242	15.4	77.0	2000	11	ACL317757	ACL317757 Rice stre	C 315	15.4	77.0	2690	8	ACD04391	ACD04391 Novel hum
C 243	15.4	77.0	2624	6	ABK12639	Abk12639 DNA encod	C 316	15.4	77.0	2690	8	ACC87832	ACC87832 Human sec
C 244	15.4	77.0	2690	2	AAZ234317	Aaz234317 Human PRO	C 317	15.4	77.0	2690	8	ACF12494	ACF12494 Human sec
C 245	15.4	77.0	2690	3	AAZ78588	Aaz78588 Human PRO	C 318	15.4	77.0	2690	8	ACA96209	ACA96209 Human PRO
C 246	15.4	77.0	2690	4	AAZ45942	Aaz45942 Human DNA	C 319	15.4	77.0	2690	8	ACA64983	ACA64983 Human PRO
C 247	15.4	77.0	2690	8	ACA89392	ACA89392 cDNA enco	C 320	15.4	77.0	2690	8	ACA73709	ACA73709 Human sec
C 248	15.4	77.0	2690	8	ACA73402	ACA73402 Human sec	C 321	15.4	77.0	2690	8	ACA74121	ACA74121 Novel hum
C 249	15.4	77.0	2690	8	ACA05717	ACA05717 Human sec	C 322	15.4	77.0	2690	8	ACA96516	ACA96516 Human PRO
C 250	15.4	77.0	2690	8	ACA66551	ACA66551 cDNA enco	C 323	15.4	77.0	2690	8	ACD10622	ACD10622 cDNA enco
C 251	15.4	77.0	2690	8	ACF20126	ACF20126 Human sec	C 324	15.4	77.0	2690	8	ACC91318	ACC91318 Human sec
C 252	15.4	77.0	2690	8	ACF19512	ACF19512 Human sec	C 325	15.4	77.0	2690	8	ACD02653	ACD02653 cDNA enco
C 253	15.4	77.0	2690	8	ACD21800	ACD21800 Human sec	C 326	15.4	77.0	2690	8	ACC87218	ACC87218 Human sec
C 254	15.4	77.0	2690	8	ACF12965	ACF12965 Human sec	C 327	15.4	77.0	2690	8	ACC85802	ACC85802 Human sec
C 255	15.4	77.0	2690	8	ACD25068	ACD25068 Human sec	C 328	15.4	77.0	2690	8	ACA65290	ACA65290 Human PRO
C 256	15.4	77.0	2690	8	ACF00117	ACF00117 Human sec	C 329	15.4	77.0	2690	8	ACA94107	ACA94107 Human sec
C 257	15.4	77.0	2690	8	ACA72174	ACA72174 Novel hum	C 330	15.4	77.0	2690	8	ACA97851	ACA97851 Human PRO
C 258	15.4	77.0	2690	8	ACD04698	ACD04698 Novel hum	C 331	15.4	77.0	2690	8	ACA91353	ACA91353 Novel hum
C 259	15.4	77.0	2690	8	ACD18159	ACD18159 Human sec	C 332	15.4	77.0	2690	8	ACA90567	ACA90567 Novel hum
C 260	15.4	77.0	2690	8	ACD08166	ACD08166 Human sec	C 333	15.4	77.0	2690	8	ACD16114	ACD16114 Human sec
C 261	15.4	77.0	2690	8	ACA88600	ACA88600 Novel hum	C 334	15.4	77.0	2690	8	ACD17275	ACD17275 Human sec
C 262	15.4	77.0	2690	8	ACA70042	ACA70042 Novel hum	C 335	15.4	77.0	2690	8	ACC91932	ACC91932 Human sec
C 263	15.4	77.0	2690	8	ACD12264	ACD12264 Novel hum	C 336	15.4	77.0	2690	8	ACA74789	ACA74789 cDNA enco
C 264	15.4	77.0	2690	8	ACC74179	ACC74179 Human sec	C 337	15.4	77.0	2690	8	ACA91660	ACA91660 Human PRO
C 265	15.4	77.0	2690	8	ACD15807	ACD15807 Human sec	C 338	15.4	77.0	2690	8	ACA71304	ACA71304 Human sec
C 266	15.4	77.0	2690	8	ACD25375	ACD25375 Novel hum	C 339	15.4	77.0	2690	8	ACC90704	ACC90704 Human sec
C 267	15.4	77.0	2690	8	ACD17852	ACD17852 Human sec	C 340	15.4	77.0	2690	8	ACA65714	ACA65714 cDNA enco
C 268	15.4	77.0	2690	8	ACD88139	ACD88139 Human sec	C 341	15.4	77.0	2690	8	ACA94859	ACA94859 cDNA enco
C 269	15.4	77.0	2690	8	ACD21493	ACD21493 Human sec	C 342	15.4	77.0	2690	8	ACD16421	ACD16421 Human sec
C 270	15.4	77.0	2690	8	ACD18560	ACD18560 Human sec	C 343	15.4	77.0	2690	8	ACD15500	ACD15500 Human sec
C 271	15.4	77.0	2690	8	ACA72049	ACA72049 Human sec	C 344	15.4	77.0	2690	8	ABX16603	ABX16603 Human cDN
C 272	15.4	77.0	2690	8	ACA98170	ACA98170 Human cDN	C 345	15.4	77.0	2690	8	ACA97544	ACA97544 Human PRO
C 273	15.4	77.0	2690	8	ACD13921	ACD13921 Human PRO	C 346	15.4	77.0	2690	8	ACA98993	ACA98993 Novel hum
C 274	15.4	77.0	2690	8	ACD09701	ACD09701 Human sec	C 347	15.4	77.0	2690	8	ACC91625	ACC91625 Human sec
C 275	15.4	77.0	2690	8	ACC88446	ACC88446 Human sec	C 348	15.4	77.0	2690	8	ACD11036	ACD11036 Novel hum
C 276	15.4	77.0	2690	8	ACD21186	ACD21186 Human sec	C 349	15.4	77.0	2690	8	ACD14886	ACD14886 Human sec
C 277	15.4	77.0	2690	8	ABX75558	ABX75558 Human cDN	C 350	15.4	77.0	2690	8	ACD11650	ACD11650 Human sec
C 278	15.4	77.0	2690	8	ABX92689	ABX92689 cDNA enco	C 351	15.4	77.0	2690	8	ACC95779	ACC95779 Human sec
C 279	15.4	77.0	2690	8	ABX97761	ABX97761 Human PRO	C 352	15.4	77.0	2690	8	ACF16342	ACF16342 Human sec
C 280	15.4	77.0	2690	8	ACA97237	ACA97237 Novel hum	C 353	15.4	77.0	2690	8	ACF02460	ACF02460 Human sec
C 281	15.4	77.0	2690	8	ACA57700	ACA57700 Human PRO	C 354	15.4	77.0	2690	8	ACF02767	ACF02767 Human sec
C 282	15.4	77.0	2690	8	ACA97700	ACA97700 Human PRO	C 355	15.4	77.0	2690	8	ACF21354	ACF21354 Human sec
C 283	15.4	77.0	2690	8	ACD14228	ACD14228 Human PRO	C 356	15.4	77.0	2690	8	ACF10038	ACF10038 Human sec
C 284	15.4	77.0	2690	8	ACC91011	ACC91011 Human sec	C 357	15.4	77.0	2690	8	ACF77931	ACF77931 Human sec
C 285	15.4	77.0	2690	8	ACC88753	ACC88753 Human sec	C 358	15.4	77.0	2690	8	ACD46636	ACD46636 Human sec
C 286	15.4	77.0	2690	8	ACD06950	ACD06950 Human PRO	C 359	15.4	77.0	2690	8	ACD49399	ACD49399 Human sec
C 287	15.4	77.0	2690	8	ACA67401	ACA67401 Human PRO	C 360	15.4	77.0	2690	8	ACF28166	ACF28166 Human sec
C 288	15.4	77.0	2690	8	ACC81456	ACC81456 Human sec	C 361	15.4	77.0	2690	8	ACD88856	ACD88856 Human sec
C 289	15.4	77.0	2690	8	ACC89060	ACC89060 Human sec	C 362	15.4	77.0	2690	8	ACD84251	ACD84251 Human PRO
C 290	15.4	77.0	2690	8	ACC86416	ACC86416 Human sec	C 363	15.4	77.0	2690	8	ACD99025	ACD99025 cDNA enco
C 291	15.4	77.0	2690	8	ACC89674	ACC89674 Human sec	C 364	15.4	77.0	2690	8	ADA77787	ADA77787 Human sec
C 292	15.4	77.0	2690	8	ACC92853	ACC92853 Human sec	C 365	15.4	77.0	2690	8	ACF48767	ACF48767 Human sec
C 293	15.4	77.0	2690	8	ACA72481	ACA72481 Human PRO	C 366	15.4	77.0	2690	8	ACD09087	ACD09087 Human sec
C 294	15.4	77.0	2690	8	ACA88999	ACA88999 Human PRO	C 367	15.4	77.0	2690	8	ACF11880	ACF11880 Human sec
C 295	15.4	77.0	2690	8	ACA69735	ACA69735 Human sec	C 368	15.4	77.0	2690	8	ACF41114	ACF41114 Human sec
C 296	15.4	77.0	2690	8	ACA96878	ACA96878 Novel hum	C 369	15.4	77.0	2690	8	ACF15728	ACF15728 Human sec
C 297	15.4	77.0	2690	8	ACA90874	ACA90874 Novel hum	C 370	15.4	77.0	2690	8	ACF16035	ACF16035 Human sec
C 298	15.4	77.0	2690	8	ACA70656	ACA70656 Human sec	C 371	15.4	77.0	2690	8	ACD31862	ACD31862 Human sec
C 299	15.4	77.0	2690	8	ACA95166	ACA95166 Novel hum	C 372	15.4	77.0	2690	8	ACF18670	ACF18670 Human sec
C 300	15.4	77.0	2690	8	ACC86109	ACC86109 Human sec	C 373	15.4	77.0	2690	8	ACF09117	ACF09117 Human sec
C 301	15.4	77.0	2690	8	ACC89981	ACC89981 Human sec	C 374	15.4	77.0	2690	8	ACF78238	ACF78238 Human sec
C 302	15.4	77.0	2690	8	ACD12589	ACD12589 Human sec	C 375	15.4	77.0	2690	8	ACF51837	ACF51837 Human sec
C 303	15.4	77.0	2690	8	ACF19819	ACF19819 Human sec	C 376	15.4	77.0	2690	8	ACF26324	ACF26324 Human sec
C 304	15.4	77.0	2690	8	ABX76763	ABX76763 Human PRO	C 377	15.4	77.0	2690	8	ACF24117	ACF24117 Human sec
C 305	15.4	77.0	2690	8	ACA73095	ACA73095 Novel hum	C 378	15.4	77.0	2690	8	ACF63428	ACF63428 Human sec
C 306	15.4	77.0	2690	8	ACA68638	ACA68638 Novel hum	C 379	15.4	77.0	2690	8	ACF50302	ACF50302 Human sec
C 307	15.4	77.0	2690	8	ACA74482	ACA74482 cDNA enco	C 380	15.4	77.0	2690	8	ACH07773	ACH07773 Human sec
C 308	15.4	77.0	2690	8	ACA70349	ACA70349 Human sec	C 381	15.4	77.0	2690	8	ACF13579	ACF13579 Human sec
C 309	15.4	77.0	2690	8	ACD14535	ACD14535 Human PRO	C 382	15.4	77.0	2690	8	ACD41505	ACD41505 Human sec
C 310	15.4	77.0	2690	8	ACA68207	ACA68207 Novel hum	C 383	15.4	77.0	2690	8	ACF31918	ACF31918 Human sec
C 311	15.4	77.0	2690	8	ABX98672	ABX98672 Novel hum	C 384	15.4	77.0	2690	8	ACF23196	ACF23196 Human sec

C 385	15.4	77.0	2690	9	ACF39886	Human sec
C 386	15.4	77.0	2690	9	ACD45408	Human sec
C 387	15.4	77.0	2690	9	ACF53065	Human sec
C 388	15.4	77.0	2690	9	ACF27245	Human sec
C 389	15.4	77.0	2690	9	ACF45083	Human sec
C 390	15.4	77.0	2690	9	ACF29701	Human sec
C 391	15.4	77.0	2690	9	ACD89777	Human sec
C 392	15.4	77.0	2690	9	ACD84558	Human PRO
C 393	15.4	77.0	2690	9	ACD98718	CDNA enco
C 394	15.4	77.0	2690	9	ACF77010	Human sec
C 395	15.4	77.0	2690	9	ACF76703	Human sec
C 396	15.4	77.0	2690	9	ACF49688	Human sec
C 397	15.4	77.0	2690	9	ACF49995	Human sec
C 398	15.4	77.0	2690	9	ACD09394	Human sec
C 399	15.4	77.0	2690	9	ACD08473	Human sec
C 400	15.4	77.0	2690	9	ACF12187	Human sec
C 401	15.4	77.0	2690	9	ACC94695	Human sec
C 402	15.4	77.0	2690	9	ACD22414	Human sec
C 403	15.4	77.0	2690	9	ACF15114	Human sec
C 404	15.4	77.0	2690	9	ACG97209	Human sec
C 405	15.4	77.0	2690	9	ACG92239	Human sec
C 406	15.4	77.0	2690	9	ACF13886	Human sec
C 407	15.4	77.0	2690	9	ACF14193	Human sec
C 408	15.4	77.0	2690	9	ACF09424	Human sec
C 409	15.4	77.0	2690	9	ACD45715	Human sec
C 410	15.4	77.0	2690	9	ACD47864	Human sec
C 411	15.4	77.0	2690	9	ACD67595	CDNA enco
C 412	15.4	77.0	2690	9	ACF23403	Human sec
C 413	15.4	77.0	2690	9	ACF29087	Human sec
C 414	15.4	77.0	2690	9	ACD84865	Human sec
C 415	15.4	77.0	2690	9	ACD83944	Human PRO
C 416	15.4	77.0	2690	9	ACD87935	Human sec
C 417	15.4	77.0	2690	9	ACF30622	Human sec
C 418	15.4	77.0	2690	9	ACF32225	Human sec
C 419	15.4	77.0	2690	9	ACH11885	CDNA enco
C 420	15.4	77.0	2690	9	ACH12192	CDNA enco
C 421	15.4	77.0	2690	9	ACD40584	Human sec
C 422	15.4	77.0	2690	9	ACF18056	Human sec
C 423	15.4	77.0	2690	9	ACF08503	Human sec
C 424	15.4	77.0	2690	9	ACF31304	Human sec
C 425	15.4	77.0	2690	9	ACF52144	Human sec
C 426	15.4	77.0	2690	9	ACD50013	Human sec
C 427	15.4	77.0	2690	9	ACF38716	Human sec
C 428	15.4	77.0	2690	9	ACF26631	Human sec
C 429	15.4	77.0	2690	9	ACF24731	Human sec
C 430	15.4	77.0	2690	9	ACF46311	Human sec
C 431	15.4	77.0	2690	9	ACF27859	Human sec
C 432	15.4	77.0	2690	9	ACD89163	Human sec
C 433	15.4	77.0	2690	9	ACF63735	Human sec
C 434	15.4	77.0	2690	9	ACF60375	Human sec
C 435	15.4	77.0	2690	9	ACH12499	CDNA enco
C 436	15.4	77.0	2690	9	ACH09922	Human sec
C 437	15.4	77.0	2690	9	ACD03777	Human sec
C 438	15.4	77.0	2690	9	ACD10315	Human sec
C 439	15.4	77.0	2690	9	ACD11957	Human sec
C 440	15.4	77.0	2690	9	ACF42342	Human sec
C 441	15.4	77.0	2690	9	ACF18363	Human sec
C 442	15.4	77.0	2690	9	ACF02153	Human sec
C 443	15.4	77.0	2690	9	ACF21661	Human sec
C 444	15.4	77.0	2690	9	ACF10345	Human sec
C 445	15.4	77.0	2690	9	ACF33797	Human sec
C 446	15.4	77.0	2690	9	ACF44759	Human sec
C 447	15.4	77.0	2690	9	ACD90391	Human sec
C 448	15.4	77.0	2690	9	ACD91004	Human sec
C 449	15.4	77.0	2690	9	ACF30315	Human sec
C 450	15.4	77.0	2690	9	ACD87014	Human sec
C 451	15.4	77.0	2690	9	ACF60068	Human sec
C 452	15.4	77.0	2690	9	ACF46618	Human sec
C 453	15.4	77.0	2690	9	ACF75475	Human sec
C 454	15.4	77.0	2690	9	ADA79579	Human sec
C 455	15.4	77.0	2690	9	ADA25053	Novel hum
C 456	15.4	77.0	2690	9	ACF17135	Human sec
C 457	15.4	77.0	2690	9	ACF22889	Human sec
C 458	15.4	77.0	2690	9	ACF39886	Human sec
C 459	15.4	77.0	2690	9	ACD45408	Human sec
C 460	15.4	77.0	2690	9	ACF53065	Human sec
C 461	15.4	77.0	2690	9	ACF27245	Human sec
C 462	15.4	77.0	2690	9	ACF45083	Human sec
C 463	15.4	77.0	2690	9	ACF29701	Human sec
C 464	15.4	77.0	2690	9	ACD89777	Human sec
C 465	15.4	77.0	2690	9	ACD84558	Human PRO
C 466	15.4	77.0	2690	9	ACD98718	CDNA enco
C 467	15.4	77.0	2690	9	ACF77010	Human sec
C 468	15.4	77.0	2690	9	ACF76703	Human sec
C 469	15.4	77.0	2690	9	ACF49688	Human sec
C 470	15.4	77.0	2690	9	ACF49995	Human sec
C 471	15.4	77.0	2690	9	ACD09394	Human sec
C 472	15.4	77.0	2690	9	ACD08473	Human sec
C 473	15.4	77.0	2690	9	ACF12187	Human sec
C 474	15.4	77.0	2690	9	ACC94695	Human sec
C 475	15.4	77.0	2690	9	ACD22414	Human sec
C 476	15.4	77.0	2690	9	ACF15114	Human sec
C 477	15.4	77.0	2690	9	ACG97209	Human sec
C 478	15.4	77.0	2690	9	ACG92239	Human sec
C 479	15.4	77.0	2690	9	ACF13886	Human sec
C 480	15.4	77.0	2690	9	ACF14193	Human sec
C 481	15.4	77.0	2690	9	ACF09424	Human sec
C 482	15.4	77.0	2690	9	ACD45715	Human sec
C 483	15.4	77.0	2690	9	ACD47864	Human sec
C 484	15.4	77.0	2690	9	ACD67595	CDNA enco
C 485	15.4	77.0	2690	9	ACF23403	Human sec
C 486	15.4	77.0	2690	9	ACF29087	Human sec
C 487	15.4	77.0	2690	9	ACD84865	Human sec
C 488	15.4	77.0	2690	9	ACD83944	Human PRO
C 489	15.4	77.0	2690	9	ACD87935	Human sec
C 490	15.4	77.0	2690	9	ACF30622	Human sec
C 491	15.4	77.0	2690	9	ACF32225	Human sec
C 492	15.4	77.0	2690	9	ACH11885	CDNA enco
C 493	15.4	77.0	2690	9	ACH12192	CDNA enco
C 494	15.4	77.0	2690	9	ACD40584	Human sec
C 495	15.4	77.0	2690	9	ACF18056	Human sec
C 496	15.4	77.0	2690	9	ACF08503	Human sec
C 497	15.4	77.0	2690	9	ACF31304	Human sec
C 498	15.4	77.0	2690	9	ACF52144	Human sec
C 499	15.4	77.0	2690	9	ACD50013	Human sec
C 500	15.4	77.0	2690	9	ACF38716	Human sec
C 501	15.4	77.0	2690	9	ACF26631	Human sec
C 502	15.4	77.0	2690	9	ACF24731	Human sec
C 503	15.4	77.0	2690	9	ACF46311	Human sec
C 504	15.4	77.0	2690	9	ACF27859	Human sec
C 505	15.4	77.0	2690	9	ACD89163	Human sec
C 506	15.4	77.0	2690	9	ACF63735	Human sec
C 507	15.4	77.0	2690	9	ACF60375	Human sec
C 508	15.4	77.0	2690	9	ACH12499	CDNA enco
C 509	15.4	77.0	2690	9	ACH09922	Human sec
C 510	15.4	77.0	2690	9	ACD03777	Human sec
C 511	15.4	77.0	2690	9	ACD10315	Human sec
C 512	15.4	77.0	2690	9	ACD11957	Human sec
C 513	15.4	77.0	2690	9	ACF42342	Human sec
C 514	15.4	77.0	2690	9	ACF18363	Human sec
C 515	15.4	77.0	2690	9	ACF02153	Human sec
C 516	15.4	77.0	2690	9	ACF21661	Human sec
C 517	15.4	77.0	2690	9	ACF10345	Human sec
C 518	15.4	77.0	2690	9	ACF33797	Human sec
C 519	15.4	77.0	2690	9	ACF44759	Human sec
C 520	15.4	77.0	2690	9	ACD90391	Human sec
C 521	15.4	77.0	2690	9	ACD91004	Human sec
C 522	15.4	77.0	2690	9	ACF30315	Human sec
C 523	15.4	77.0	2690	9	ACD87014	Human sec
C 524	15.4	77.0	2690	9	ACF60068	Human sec
C 525	15.4	77.0	2690	9	ACF46618	Human sec
C 526	15.4	77.0	2690	9	ACF75475	Human sec
C 527	15.4	77.0	2690	9	ADA79579	Human sec
C 528	15.4	77.0	2690	9	ADA25053	Novel hum
C 529	15.4	77.0	2690	9	ACF17135	Human sec
C 530	15.4	77.0	2690	9	ACF22889	Human sec
C 531	15.4	77.0	2690	9	ACF39886	Human sec
C 532	15.4	77.0	2690	9	ACD45408	Human sec
C 533	15.4	77.0	2690	9	ACF53065	Human sec
C 534	15.4	77.0	2690	9	ACF27245	Human sec
C 535	15.4	77.0	2690	9	ACF45083	Human sec
C 536	15.4	77.0	2690	9	ACF29701	Human sec
C 537	15.4	77.0	2690	9	ACD89777	Human sec
C 538	15.4	77.0	2690	9	ACD84558	Human PRO
C 539	15.4	77.0	2690	9	ACD98718	CDNA enco
C 540	15.4	77.0	2690	9	ACF77010	Human sec
C 541	15.4	77.0	2690	9	ACF76703	Human sec
C 542	15.4	77.0	2690	9	ACF49688	Human sec
C 543	15.4	77.0	2690	9	ACF49995	Human sec
C 544	15.4	77.0	2690	9	ACD09394	Human sec
C 545	15.4	77.0	2690	9	ACD08473	Human sec
C 546	15.4	77.0	2690	9	ACF12187	Human sec
C 547	15.4	77.0	2690	9	ACC94695	Human sec
C 548	15.4	77.0	2690	9	ACD22414	Human sec
C 549	15.4	77.0	2690	9	ACF15114	Human sec
C 550	15.4	77.0	2690	9	ACG97209	Human sec
C 551	15.4	77.0	2690	9	ACG92239	Human sec
C 552	15.4	77.0	2690	9	ACF13886	Human sec
C 553	15.4	77.0	2690	9	ACF14193	Human sec
C 554	15.4	77.0	2690	9	ACF09424	Human sec
C 555	15.4	77.0	2690	9	ACD45715	Human sec
C 556	15.4	77.0	2690	9	ACD47864	Human sec
C 557	15.4	77.0	2690	9	ACD67595	CDNA enco
C 558	15.4	77.0	2690	9	ACF23403	Human sec
C 559	15.4	77.0	2690	9	ACF29087	Human sec
C 560	15.4	77.0	2690	9	ACD84865	Human sec
C 561	15.4	77.0	2690	9	ACD83944	Human PRO
C 562	15.4	77.0	2690	9	ACD87935	Human sec
C 563	15.4	77.0	2690	9	ACF30622	Human sec
C 564	15.4	77.0	2690	9	ACF32225	Human sec
C 565	15.4	77.0	2690	9	ACH11885	CDNA enco
C 566	15.4	77.0	2690	9	ACH12192	CDNA enco
C 567	15.4	77.0	2690	9	ACD40584	Human sec
C 568	15.4	77.0	2690	9	ACF18056	Human sec
C 569	15.4	77.0	2690	9	ACF08503	Human sec
C 570	15.4	77.0	2690	9	ACF31304	Human sec
C 571	15.4	77.0	2690	9	ACF52144	Human sec
C 572	15.4	77.0	2690	9	ACD50013	Human sec
C 573	15.4	77.0	2690	9	ACF38716	

XX TSANG S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; S76769.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of ABB56764  
 CC to ABB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 20; DB 14; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 9.9;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 100 AAGGAACACGGACACCCAA 81

RESULT 2  
 ABB56868/c  
 ID ABB56868 standard; DNA; 106 BP.  
 AC ABB56868;  
 XX 22-SEP-2005 (first entry)  
 DT Human echovirus 30 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 KW Human echovirus 30.  
 OS US2005158710-A1.  
 PN 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 PR (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; S76768.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX

PS Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of ABB56764  
 CC to ABB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 106 BP; 21 A; 26 C; 27 G; 32 T; 0 U; 0 Other;  
 SQ

Query Match 100.0%; Score 20; DB 14; Length 106;  
 Best Local Similarity 100.0%; Pred. No. 9.9;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 101 AAGGAACACGGACACCCAA 82

RESULT 3  
 ABB56814/c  
 ID ABB56814 standard; DNA; 107 BP.  
 XX ABB56814;  
 AC ABB56814;  
 XX 22-SEP-2005 (first entry)  
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.  
 DE DNA detection; enteroviral detection; ds.  
 KW DNA detection; enteroviral detection; ds.  
 OS Unidentified.  
 XX US2005158710-A1.  
 PN 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 PR (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 53; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of ABB56764  
 CC to ABB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX

CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 9.9;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 102 AAGGAAACACGGACACCCAA 83  
 |||||

RESULT 4  
 AEB56813/c  
 ID AEB56813 standard; DNA; 110 BP.  
 XX AC AEB56813;  
 XX  
 XX 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:52.  
 XX  
 XX DNA detection; enteroviral detection; ds.  
 XX Unidentified.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 52; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 110 BP; 21 A; 28 C; 29 G; 32 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 110;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 105 AAGGAAACACGGACACCCAA 86  
 |||||

RESULT 5  
 AEB56779/c  
 ID AEB56779 standard; DNA; 126 BP.  
 XX AC AEB56779;  
 XX  
 XX 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.  
 XX  
 XX DNA detection; enteroviral detection; ds.  
 XX Unidentified.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 18; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 105 AAGGAAACACGGACACCCAA 86  
 |||||



RESULT 6  
 AA258488/c  
 ID AA258488 standard; RNA; 176 BP.  
 XX AC  
 XX AA258488;  
 XX 15-SEP-2003 (revised)  
 XX 23-MAY-2000 (first entry)  
 XX  
 DE Recombinant poliovirus PVI (pr) IRES domain V-VI region.  
 XX  
 KW Internal ribosomal entry site; IRES; picornavirus; PVI (pr); tumour;  
 KW cancer; glioblastoma multiforme; medulloblastoma; mammary carcinoma;  
 KW prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;  
 KW bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.  
 XX OS  
 OS Human poliovirus 1.  
 OS Human rhinovirus sp; type 2.  
 OS Chimeric.  
 XX  
 FH Key Location/Qualifiers  
 FT stem\_loop . 1..109  
 FT /\*tag= a  
 FT /\*note= "domain V"  
 FT 138..176  
 FT /\*tag= b  
 FT /\*note= "domain VI"  
 FT  
 FN WO200008166-A1.  
 XX  
 XX 17-FEB-2000.  
 XX  
 XX 09-APR-1999; 99WO-US007839.  
 XX  
 XX 05-AUG-1998; 98US-00129686.  
 XX  
 XX (UUNY ) UNIV NEW YORK STATE RES FOUND.  
 XX  
 XX Gromeier M, Wimmer E;  
 XX  
 XX WPI; 2000-205717/18.  
 XX  
 XX Chimeric recombinant poliovirus useful for treating malignant tumors  
 XX comprises internal ribosomal entry site derived from picornaviruses.  
 XX  
 XX Example 6; Fig 7; 99pp; English.  
 XX  
 XX This sequence represents domains V-VI of the internal ribosomal entry  
 XX site (IRES) of PVI (pr), a recombinant, non-pathogenic oncolytic  
 XX poliovirus that carries the IRES of poliovirus type 1 Mahoney where the  
 XX terminal loop of regions of domain V and domain VI are substituted with  
 XX the corresponding fragments of human rhinovirus type 2 (HRV2). PVI (pr)  
 XX was characterized by a loss of neurovirulence, demonstrated by its  
 XX reduced ability to propagate within cells of neuronal origin and failure  
 XX to cause neurological disease in C155 tg mice. Oncolytic potential was  
 XX demonstrated against a panel of malignant cell lines. PVI (pr) is an  
 XX example of novel recombinant polioviruses (I) of the invention in which  
 XX the IRES of wild-type poliovirus is exchanged with the IRES of another  
 XX picornavirus, such as HRV2, and optionally the P1, P3 or 3' untranslated  
 XX region is exchanged with that of Sabin poliovirus. (I) are useful for  
 XX treating malignant tumors such as glioblastoma multiforme,  
 XX medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial  
 XX and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to  
 XX standardise OS field)  
 XX  
 XX Sequence 176 BP; 42 A; 43 C; 40 G; 0 T; 51 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 3; Length 176;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 |||||||||||||||||||

Db 118 AAGGAACACGGACACCCAA 99  
 RESULT 7  
 AEB56834/c  
 ID AEB56834 standard; DNA; 180 BP.  
 XX AC  
 XX AEB56834;  
 XX 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B1 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B1.  
 XX  
 XX US2005158710-A1.  
 XX  
 XX 21-JUL-2005.  
 XX  
 XX 16-JAN-2004; 2004US-00760048.  
 XX  
 XX 16-JAN-2004; 2004US-00760048.  
 XX  
 XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX  
 XX WPI; 2005-512251/52.  
 XX  
 XX GENBANK; S76767.  
 XX  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX target binding sequence of an oligonucleotide chosen from any one of the  
 XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 XX selected amplification or detection reaction. Also described: (1) a kit  
 XX (K1) comprising (I), and one or more container that contains (I); and (2)  
 XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 XX the target sequence using first amplification primer having a sequence  
 XX consisting essentially of target binding sequence of any one of AEB56764  
 XX to AEB56771 and optionally a sequence required for selected amplification  
 XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 XX (K1) are useful for detecting enterovirus target sequences. (I)  
 XX specifically and selectively recognizes the enterovirus genome. (I)  
 XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
 XX genome and allows detection of broad range of enterovirus serotypes. The  
 XX present sequence represents a viral 5' untranslated polynucleotide  
 XX sequence given in the exemplification of the present invention.  
 XX  
 XX Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 20; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 |||||||||||||||||||  
 Db 159 AAGGAACACGGACACCCAA 140  
 RESULT 8  
 ABZ69931/c  
 ID ABZ69931 standard; DNA; 195 BP.  
 XX AC  
 XX ABZ69931;  
 XX

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DT 04-APR-2003 (first entry)
XX Poliovirus type 3 sequence.
DE Analysis; detection; quantification; ss.
XX Poliovirus.
XX FR2824001-A1.
XX 31-OCT-2002.
XX 26-APR-2001; 2001FR-00005639.
XX 26-APR-2001; 2001FR-00005639.
XX (INMR ) BIO MERIEUX.
XX Perrin A, Theretz A, Delair T, Mandrand B;
XX WPI; 2003-186349/19.
XX Preparing a spot on a substrate surface, the sample is contained within a
XX liquid with magnetic particles to be deposited as a droplet, to be dried
XX together with a magnetic field to distribute the particles/molecules
XX evenly in the spot.
XX Example 3; Page 17; 26pp; French.
XX The present invention relates to a method for depositing a spot on a
XX substrate, containing a sample for study, comprising preparing the sample
XX in a liquid vehicle together with a magnetic support, to be deposited on
XX the surface of a substrate as a droplet. The sample bonds to the magnetic
XX support as particles. The sample material for analysis/ detection/
XX quantification can be cells, organisms, viruses and bacteria, antibodies,
XX antibody fragments, antigens, haptens, lectins, sugars, RNA and DNA,
XX proteins, hormones, hormone receptors, natural or synthetic molecules and
XX macro molecules, and the like. The present oligonucleotide from
XX Poliovirus type 3 was used in an example from the invention
XX SQ Sequence 195 BP; 42 A; 51 C; 50 G; 52 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 10; Length 195;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 122 AAGGAAACACGGACACCCAA 103
RESULT 9
AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX AC AEB56860;
XX 22-SEP-2005 (first entry)
XX Human echovirus 9 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 9.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11709.
XX
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PA (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11710.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 198;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGGACACCCAA 20
Db 121 AAGGAAACACGGACACCCAA 102
RESULT 10
AEB56858/c
ID AEB56858 standard; DNA; 198 BP.
XX AC AEB56858;
XX 22-SEP-2005 (first entry)
XX Human echovirus 6 5' untranslated polynucleotide sequence.
XX DNA detection; enteroviral detection; ds.
XX Human echovirus 6.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11709.
XX
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PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771; and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 198 BP; 37 A; 47 C; 55 G; 59 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGACACCCAA 20  
 |||||  
 DB 121 AAGGAACACGACACCCAA 102

RESULT 11

AEBS6863/c  
 ID AEB56863 standard; DNA; 198 BP.

XX AC AEB56863;

XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 11 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 11.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.  
 XX PR (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.  
 XX DR GENBANK; U11705.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771; and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;

Best Local Similarity 100.0%; Pred. No. 10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGACACCCAA 20  
 |||||  
 DB 121 AAGGAACACGACACCCAA 102

RESULT 12

AEBS6854/c

ID AEB56854 standard; DNA; 198 BP.

XX AC AEB56854;

XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 4 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human echovirus 4.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.  
 XX PR (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.  
 XX DR GENBANK; U11708.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771; and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 198 BP; 43 A; 48 C; 50 G; 57 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 10;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 121 AAGGAACACGGACACCCAA 102

## RESULT 13

AEBS6816/c  
 ID AEB56816 standard; DNA; 236 BP.

XX AC AEB56816;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:55.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX FA (PRIC/) PRICE J A.

XX FA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 55; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 236 BP; 59 A; 51 C; 46 G; 80 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 100.0%; Score 20; DB 14; Length 236;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 105 AAGGAACACGGACACCCAA 86

## RESULT 14

AEBS6837/c

ID AEB56837 standard; DNA; 237 BP.

XX AC AEB56837;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B2 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B2.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX DR GENBANK; AF081485.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 237 BP; 46 A; 54 C; 66 G; 71 T; 0 U; 0 Other;

## Query Match

Best Local Similarity 100.0%; Score 20; DB 14; Length 237;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 |||||  
 Db 161 AAGGAACACGGACACCCAA 142

## RESULT 15

AEBS6862/c

ID AEB56862 standard; DNA; 237 BP.

XX



PA (TSAN//) TSANG S.  
PA (PRIC//) PRICE J A.  
PA (HELL//) HELLYER T J.  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
DR GENBANK; X00925.  
DR  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; Fig 1A-D; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 237 BP; 54 A; 56 C; 65 G; 62 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AAGGAACACGGACACCCAA 20  
DB 161 AAGGAACACGGACACCCAA 142  
  
RESULT 18  
AEB56827/C  
ID AEB56827 standard; DNA; 237 BP.  
XX  
AC AEB56827;  
XX  
XX 22-SEP-2005 (first entry)  
XX  
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:66.  
XX  
XX DNA detection; enteroviral detection; ds.  
XX  
XX Unidentified.  
XX  
XX US2005158710-A1.  
XX  
XX 21-JUL-2005.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX (TSAN//) TSANG S.  
XX (PRIC//) PRICE J A.  
XX (HELL//) HELLYER T J.  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; SEQ ID NO 66; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AAGGAACACGGACACCCAA 20  
DB 105 AAGGAACACGGACACCCAA 86  
  
RESULT 19  
AEB56875/C  
ID AEB56875 standard; DNA; 237 BP.  
XX  
AC AEB56875;  
XX  
XX 22-SEP-2005 (first entry)  
XX  
XX Human poliovirus 1 5' untranslated polynucleotide sequence.  
XX  
XX DNA detection; enteroviral detection; ds.  
XX  
XX Human poliovirus 1.  
XX  
XX US2005158710-A1.  
XX  
XX 21-JUL-2005.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX (TSAN//) TSANG S.  
XX (PRIC//) PRICE J A.  
XX (HELL//) HELLYER T J.  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX GENBANK; V01149.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; Fig 1A-D; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 237 BP; 54 A; 56 C; 65 G; 62 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 20; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 AAGGAACACGGACACCCAA 20  
DB 161 AAGGAACACGGACACCCAA 142  
  
RESULT 18  
AEB56827/C  
ID AEB56827 standard; DNA; 237 BP.  
XX  
AC AEB56827;  
XX  
XX 22-SEP-2005 (first entry)  
XX  
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:66.  
XX  
XX DNA detection; enteroviral detection; ds.  
XX  
XX Unidentified.  
XX  
XX US2005158710-A1.  
XX  
XX 21-JUL-2005.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX 16-JAN-2004; 2004US-00760048.  
XX  
XX (TSAN//) TSANG S.  
XX (PRIC//) PRICE J A.  
XX (HELL//) HELLYER T J.  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 57 A; 54 C; 62 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
 |||||  
 DB 161 AAGGAACACGACACCCAA 142

RESULT 20  
 AEB56876/c  
 ID AEB56876 standard; DNA; 237 BP.  
 XX  
 AC AEB56876;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human poliovirus 1 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human poliovirus 1.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.

16-JAN-2004; 2004US-00760048.  
 16-JAN-2004; 2004US-00760048.  
 (TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.

TSang S, Price JA, Hellyer TJ;  
 WPI; 2005-512251/52.  
 GENBANK; V01150.

Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 56 A; 54 C; 63 G; 64 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
 |||||  
 DB 161 AAGGAACACGACACCCAA 142

RESULT 21  
 AEB56880/c  
 ID AEB56880 standard; DNA; 237 BP.

XX  
 AC AEB56880;  
 XX  
 DT 22-SEP-2005 (first entry)

XX Human poliovirus 3 5' untranslated polynucleotide sequence.  
 XX DNA detection; enteroviral detection; ds.  
 XX Human poliovirus 3.

OS US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.

16-JAN-2004; 2004US-00760048.  
 (TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.

TSang S, Price JA, Hellyer TJ;  
 WPI; 2005-512251/52.  
 GENBANK; X00596.

Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 237 BP; 55 A; 56 C; 65 G; 61 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
|||||  
Db 161 AAGGAACACGGACACCCAA 142

RESULT 22  
AEB56825/c  
ID AEB56825 standard; DNA; 237 BP.

XX AEB56825;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:64.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 64; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (I), and one or more container that contains (I); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
XX specifically and selectively recognizes the enterovirus genome. (I)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The  
XX present sequence represents a viral 5' untranslated polynucleotide  
XX sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 53 A; 58 C; 55 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 105 AAGGAACACGGACACCCAA 86

RESULT 23

AEB56805/c

ID AEB56805 standard; DNA; 237 BP.

XX AEB56805;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:44.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 44; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (I), and one or more container that contains (I); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
XX specifically and selectively recognizes the enterovirus genome. (I)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The  
XX present sequence represents a viral 5' untranslated polynucleotide  
XX sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20

Db 105 AAGGAACACGGACACCCAA 86

RESULT 24

AEB56818/c

ID AEB56818 standard; DNA; 237 BP.

XX AEB56818;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:57.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.



```
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PP 16-JAN-2004; 2004US-00760048.
XX PR (TSAN//) TSANG S.
XX PA (PRIC//) PRICE J A.
XX PA (HELL//) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX PP WPI; 2005-512251/52.
XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 57; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 237 BP; 50 A; 55 C; 59 G; 73 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAGGAACACGACACCCAA 20
Db 105 AAGGAACACGACACCCAA 86
RESULT 25
AEB56873/c
ID AEB56873 standard; DNA; 237 BP.
XX AC AEB56873;
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 1 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human poliovirus 1.
XX FN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN//) TSANG S.
XX PA (PRIC//) PRICE J A.
XX PA (HELL//) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX PP WPI; 2005-512251/52.
XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 57; 34pp; English.
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX SQ Sequence 237 BP; 50 A; 55 C; 59 G; 73 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 AAGGAACACGACACCCAA 20
Db 105 AAGGAACACGACACCCAA 86
RESULT 26
AEB56806/c
ID AEB56806 standard; DNA; 237 BP.
XX AC AEB56806;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:45.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX FN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN//) TSANG S.
XX PA (PRIC//) PRICE J A.
XX PA (HELL//) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX PP WPI; 2005-512251/52.
XX DR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 45; 34pp; English.
```

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 54 A; 53 C; 56 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 105 AAGGAACACGACACCCAA 86

RESULT 27  
 AEB56861/c  
 ID AEB56861 standard; DNA; 237 BP.  
 AC AEB56861;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human echovirus 9 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human echovirus 9.  
 XX  
 FN US2005158710-A1.  
 XX  
 XX 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.  
 XX  
 PI Teang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; X84981.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 CC

CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 160 AAGGAACACGACACCCAA 141

RESULT 28  
 AEB56817/c  
 ID AEB56817 standard; DNA; 237 BP.  
 AC AEB56817;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:56.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 FN US2005158710-A1.  
 XX  
 XX 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.  
 XX  
 PI Teang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; SEQ ID NO 56; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 52 A; 56 C; 58 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
 DB 105 AAGGAACACGACACCCAA 86

RESULT 29  
 AEB56820/c  
 ID AEB56820 standard; DNA; 237 BP.  
 AC AEB56820;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:59.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 OS US2005158710-A1.  
 PN  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 XX WPI; 2005-512251/52.  
 DR  
 DR GENBANK; D00820.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 PS Disclosure; SEQ ID NO 59; 34pp; English.  
 XX  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 XX Sequence 237 BP; 50 A; 53 C; 60 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
 DB 105 AAGGAACACGACACCCAA 86

RESULT 30  
 AEB56871/c  
 ID AEB56871 standard; DNA; 237 BP.  
 XX  
 AC AEB56871;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human enterovirus 70 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human enterovirus 70.  
 XX  
 XX US2005158710-A1.  
 PN  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 XX WPI; 2005-512251/52.  
 DR  
 DR GENBANK; D00820.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 XX Sequence 237 BP; 54 A; 52 C; 60 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
 DB 161 AAGGAACACGACACCCAA 142

RESULT 31  
 AEB56821/c  
 ID AEB56821 standard; DNA; 237 BP.  
 XX  
 AC AEB56821;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:60.

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XX DNA detection; enteroviral detection; ds.
XX Unidentified.
XX US2005158710-A1.
XX 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 60; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 237 BP; 49 A; 51 C; 61 G; 76 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCAA 20
Db |||||
105 AAGGAACACGGACACCCAA 86
RESULT 32
AEB56872/c
ID AEB56872 standard; DNA; 237 BP.
XX AC AEB56872;
XX DT 22-SEP-2005 (first entry)
XX DE Human poliovirus 1 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human poliovirus 1.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX DNA detection; enteroviral detection; ds.
XX Human poliovirus 1.
XX OS US2005158710-A1.
XX PN 21-JUL-2005.
XX PD 16-JAN-2004; 2004US-00760048.
XX PF
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XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I), (M1) and
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 237 BP; 54 A; 56 C; 64 G; 63 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 14; Length 237;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AAGGAACACGGACACCCAA 20
Db |||||
161 AAGGAACACGGACACCCAA 142
RESULT 33
AEB56782/c
ID AEB56782 standard; DNA; 237 BP.
XX AC AEB56782;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:21.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX 16-JAN-2004; 2004US-00760048.
XX 16-JAN-2004; 2004US-00760048.
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX Tsang S, Price JA, Hellyer TJ;
XX
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DR WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 21; 34pp; English.

PS

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence, involving: (a) amplifying

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I) and (2)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 46 A; 52 C; 61 G; 78 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 34

AEB56824/C

ID AEB56824 standard; DNA; 237 BP.

XX AC AEB56824;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:63.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 63; 34pp; English.

PS

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence, involving: (a) amplifying

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I) and (2)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 46 A; 52 C; 61 G; 78 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 35

AEB56791/C

ID AEB56791 standard; DNA; 238 BP.

XX AC AEB56791;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:30.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 30; 34pp; English.

PS

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence, involving: (a) amplifying

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I) and (2)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 53 A; 59 C; 55 G; 70 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

RESULT 35

AEB56791/C

ID AEB56791 standard; DNA; 238 BP.

XX AC AEB56791;

XX 22-SEP-2005 (first entry)

XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:30.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 30; 34pp; English.

PS

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence, involving: (a) amplifying

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I) and (2)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX Sequence 237 BP; 53 A; 59 C; 55 G; 70 T; 0 U; 0 Other;

SQ

Query Match 100.0%; Score 20; DB 14; Length 237;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAGGAACACGGACACCCAA 20

DB 105 AAGGAACACGGACACCCAA 86

CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX  
SQ Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
|||||  
Db 105 AAGGAACACGGACACCCAA 86

RESULT 36  
AEB56826/c  
ID AEB56826 standard; DNA; 238 BP.

XX AC AEB56826;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:65.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 65; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 56 A; 52 C; 55 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
|||||  
Db 105 AAGGAACACGGACACCCAA 86

RESULT 37

AEB56849/c

ID AEB56849 standard; DNA; 238 BP.

XX AC AEB56849;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B5 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B5.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Teang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; X67706.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
|||||  
Db 161 AAGGAACACGGACACCCAA 142

RESULT 38

AEB56846/c

ID AEB56846 standard; DNA; 238 BP.

XX

```

AC AEB56846;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human coxsackievirus B4.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
XX (PRIC/) PRICE J A.
XX (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
XX GENBANK; D00149.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 1 AAGGAACACGGACACCCAA 20
XX |||||
XX Db 161 AAGGAACACGGACACCCAA 142
XX
XX RESULT 39
XX AEB56847/c
XX ID AEB56847 standard; DNA; 238 BP.
XX
XX AC AEB56847;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus B4 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Human coxsackievirus B4.
XX
XX RESULT 40
XX AEB56819/c
XX ID AEB56819 standard; DNA; 238 BP.
XX
XX AC AEB56819;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:58.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX

```





CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX  
SQ Sequence 238 BP; 55 A; 51 C; 56 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
DB 105 AAGGAACACGACACCCAA 86  
|||||

RESULT 43  
AEB56799/c  
ID AEB56799 standard; DNA; 238 BP.

XX AC AEB56799;

DT 22-SEP-2005 (first entry)

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:38.

KW DNA detection; enteroviral detection; ds.

XX Unidentified.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; SEQ ID NO 38; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX

SQ Sequence 238 BP; 57 A; 50 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
DB 105 AAGGAACACGACACCCAA 86  
|||||

RESULT 44  
AEB56874/c  
ID AEB56874 standard; DNA; 238 BP.

XX AC AEB56874;

DT 22-SEP-2005 (first entry)

XX Human poliovirus 1 5' untranslated polynucleotide sequence.

KW DNA detection; enteroviral detection; ds.

XX Human poliovirus 1.

PN US2005158710-A1.

PD 21-JUL-2005.

PF 16-JAN-2004; 2004US-00760048.

PR 16-JAN-2004; 2004US-00760048.

PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; V01148.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.

PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
DB 162 AAGGAACACGACACCCAA 143  
|||||

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RESULT 45
AEB56803/c
ID AEB56803 standard; DNA; 238 BP.
XX
XX AC AEB56803;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:42.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX PA (TSAN/) TSANG S.
XX
XX PA (PRIC/) PRICE J A.
XX
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 42; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 49 A; 52 C; 60 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB |||||||||||||||||||

RESULT 46
AEB56829/c
ID AEB56829 standard; DNA; 238 BP.
XX
XX AC AEB56829;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
XX PF 16-JAN-2004; 2004US-00760048.
XX
XX PR 16-JAN-2004; 2004US-00760048.
XX
XX PA (TSAN/) TSANG S.
XX
XX PA (PRIC/) PRICE J A.
XX
XX PA (HELL/) HELLYER T J.
XX
XX PI Tsang S, Price JA, Hellyer TJ;
XX
XX WPI; 2005-512251/52.
XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX
XX PS Disclosure; SEQ ID NO 42; 34pp; English.
XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (KI) comprising (I), and one or more container that contains (I); and (2)
XX detecting (MI) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (KI) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX
XX SQ Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20
DB |||||||||||||||||||

RESULT 47
AEB56774/c
ID AEB56774 standard; DNA; 238 BP.
XX
XX AC AEB56774;
XX
XX DT 22-SEP-2005 (first entry)
XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.
XX
XX KW DNA detection; enteroviral detection; ds.
XX
XX OS Unidentified.
XX
XX PN US2005158710-A1.
XX
XX PD 21-JUL-2005.
XX
```

XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.  
 XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX DR WPI; 2005-512251/52.  
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; SEQ ID NO 13; 34pp; English.  
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 Db ||||||||||||||||  
 105 AAGGAACACGGACACCCAA 86  
 RESULT 48  
 AEB56792/c  
 ID AEB56792 standard; DNA; 238 BP.  
 AC AEB56792;  
 XX 22-SEP-2005 (first entry)  
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:31.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.  
 XX CC Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; SEQ ID NO 31; 34pp; English.  
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 Db ||||||||||||||||  
 105 AAGGAACACGGACACCCAA 86  
 RESULT 49  
 AEB56864/c  
 ID AEB56864 standard; DNA; 238 BP.  
 AC AEB56864;  
 XX 22-SEP-2005 (first entry)  
 DT Human echovirus 11 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 KW Human echovirus 11.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX DR WPI; 2005-512251/52.  
 XX DR GENBANK; X80059.  
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; Fig 1A-D; 34pp; English.  
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 161 AAGGAACACGACACCCAA 142

RESULT 50  
 AEB56877/c  
 ID AEB56877 standard; DNA; 238 BP.  
 XX  
 AC AEB56877;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human poliovirus 2 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human poliovirus 2.  
 XX  
 FN US2005158710-A1.  
 XX  
 XX 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; M12197.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and

CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 56 A; 56 C; 63 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 161 AAGGAACACGACACCCAA 142

RESULT 51  
 AEB56794/c  
 ID AEB56794 standard; DNA; 238 BP.  
 XX  
 AC AEB56794;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:33.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 FN US2005158710-A1.  
 XX  
 XX 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

(TSAN/) TSANG S.  
 (PRIC/) PRICE J A.  
 (HELL/) HELLYER T J.  
 XX  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; SEQ ID NO 33; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 59 A; 53 C; 53 G; 73 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;

```
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 52
AEB56859/c
ID AEB56859 standard; DNA; 238 BP.
XX AC AEB56859;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:15.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TSAN// TSANG S.
XX PRIC// PRICE J A.
XX HELL// HELLYER T J.
XX TSang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 15; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 161 AAGGAAACACGGACACCCAA 142

RESULT 53
AEB56809/c
ID AEB56809 standard; DNA; 238 BP.
XX AC AEB56809;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TSAN// TSANG S.
XX PRIC// PRICE J A.
XX HELL// HELLYER T J.
XX TSang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 47 A; 53 C; 66 G; 72 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 54
AEB56809/c
ID AEB56809 standard; DNA; 238 BP.
XX AC AEB56809;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TSAN// TSANG S.
XX PRIC// PRICE J A.
XX HELL// HELLYER T J.
XX TSang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 15; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 58 A; 55 C; 55 G; 70 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 14; Length 238;
XX Best Local Similarity 100.0%; Pred. No. 11;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
Db 105 AAGGAAACACGGACACCCAA 86

RESULT 55
AEB56776/c
ID AEB56776 standard; DNA; 238 BP.
XX AC AEB56776;
XX DT 22-SEP-2005 (first entry)
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:15.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX TSAN// TSANG S.
XX PRIC// PRICE J A.
XX HELL// HELLYER T J.
XX TSang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; SEQ ID NO 15; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX Sequence 238 BP; 58 A; 55 C; 55 G; 70 T; 0 U; 0 Other;
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XX OS Unidentified.
XX PA
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.
XX PT
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; SEQ ID NO 48; 34pp; English.
XX CC
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 105 AAGGAACACGGACACCCAA 86

RESULT 55
AEB56831/C
ID AEB56831 standard; DNA; 238 BP.
AC AEB56831;
XX XX
XX DT 22-SEP-2005 (first entry)
XX XX
XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human coxsackievirus A16.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.

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XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.
XX DR GENBANK; U05876.
XX XX
XX PT Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PS Disclosure; Fig 1A-D; 34pp; English.
XX CC
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of AEB56764
XX CC to AEB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 161 AAGGAACACGGACACCCAA 142

RESULT 56
AEB56808/C
ID AEB56808 standard; DNA; 238 BP.
XX XX
XX AC AEB56808;
XX XX
XX DT 22-SEP-2005 (first entry)
XX XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:47.
XX KW DNA detection; enteroviral detection; ds.
XX OS Unidentified.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI
XX PI Tsang S, Price JA, Hellyer TJ;
XX DR WPI; 2005-512251/52.
XX XX

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PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 PS Disclosure; SEQ ID NO 47; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
 |||||  
 DB 105 AAGGAAACACGGACACCCAA 86

RESULT 57  
 AEB56882/c  
 ID AEB56882 standard; DNA; 238 BP.  
 XX  
 AC AEB56882;  
 XX  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human poliovirus 3 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human poliovirus 3.  
 XX  
 FN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; X04468.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 57 A; 54 C; 62 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCAA 20  
 |||||  
 DB 161 AAGGAAACACGGACACCCAA 142

RESULT 58  
 AEB56804/c  
 ID AEB56804 standard; DNA; 238 BP.  
 XX  
 AC AEB56804;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:43.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 FN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; SEQ ID NO 43; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20  
Db 105 AAGGAACACGACCCCAA 86  
|||||

RESULT 59  
AAZ58487/C  
ID AAZ58487 standard; RNA; 514 BP.

XX AAZ58487;  
XX 15-SEP-2003 (revised)  
XX 23-MAY-2000 (first entry)  
XX Poliovirus IRES domain II-VI region.

XX Internal ribosomal entry site; IRES; picornavirus; tumour; cancer;  
XX glioblastoma multiforme; medulloblastoma; mammary carcinoma;  
XX prostate carcinoma; colorectal carcinoma; hepatocellular carcinoma;  
XX bronchial carcinoma; epidermoid carcinoma; cytostatic; therapy; ss.  
XX Human poliovirus 1.

XX Key Location/Qualifiers  
FT stem\_loop 25..63  
FT /\*tag= a  
FT /note= "domain II"  
FT stem\_loop 70..83  
FT /\*tag= b  
FT stem\_loop 84..120  
FT /\*tag= c  
FT /note= "domain III"  
FT stem\_loop 132..338  
FT /\*tag= d  
FT /note= "domain IV"  
FT stem\_loop 183..209  
FT /\*tag= e  
FT stem\_loop 273..292  
FT /\*tag= f  
FT stem\_loop 346..454  
FT /\*tag= g  
FT /note= "domain V"  
FT stem\_loop 481..513  
FT /\*tag= h  
FT /note= "domain VI"

XX WO200008166-A1.  
XX 17-FEB-2000.  
XX 09-APR-1999; 99WO-US007839.  
XX 05-AUG-1998; 98US-00129686.  
XX (UYNV ) UNIV NEW YORK STATE RES FOUND.

XX Gromeier M, Wimmer E;

XX WPI; 2000-205717/18.

XX Chimeric recombinant poliovirus useful for treating malignant tumors  
XX comprises internal ribosomal entry site derived from picornaviruses.

XX Disclosure; Fig 2; 99pp; English.

XX This sequence represents domains II-VI of the internal ribosomal entry  
CC site (IRES) of wild-type poliovirus type 1 Mahoney. The invention  
CC provides non-pathogenic, oncolytic, recombinant polioviruses (I) in which  
CC the IRES of the wild-type poliovirus is exchanged with the IRES of  
CC another picornavirus, such as human rhinovirus type 2, and optionally the  
CC P1, P3 or 3' untranslated region is exchanged with that of Sabin  
CC poliovirus. (I) may contain a composite IRES encompassing IRES domains  
CC from both wild-type poliovirus and from another virus. (I) are useful for  
CC treating malignant tumors such as glioblastoma multiforme,  
CC medulloblastoma, mammary, prostate, colorectal, hepatocellular, bronchial  
CC and epidermoid carcinomas (claimed). (Updated on 15-SEP-2003 to  
CC standardise OS field)

SQ Sequence 514 BP; 122 A; 134 C; 132 G; 0 T; 126 U; 0 Other;  
Query Match 100.0%; Score 20; DB 3; Length 514;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACCCCAA 20  
Db 463 AAGGAACACGACCCCAA 444  
|||||

RESULT 60  
AAQ58715/C  
ID AAQ58715 standard; DNA; 628 BP.

XX AAQ58715;  
XX 27-AUG-2003 (revised)  
XX 25-MAR-2003 (revised)  
XX 29-SEP-1994 (first entry)  
XX Poliovirus type 1 5'-UTR with C to G substn. at position 610.  
XX Platelet-Derived Growth Factor; heterodimer; PDGF-AB;  
XX recombinant protein production; PDGF-A chain; PDGF-B chain;  
XX bicistronic vector system; ss.

XX Human poliovirus 1 Mahoney.

XX Key Location/Qualifiers  
FT 5'UTR 1..628  
FT /\*tag= a  
FT mutation 610  
FT /\*tag= b  
FT /note= "wild-type C has been substituted by G"

XX WO9405786-A1.

XX 17-MAR-1994.

XX 26-AUG-1993; 93WO-EP002295.

XX 27-AUG-1992; 92DE-04228457.

XX (BEIE ) BEIERSDORF AG.  
XX (GBFB ) GBF GES BIOTECH FORSCHUNG GMBH.

XX Eichner W, Achterberg V, Doerschner A, Meyer-Ingold W, Mielke H;  
XX Dirks W, Wirth M, Hauser H;

XX WPI; 1994-101191/12.

XX Heterodimer platelet-derived-growth factor (PDGF) prodn. - using a  
XX polycistronic vector system in mammalian host cells for equimolar prodn  
XX of A- and B-chains.

XX Claim 5; Page 41; 64pp; German.

XX A PDGF-AB heterodimer is recombinantly produced using a bicistronic



CC expression unit in which a sequence responsible for internal translation  
CC start (designated "IRES") is located between cistrons coding for the PDGF  
CC -B and PDGF-A chains. The preferred IRES sequence for inclusion in the  
CC bicistronic construct is the 5'-UTR from Poliovirus type 1 Mahoney strain  
CC of sequence AAQ58715. (Updated on 25-MAR-2003 to correct PN field.)  
CC (Updated on 27-AUG-2003 to correct OS field.)  
XX  
SQ Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 628;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
DB 565 AAGGAACACGACACCCAA 546

RESULT 61  
AAQ58726/c  
ID AAQ58726 standard; DNA; 628 BP.  
XX  
AC AAQ58726;  
DT 27-AUG-2003 (revised)  
DT 25-MAR-2003 (revised)  
DT 29-SEP-1994 (first entry)  
XX  
DE Poliovirus type 1 5'-UTR with C to G substn. at position 610.  
XX  
KW Multicistronic expression unit; recombinant protein production;  
KW internal translation start; initiation; 5'-untranslated region; ss.  
XX  
OS Human poliovirus 1 Mahoney.

Key Location/Qualifiers  
FH 5'UTR 1..628  
FT mutation /tag= a  
FT 610  
FT /tag= b  
FT /note= "wild-type C has been substituted by G"  
XX  
PN WO9405785-A1.

XX 17-MAR-1994.  
XX  
XX 26-AUG-1993; 93WO-EP002294.  
XX  
XX 27-AUG-1992; 92DE-04228458.  
XX  
XX (BEIE ) BEIERSDORF AG.  
XX (GBPB ) GBF GBS BIOTECH FORSCHUNG GMBH.

XX Dirks W, Wirth M, Hauser H, Eichner W, Achterberg V;  
XX Doerschner A, Meyer-Ingold W, Mielke H;  
XX WPI; 1994-101190/12.

XX New multicistronic expression units - for producing equimolar amts. of  
XX polypeptide(s) in mammalian cells as hosts.

XX Claim 6; Page 50; 109pp; German.

XX Heterodimeric proteins can be recombinantly produced using a  
XX multicistronic (esp. bicistronic) expression unit in which a sequence  
XX responsible for internal translation start (designated "IRES") is located  
XX between cistrons coding for the different subunits. The preferred IRES  
XX sequence is the 5'-UTR from Poliovirus type 1 Mahoney strain of sequence  
XX AAQ58726. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-  
XX AUG-2003 to correct OS field.)

XX Sequence 628 BP; 143 A; 165 C; 162 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 628;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGGAACACGACACCCAA 20  
DB 565 AAGGAACACGACACCCAA 546

RESULT 62  
ADP74707/c  
ID ADP74707 standard; DNA; 639 BP.  
XX  
AC ADP74707;  
DT 26-AUG-2004 (first entry)  
XX

XX Novel bicistronic retroviral vector related poliovirus IRES sequence.  
XX  
KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
KW severe combined immune deficiency syndrome; protein expression;  
KW antisense; ds; gene.  
XX  
OS Unidentified.  
XX  
XX EP1428886-A1.  
XX 16-JUN-2004.  
XX  
XX 09-DEC-2002; 2002EP-00027555.  
XX  
XX 09-DEC-2002; 2002EP-00027555.

XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.  
XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
XX WPI; 2004-452367/43.  
XX  
XX Bicistronic retroviral vector, useful in gene therapy, particularly of  
XX graft versus host disease, contains components of both murine embryonic  
XX stem cell and myeloproliferative sarcoma viruses.

XX Disclosure; Page 70; 91pp; German.

XX The present invention relates to a new bicistronic retroviral vector.  
XX These are used for (over)expression of proteins, suppressing expression  
XX of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
XX suppress a dominant-negative phenotype, also infectious viral particles  
XX that contain the vectors, in gene therapy, particularly for control of  
XX guest versus host disease, especially where haematopoietic cells are  
XX transduced with the vector or where T cells are transduced, for adoptive  
XX immunotherapy, but also for treating severe combined immune deficiency  
XX syndrome and for expression cloning of genes. The present sequence is a  
XX vector sequence fragment shown in the exemplification of the invention.

SQ Sequence 639 BP; 146 A; 171 C; 164 G; 158 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 639;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCAA 20  
DB 569 AAGGAACACGACACCCAA 550

RESULT 63  
ADU77356/c  
ID ADU77356 standard; DNA; 682 BP.  
XX  
XX AC ADU77356;  
XX

DT	10-FEB-2005	(first entry)	
XX			
DE	Prima7 virus 5' UTR region DNA.		
XX			
KW	Enteroviral genus related disease; Prima7-related disease; gene therapy;		
KW	ds.		
XX			
OS	Prima7 virus.		
XX			
PN	EP1479761-A1.		
XX			
PD	24-NOV-2004.		
XX			
PF	21-MAY-2003; 2003EP-00076529.		
XX			
PR	21-MAY-2003; 2003EP-00076529.		
XX			
PA	(PRIM-) PRIMAGEN HOLDING BV.		
XX			
PI	Maas HCGL, Van Den Broek PJM, Mang R;		
XX			
DR	WPI; 2004-823915/82.		
XX			
XX	New isolated or recombinant virus, useful for detecting a molecule		
PT	capable of specifically binding the virus in a sample, and as a vaccine		
PT	or medicament for treating or preventing Prima7-related disease.		
XX			
PS	Example; SEQ ID NO 39; 51pp; English.		
XX			
CC	The present invention provides a new isolated or recombinant virus called		
CC	Prima7 (which belong to enteroviral species) comprising a nucleic acid		
CC	sequence or its functional part, derivative or analogue of the said		
CC	virus. The invention is useful for detecting and/or identifying a Prima7		
CC	enterovirus in a sample and for diagnosing an enteroviral genus related		
CC	disease. The vaccine or medicament prepared from the Prima7 virus is		
CC	useful for preventing and/or treating a Prima7-related disease. The		
CC	invention is also useful in gene therapy. The present sequence is Prima7		
CC	virus 5' UTR region DNA.		
XX			
SQ	Sequence 682 BP; 176 A; 157 C; 159 G; 190 T; 0 U; 0 Other;		
	Query Match 100.0%; Score 20; DB 13; Length 682;		
	Best Local Similarity 100.0%; Pred. No. 11;		
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1 AAGGAAACACGGACACCCAA 20		
DB	504 AAGGAAACACGGACACCCAA 485		
RESULT 64			
AEAA00424/C			
ID	AEAA00424 standard; DNA; 709 BP.		
XX			
AC	AEAA00424;		
XX			
DT	28-JUL-2005 (first entry)		
XX			
DE	Enterovirus 71 5' untranslated region internal ribosome entry site DNA.		
XX			
KW	vector; neurological disease; ds; gene therapy;		
KW	internal ribosome entry site; cystic fibrosis; cns-gen.;		
KW	respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;		
KW	factor IX deficiency; Duchenne dystrophy; muscular-gen.;		
KW	Becker's disease; cancer; cytostatic; neoplasm;		
KW	acquired immune deficiency syndrome; anti-hiv; infectious disease;		
XX	antimicrobial.		
XX			
OS	Human enterovirus 71; strain TW/2086/98.		
XX			
PN	US2005112095-A1.		
XX			
PD	26-MAY-2005.		

DR WPI; 2005-065191/07.  
 XX  
 PT New system comprising one or more recombinant vectors that expresses the  
 PT SARS-CoV E-protein, SARS-CoV M-protein, and SARS-CoV S-protein, useful  
 PT for making SARS-coronavirus virus-like particles.  
 XX  
 PS Example 2; SEQ ID NO 21; 111pp; English.  
 XX  
 CC The present invention provides a system for making SARS-coronavirus virus  
 CC -like particles (SARS-CoV-VLPs) comprising one or more recombinant  
 CC vectors that express the SARS-CoV E (small membrane)-protein, SARS-CoV  
 CC M (membrane)-protein and SARS-CoV S (spike)-protein. The invention is  
 CC useful for inducing cellular and/or humoral immune response. The  
 CC invention is also useful to reduce the symptoms of SARS-CoV infections  
 CC and in vaccine preparations. The present sequence is Poliovirus type 1  
 CC strain mahoney internal ribosomal entry site (IRES) cDNA. This cDNA  
 CC sequence is used in the preparation of plasmid for the expression of SARS  
 CC -CoV M, E and S proteins.  
 XX  
 SQ Sequence 743 BP; 175 A; 185 C; 181 G; 202 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 14; Length 743;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 DB 563 AAGGAACACGGACACCCAA 544  
 RESULT 66  
 ACC48197/c  
 ID ACC48197 standard; cDNA; 745 BP.  
 XX  
 AC ACC48197;  
 XX  
 DT 11-AUG-2003 (first entry)  
 XX  
 DE Poliovirus internal ribosome entry site-containing mRNA 5' UTR.  
 XX  
 KW Internal ribosome entry site; IRES; translation; ss.  
 XX  
 OS Poliovirus.  
 XX  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..742  
 FT /\*tag= a  
 XX  
 PN WO200302927-A2.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 03-SEP-2002; 2002WO-EP009843.  
 XX  
 PR 04-SEP-2001; 2001DE-01043237.  
 XX  
 PA (ICON-) ICON GENETICS INC.  
 XX  
 PI Atabekov J, Dorokhov Y, Skulachev M, Ivanov P, Gleba Y;  
 DR WPI; 2003-313089/30.  
 XX  
 PT Creating nucleic acid sequence for carrying out translation by internal  
 PT ribosome entry site element and expressing nucleotide sequence of  
 PT interest in eukaryotic cell, by creating a nucleic acid having adenine-  
 PT rich block.  
 XX  
 PS Disclosure; Fig 3; 48pp; English.  
 XX  
 CC The present sequence is that of a known internal ribosome entry site  
 CC (IRES) element contained in the 5' untranslated region of poliovirus  
 CC mRNA. The invention provides a method of creating an artificial IRES  
 CC element having an adenine-rich (40-100 mol%) nucleic acid block of at

CC least 25 nucleotides and capable of causing cap-independent translation  
 CC of a downstream nucleotide sequence of interest in eukaryotic cells, such  
 CC as plant, animal or yeast cells (claimed). A method of identifying  
 CC nucleic acid elements having IRES activity involving genome database  
 CC searches is also provided. The methods allow the creation or  
 CC identification of IRES elements that are universal with cross-kingdom and  
 CC tailor-made activity  
 XX  
 SQ Sequence 745 BP; 163 A; 202 C; 193 G; 187 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 745;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGGACACCCAA 20  
 DB 568 AAGGAACACGGACACCCAA 549  
 RESULT 67  
 ABK14791/c  
 ID ABK14791 standard; DNA; 2076 BP.  
 XX  
 AC ABK14791;  
 XX  
 DT 08-MAY-2002 (first entry)  
 XX  
 DE Platelet-derived growth factor expression cassette insert used in pBC701.  
 XX  
 KW Platelet-derived growth factor; PDGF; transgenic; milk; gene;  
 KW wound healing; diabetic foot ulcer; decubitus ulcer; ophthalmic disease;  
 KW venous stasis ulcer; periodontal regeneration; bone formation;  
 KW prosthetic vascular graft; pBC701; ds.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200198520-A1.  
 XX  
 PD 27-DEC-2001.  
 XX  
 PF 19-JUN-2001; 2001WO-US041044.  
 XX  
 PR 19-JUN-2000; 2000US-0212406P.  
 XX  
 PA (GENZ) GENZYME TRANSGENICS CORP.  
 XX  
 PI Echelard Y, Meade H, Eichner W, Sommermeyer K;  
 XX  
 DR WPI; 2002-083329/11.  
 XX  
 PT Production of platelet derived growth factor (PDGF) comprises expression  
 PT in the milk of a non-human transgenic animal.  
 XX  
 PS Example 1; Fig 1; 59pp; English.  
 XX  
 CC The invention relates to the production of platelet-derived growth factor  
 CC (PDGF) comprising a transgenic mammal whose somatic and germ cells  
 CC comprise a nucleic acid sequence (I) encoding PDGF, operably linked to a  
 CC promoter directing expression into mammalian gland epithelial cells, and  
 CC obtaining the milk from the transgenic mammal where at least 30% of the  
 CC PDGF in the milk is as a dimer. Also described is a method of producing a  
 CC transgenic mammal capable of expressing an active PDGF molecule in milk.  
 CC Pharmaceutical compositions can be obtained from this milk and can be  
 CC used to stimulate or enhance the wound healing process, in particular  
 CC diabetic foot ulcers, decubitus ulcers and venous stasis ulcers.  
 CC Transgenic PGF (II) can also be used in the treatment of periodontal  
 CC regeneration, stimulation of bone formation, ophthalmic diseases or  
 CC healing of prosthetic vascular grafts. (II) can also be used for non-  
 CC medical applications, e.g., as a supplement for cell culture media or as  
 CC a component of diagnostic kits. The present sequence represents the  
 CC platelet-derived growth factor expression cassette insert used in pBC701  
 CC vector of the invention

1 AAGGAAACACGGACACCCAA 20

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XX OS Synthetic.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /tag= a
XX FT /standard_name= "5'-LTR"
XX FT 5'UTR 995..1487
XX FT CDS 1488..2615
XX FT /tag= b
XX FT /tag= c
XX FT /product= "HSV-TK"
XX FT misc_RNA 2626..3250
XX FT /tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3298..4098
XX FT /tag= e
XX FT /product= "neo"
XX FT LTR 4345..4931
XX FT /tag= f
XX FT /standard_name= "3'-LTR"
XX PN EP1428886-A1.
XX XX 16-JUN-2004.
XX PD 09-DEC-2002; 2002EP-00027555.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX XX Bistronic retroviral vector, useful in gene therapy, particularly of
XX FT graft versus host disease, contains components of both murine embryonic
XX FT stem cell and myeloproliferative sarcoma viruses.
XX PS Disclosure; Page 58-59; 91pp; German.
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7185 BP; 1579 A; 2013 C; 1943 G; 1650 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 12; Length 7185;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAAACACGGACCCCAA 20
DB 3188 AAGGAAACACGGACCCCAA 3169
RESULT 71
ID ADP74701/c
XX ADP74701 standard; DNA; 7185 BP.
XX AC ADP74701;
XX DT 26-AUG-2004 (first entry)
XX XX

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DE XX Novel bicistronic retroviral vector related vector #3.
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;
XX KW severe combined immune deficiency syndrome; protein expression;
XX KW antisense; ds; gene.
XX OS Synthetic.
XX OS Unidentified.
XX PH Key Location/Qualifiers
XX FT LTR 424..994
XX FT /tag= a
XX FT /standard_name= "5'-LTR"
XX FT 5'UTR 995..1487
XX FT CDS 1488..2615
XX FT /tag= b
XX FT /tag= c
XX FT /product= "HSV-TK splice variant"
XX FT misc_RNA 2626..3250
XX FT /tag= d
XX FT /standard_name= "IRES"
XX FT CDS 3298..4098
XX FT /tag= e
XX FT /product= "neo"
XX FT LTR 4345..4931
XX FT /tag= f
XX FT /standard_name= "3'-LTR"
XX PN EP1428886-A1.
XX XX 16-JUN-2004.
XX PD 09-DEC-2002; 2002EP-00027555.
XX PF 09-DEC-2002; 2002EP-00027555.
XX PR (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.
XX PI Heberlein C, Gindullis F, Hannemann J, Strathmann G;
XX DR WPI; 2004-452367/43.
XX XX Bistronic retroviral vector, useful in gene therapy, particularly of
XX FT graft versus host disease, contains components of both murine embryonic
XX FT stem cell and myeloproliferative sarcoma viruses.
XX PS Disclosure; Page 63-65; 91pp; German.
XX CC The present invention relates to a new bicistronic retroviral vector.
XX CC These are used for (over)expression of proteins, suppressing expression
XX CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to
XX CC suppress a dominant-negative phenotype, also infectious viral particles
XX CC that contain the vectors, in gene therapy, particularly for control of
XX CC guest versus host disease, especially where haematopoietic cells are
XX CC transduced with the vector or where T cells are transduced, for adoptive
XX CC immunotherapy, but also for treating severe combined immune deficiency
XX CC syndrome and for expression cloning of genes. The present sequence is a
XX CC vector sequence shown in the exemplification of the invention.
XX SQ Sequence 7185 BP; 1581 A; 2013 C; 1942 G; 1649 T; 0 U; 0 Other;
XX Query Match 100.0%; Score 20; DB 12; Length 7185;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAGGAAACACGGACCCCAA 20
DB 3188 AAGGAAACACGGACCCCAA 3169
RESULT 72
ID ADP74714/c
XX ADP74714 standard; DNA; 7235 BP.
XX XX

```

XX ADP74714;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Novel bicistronic retroviral vector related vector #6.  
 XX  
 XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
 KW severe combined immune deficiency syndrome; protein expression;  
 KW antisense; ds; gene.  
 XX  
 XX Synthetic.  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT LTR 424..994  
 FT /\*tag= a  
 FT /\*standard\_name= "5'-LTR"  
 FT 5'UTR 995..1537  
 FT /\*tag= b  
 FT CDS 1538..2665  
 FT /\*tag= c  
 FT /\*product= "HSV-TK splice variant"  
 FT 2676..3300  
 FT /\*tag= d  
 FT /\*standard\_name= "IRES"  
 FT CDS 3348..4148  
 FT /\*tag= e  
 FT /\*product= "neo"  
 FT 4395..4981  
 FT /\*tag= f  
 FT /\*standard\_name= "3'-LTR"  
 XX  
 XX EP1428886-A1.  
 XX  
 XX 16-JUN-2004.  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX  
 XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.  
 XX  
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
 XX  
 XX WPI; 2004-452367/43.  
 XX  
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 PT stem cell and myeloproliferative sarcoma viruses.  
 XX  
 XX Disclosure; Page 75-77; 91pp; German.  
 XX  
 XX The present invention relates to a new bicistronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX  
 XX Sequence 7235 BP; 1594 A; 2025 C; 1950 G; 1666 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 12; Length 7235;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 AAGGAACACGACCCAA 20  
 Db 3238 AAGGAACACGACCCAA 3219

RESULT 73  
 ADP74715/c  
 ID ADF74715 standard; DNA; 7235 BP.  
 XX  
 AC ADP74715;  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Novel bicistronic retroviral vector related vector #7.  
 XX  
 XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
 KW severe combined immune deficiency syndrome; protein expression;  
 KW antisense; ds; gene.  
 XX  
 XX Synthetic.  
 OS Unidentified.  
 XX  
 XX Key Location/Qualifiers  
 FT LTR 424..994  
 FT /\*tag= a  
 FT /\*standard\_name= "5'-LTR"  
 FT 5'UTR 995..1537  
 FT /\*tag= b  
 FT CDS 1538..2665  
 FT /\*tag= c  
 FT /\*product= "HSV-TK splice variant"  
 FT 2676..3300  
 FT /\*tag= d  
 FT /\*standard\_name= "IRES"  
 FT CDS 3348..4148  
 FT /\*tag= e  
 FT /\*product= "neo"  
 FT 4395..4981  
 FT /\*tag= f  
 FT /\*standard\_name= "3'-LTR"  
 XX  
 XX EP1428886-A1.  
 XX  
 XX 16-JUN-2004.  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX  
 XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.  
 XX  
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
 XX  
 XX WPI; 2004-452367/43.  
 XX  
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 PT stem cell and myeloproliferative sarcoma viruses.  
 XX  
 XX Disclosure; Page 78-79; 91pp; German.  
 XX  
 XX The present invention relates to a new bicistronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX  
 XX Sequence 7235 BP; 1595 A; 2025 C; 1949 G; 1666 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 20; DB 12; Length 7235;  
 Best Local Similarity 100.0%; Pred. No. 13;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3238 AAGGAAACACGACACCCAA 3219

RESULT 74  
ADP74700/c  
ID ADP74700 standard; DNA; 7235 BP.  
XX AC  
XX ADP74700;  
XX 26-AUG-2004 (first entry)  
XX DE Novel bicistronic retroviral vector related vector #2.  
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
XX KW severe combined immune deficiency syndrome; protein expression;  
XX KW antisense; ds; gene.  
XX OS Synthetic.  
XX OS Unidentified.  
XX FH Key  
XX LTR Location/Qualifiers  
424..994  
/\*tag= a  
/standard\_name= "5'-LTR"  
995..1537  
/\*tag= b  
1538..2665  
/\*tag= c  
/product= "HSV-TK"  
2676..3300  
/\*tag= d  
/standard\_name= "IRES"  
3348..4148  
/\*tag= e  
/product= "neo"  
4395..4981  
/\*tag= f  
/standard\_name= "3'-LTR"  
EPI428886-A1.  
16-JUN-2004.  
09-DEC-2002; 2002EP-00027555.  
09-DEC-2002; 2002EP-00027555.  
(CELL-) CELLSGMBH BIOTECHNOLOGIE.  
Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
WPI; 2004-452367/43.  
Bicistronic retroviral vector, useful in gene therapy, particularly of  
graft versus host disease, contains components of both murine embryonic  
stem cell and myeloproliferative sarcoma viruses.  
Disclosure; Page 60-62; 91pp; German.  
The present invention relates to a new bicistronic retroviral vector.  
These are used for (over)expression of proteins, suppressing expression  
of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
suppress a dominant-negative phenotype, also infectious viral particles  
that contain the vectors, in gene therapy, particularly for control of  
graft versus host disease, especially where haematopoietic cells are  
transduced with the vector or where T cells are transduced, for adoptive  
immunotherapy, but also for treating severe combined immune deficiency  
syndrome and for expression cloning of genes. The present invention is a  
vector sequence shown in the exemplification of the invention.

XX SQ Sequence 7235 BP; 1592 A; 2025 C; 1951 G; 1667 T; 0 U; 0 Other;  
Query Match 100.0%; Score 20; DB 12; Length 7235;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAAACACGACACCCAA 20  
| | | | | | | | | | | | | | | | | | | | | |  
Db 3238 AAGGAAACACGACACCCAA 3219

RESULT 75  
ADP74713/c  
ID ADP74713 standard; DNA; 7235 BP.  
XX AC  
XX ADP74713;  
XX DT 26-AUG-2004 (first entry)  
XX DE Novel bicistronic retroviral vector related vector #5.  
XX KW immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
XX KW severe combined immune deficiency syndrome; protein expression;  
XX KW antisense; ds; gene.  
XX OS Synthetic.  
XX OS Unidentified.  
XX FH Key  
XX LTR Location/Qualifiers  
424..994  
/\*tag= a  
/standard\_name= "5'-LTR"  
995..1537  
/\*tag= b  
1538..2665  
/\*tag= c  
/product= "HSV-TK"  
2676..3300  
/\*tag= d  
/standard\_name= "IRES"  
3348..4148  
/\*tag= e  
/product= "neo"  
4395..4981  
/\*tag= f  
/standard\_name= "3'-LTR"  
EPI428886-A1.  
16-JUN-2004.  
09-DEC-2002; 2002EP-00027555.  
09-DEC-2002; 2002EP-00027555.  
(CELL-) CELLSGMBH BIOTECHNOLOGIE.  
Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
WPI; 2004-452367/43.  
Bicistronic retroviral vector, useful in gene therapy, particularly of  
graft versus host disease, contains components of both murine embryonic  
stem cell and myeloproliferative sarcoma viruses.  
Disclosure; Page 72-74; 91pp; German.  
The present invention relates to a new bicistronic retroviral vector.  
These are used for (over)expression of proteins, suppressing expression  
of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
suppress a dominant-negative phenotype, also infectious viral particles  
that contain the vectors, in gene therapy, particularly for control of

CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX

SQ Sequence 7235 BP; 1593 A; 2025 C; 1950 G; 1667 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 12; Length 7235;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20

Db 3238 AAGGAACACGGACACCCAA 3219

RESULT 76

ABX12440/C

ID ABX12440 standard; DNA; 7392 BP.

AC ABX12440;

XX 10-MAY-2003 (first entry)

XX Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.

XX Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
 KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
 KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
 KW renal failure; leg amputation; ds.

XX Coxsackievirus.

XX Key Location/Qualifiers

FH misc\_feature 1..87  
 FT /note= "Specifically claimed in claim 16"  
 FT /tag= a  
 FT misc\_feature 88..512  
 FT /note= "Specifically claimed in claim 19"  
 FT /tag= b  
 FT misc\_feature 513..742  
 FT /note= "Specifically claimed in claim 22"  
 FT /tag= c  
 FT misc\_feature 742  
 FT /note= "Specifically claimed in claim 25"  
 FT /tag= d  
 FT CDS 743..7303  
 FT /tag= f  
 FT /product= "Polyprotein"  
 FT /tag= e  
 FT misc\_feature 743..952  
 FT /note= "Specifically claimed in claim 26"  
 FT /tag= g  
 FT misc\_feature 953..1726  
 FT /note= "Specifically claimed in claim 29"  
 FT /tag= h  
 FT misc\_feature 1727..2441  
 FT /note= "Specifically claimed in claim 32"  
 FT /tag= i  
 FT misc\_feature 2442..3296  
 FT /note= "Specifically claimed in claim 35"  
 FT /tag= j  
 FT misc\_feature 3297..3737  
 FT /note= "Specifically claimed in claim 38"  
 FT /tag= k  
 FT misc\_feature 3738..4033  
 FT /note= "Specifically claimed in claim 41"  
 FT /tag= l  
 FT misc\_feature 4034..5029  
 FT /note= "Specifically claimed in claim 44"

XX WO2002103060-A2.

XX 27-DEC-2002.

XX 19-JUN-2002; 2002WO-IB003278.

XX 20-JUN-2001; 2001SE-00002198.

XX (INNO-) INNOVENTUS PROJECT AB.

XX Tuvemo HT, Frisk GE, Yin H;

XX WPI; 2003-278229/27.

XX P-PSDB; ABG75961.

XX Polymerase chain reaction and primers for detecting nucleic acids from  
 the diabetogenic coxsackie B virus-4 strain VD2921.

XX Example 5; Page 64-66; 79pp; English.

XX The invention describes a polymerase chain reaction (PCR) and primers for  
 detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 P3C and P3D nucleic acids). The methods and primers are used for the  
 detection of CBV-4 strain VD2921 which is associated with diabetes  
 (diabetogenic enterovirus). Early detection of the diabetes e.g.  
 detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 cells, can improve prognosis by allowing treatment e.g. with antiviral  
 drugs, to prevent further loss of beta cells and severe long term  
 consequences of diabetes including blindness, renal failure and leg  
 amputations. This sequence represents the genome of diabetogenic  
 coxsackie B virus 4 (CBV-4) strain VD2921

SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 8; Length 7392;

Best Local Similarity 100.0%; Pred. No. 13;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20

Db 568 AAGGAACACGGACACCCNA 549

RESULT 77

AAZ98719/C

ID AAZ98719 standard; cDNA; 7400 BP.

XX AAZ98719;

XX 20-JUN-2000 (first entry)

XX Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.

XX Swine vesicular disease virus; SVDV; swine vesicular disease;  
 Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 differentiation; vaccine; prevent; ss.

XX Swine vesicular disease virus.

XX Key Location/Qualifiers

FH misc\_feature 2693..2710

FT /note= "Nucleotides in this position replace the wild-

type nucleotide sequence of strain Taiwan Yu-Li (see  
 AAZ98717)"

XX EP982403-A1.

XX 01-MAR-2000.

XX 14-AUG-1998; 98EP-00306486.

XX 14-AUG-1998; 98EP-00306486.



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XX PA (BIOT-) DEV CENT BIOTECHNOLOGY.
XX PI Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX DR WPI; 2000-258616/23.
XX PT Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX FT to prevent swine vesicular disease.
XX PS Claim 4; Page; 66pp; English.
XX CC This sequence represents the full length Swine vesicular disease virus
XX CC (SVDV) gene sequence from the SVDV strain N3. SVDV is the causative agent
XX CC of swine vesicular disease, which is very similar to foot and mouth
XX CC disease. The invention relates to the wild-type Taiwan Yu-Li strain CDNA
XX CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
XX CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
XX CC prophylaxis of swine vesicular disease. The invention also includes a
XX CC method for differentiating the mutant SVDV nucleotide sequences from the
XX CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
XX CC virus through the use of polymerase chain reaction. Note: This sequence
XX CC is not present in the specification, but has been derived from the wild-
XX CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
XX CC 34-38 of the specification
XX SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 78
AAZ98717/c
ID AAZ98717 standard; cDNA; 7400 BP.
XX AC AAZ98718;
XX AC 20-JUN-2000 (first entry)
XX DT Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.
XX DE Swine vesicular disease virus; SVDV; swine vesicular disease;
XX KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
XX KW differentiation; vaccine; prevent; ss.
XX OS Swine vesicular disease virus.
XX OS

Key Location/Qualifiers
FT misc_feature 2705..2710
FT /*tag= a
FT /note= "Nucleotides in this position replace the wild-
FT type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"
XX PN EP982403-A1.
XX PD 01-MAR-2000.
XX PF 14-AUG-1998; 98EP-00306486.
XX PP 14-AUG-1998; 98EP-00306486.
XX PR (BIOT-) DEV CENT BIOTECHNOLOGY.
XX PA Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX PI WPI; 2000-258616/23.
XX DR Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX FT to prevent swine vesicular disease.
XX PS Claim 3; Page; 66pp; English.
XX CC This sequence represents the full length Swine vesicular disease virus
XX CC (SVDV) gene sequence from the SVDV strain H21. SVDV is the causative
XX CC agent of swine vesicular disease, which is very similar to foot and mouth
XX CC disease. The invention relates to the wild-type Taiwan Yu-Li strain CDNA
XX CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
XX CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
XX CC prophylaxis of swine vesicular disease. The invention also includes a
XX CC method for differentiating the mutant SVDV nucleotide sequences from the
XX CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
XX CC virus through the use of polymerase chain reaction. Note: This sequence
XX CC is not present in the specification, but has been derived from the wild-
XX CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
XX CC 34-38 of the specification
XX SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 79
AAZ98718/c
ID AAZ98718 standard; cDNA; 7400 BP.
XX AC AAZ98718;
XX AC 20-JUN-2000 (first entry)
XX DT Swine vesicular disease virus (SVDV) H21 mutant strain gene sequence.
XX DE Swine vesicular disease virus; SVDV; swine vesicular disease;
XX KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
XX KW differentiation; vaccine; prevent; ss.
XX OS Swine vesicular disease virus.
XX OS

Key Location/Qualifiers
FT misc_feature 2705..2710
FT /*tag= a
FT /note= "Nucleotides in this position replace the wild-
FT type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"
XX PN EP982403-A1.
XX PD 01-MAR-2000.
XX PF 14-AUG-1998; 98EP-00306486.
XX PP 14-AUG-1998; 98EP-00306486.
XX PR (BIOT-) DEV CENT BIOTECHNOLOGY.
XX PA Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX PI WPI; 2000-258616/23.
XX DR Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX FT to prevent swine vesicular disease.
XX PS Claim 3; Page; 66pp; English.
XX CC This sequence represents the full length Swine vesicular disease virus
XX CC (SVDV) gene sequence from the SVDV strain H21. SVDV is the causative
XX CC agent of swine vesicular disease, which is very similar to foot and mouth
XX CC disease. The invention relates to the wild-type Taiwan Yu-Li strain CDNA
XX CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
XX CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
XX CC prophylaxis of swine vesicular disease. The invention also includes a
XX CC method for differentiating the mutant SVDV nucleotide sequences from the
XX CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
XX CC virus through the use of polymerase chain reaction. Note: This sequence
XX CC is not present in the specification, but has been derived from the wild-
XX CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
XX CC 34-38 of the specification
XX SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAGGAACACGACACCCAA 20
Db 568 AAGGAACACGACACCCAA 549

RESULT 78
AAZ98717/c
ID AAZ98717 standard; cDNA; 7400 BP.
XX AC AAZ98717;
XX AC 20-JUN-2000 (first entry)
XX DT Swine vesicular disease virus (SVDV) gene sequence.
XX DE Swine vesicular disease virus; SVDV; swine vesicular disease;
XX KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
XX KW differentiation; vaccine; prevent; ss.
XX OS Swine vesicular disease virus.
XX OS

Key Location/Qualifiers
FT misc_feature 2705..2710
FT /*tag= a
FT /note= "Nucleotides in this position replace the wild-
FT type nucleotide sequence of strain Taiwan Yu-Li AAZ98717"
XX PN EP982403-A1.
XX PD 01-MAR-2000.
XX PF 14-AUG-1998; 98EP-00306486.
XX PP 14-AUG-1998; 98EP-00306486.
XX PR (BIOT-) DEV CENT BIOTECHNOLOGY.
XX PA Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX PI WPI; 2000-258616/23.
XX DR Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX FT to prevent swine vesicular disease.
XX PS Claim 1; Page 34-38; 66pp; English.
XX CC This sequence represents the full length Swine vesicular disease virus

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```
CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
CC 34-38 of the specification
XX
SQ Sequence 7400 BP; 2082 A; 1785 C; 1863 G; 1670 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 568 AAGGAACACGGACACCCAA 549

RESULT 80
AAZ9863/C
ID AAA29863 standard; cDNA; 7400 BP.
XX
AC AAA29863;
XX
DT 30-AUG-2000 (first entry)
XX
XX Swine vesicular disease virus (SVDV) nucleotide sequence.
DE
XX Swine vesicular disease virus; SVDV; vesicular disease; vaccine; ss.
KW
XX Swine vesicular disease virus.
OS
XX CN1244583-A.
XX
XX 16-FEB-2000.
XX
XX 12-AUG-1998; 98CN-00117165.
XX
XX 12-AUG-1998; 98CN-00117165.
XX
XX (BIOL-) BIOLOGICAL TECHNOLOGY DEV CENT.
XX
XX Huang Q, Luo Z, Yang Y;
XX WPI; 2000-388169/34.
XX
XX Native swine vascular disease virus gene and its variant - useful as
XX vaccines.
XX
XX Claim 1; Page 1-5; 54pp; Chinese.
XX
XX The present invention describes a native swine vascular disease virus
XX (SVDV) gene and its variant. Also described are: (1) an expression
XX plasmid containing the gene; (2) preparation of the gene and its variant;
XX and (3) a vaccine comprising the gene or its variant. The new gene is
XX useful for the treatment of vesicular disease. The present sequence
XX represents a specifically claimed SVDV nucleotide sequence from the
XX present invention
XX
XX Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7400;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 568 AAGGAACACGGACACCCAA 549

RESULT 81
AAZ98720/C
ID AAZ98720 standard; cDNA; 7421 BP.
XX
XX AAZ98720;
AC
XX
XX 20-JUN-2000 (first entry)
DT
```

```
XX Swine vesicular disease virus (SVDV) SP7 mutant strain gene sequence.
DE
XX Swine vesicular disease virus; SVDV; swine vesicular disease;
KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;
KW differentiation; vaccine; prevent; ss.
XX
XX Swine vesicular disease virus.
OS
XX
XX Key Location/Qualifiers
XX misc_feature /tag= a
XX 2705..2731
XX /note= "Nucleotides in this position replace the
XX nucleotides at position 2705-2710 of the SVDV wild-type
XX Taiwan Yu-Li strain (see AAZ98717)."
XX
XX EP982403-A1.
XX
XX 01-MAR-2000.
XX
XX 14-AUG-1998; 98EP-00306486.
XX
XX 14-AUG-1998; 98EP-00306486.
XX
XX (BIOT-) DEV CENT BIOTECHNOLOGY.
XX
XX Hong CL, Lo C, Yang Y, Jeng K, Chang EL;
XX WPI; 2000-258616/23.
XX
XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines
XX to prevent swine vesicular disease.
XX
XX Claim 5; Page: 66pp; English.
XX
XX This sequence represents the full length Swine vesicular disease virus
XX (SVDV) gene sequence from the SVDV strain SP7. SVDV is the causative
XX agent of swine vesicular disease, which is very similar to foot and mouth
XX disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA
XX sequence, and the gene sequences of the mutant SVDV strains N3, H21 and
XX SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the
XX prophylaxis of swine vesicular disease. The invention also includes a
XX method for differentiating the mutant SVDV nucleotide sequences from the
XX wild type strain of SVDV, coxsackie virus and foot-and-mouth disease
XX virus through the use of polymerase chain reaction. Note: This sequence
XX is not present in the specification, but has been derived from the wild-
XX type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages
XX 34-38 of the specification
XX
XX Sequence 7421 BP; 2090 A; 1792 C; 1867 G; 1672 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 3; Length 7421;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 568 AAGGAACACGGACACCCAA 549

RESULT 82
AAQ30148/C
ID AAQ30148 standard; cDNA; 7431 BP.
XX
XX AAQ30148;
AC
XX
XX 24-OCT-2003 (revised)
DT 16-APR-1993 (first entry)
XX
XX Attenuated (472U, 537A) poliovirus type 3 Leon strain.
DE
XX vaccine; polioviruses; poliomyelitus; virulence; immunise; inoculate.
XX
```

```

OS Human poliovirus 3; strain Leon.
XX AU9176128-A.
XX
XX
XX 15-OCT-1992.
XX
XX 29-APR-1991; 91AU-00076128.
XX
XX 10-APR-1991; 91GB-00007552.
XX
XX (ALMO/) ALMOND J W.
XX (MINO/) MINOR P D.
XX (MACA/) MACADAM A J.
XX (STON/) STONE D M.
XX
XX Macadam AJ, Minor PD, Stone DM, Almond JW;
XX WPI; 1992-399255/49.
XX
XX New attenuated poliovirus for vaccines - in which 5-non-coding region of
XX genome is 5 non-coding region of polio-virus type 3 Leon strain modified
XX by uracil and adenine etc.
XX
XX Claim 1; Page 12; 14pp; English.
XX
XX This is an attenuated poliovirus type 3 Leon strain in which the 5' non-
XX coding region of the genome is modified by substitution with U at posn.
XX 472, and A at posn. 537. The attenuated poliovirus may be used in a
XX vaccine against polioviruses. They may be administered orally, as a nasal
XX spray, or parenterally. A dose corresp. to the amt. admin. for a
XX conventional live virus vaccine, such as up to 10power6 TCID50 for a
XX sabin vaccine strain in the case of poliovirus may be admin. (Updated on
XX 24-OCT-2003 to standardise OS field)
XX
XX Sequence 7431 BP; 2148 A; 1738 C; 1749 G; 1796 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 7431;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
DB 568 AAGGAACACGGACACCCAA 549

RESULT 83
AAQ22965/C
ID AAQ22965 standard; cDNA; 7432 BP.
XX
XX AAQ22965;
XX
XX 25-MAR-2003 (revised)
XX 14-JUL-1992 (first entry)
XX
XX True type 3 poliovirus vaccine strain cDNA.
XX
XX RNA virus; error reduction; ss.
XX
XX Poliovirus.
XX
XX Key Location/Qualifiers
XX CDS 743..7364
XX FT /*tag= b
XX mutation 2493
XX FT /*tag= a
XX FT /*note= "want to maintain C"
XX
XX WO9203538-A.
XX
XX 05-MAR-1992.
XX
XX 20-AUG-1991; 91WO-US005890.
XX
XX

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```

PR 20-AUG-1990; 90US-00569916.
PR 20-AUG-1990; 90US-00570000.
XX
XX (UYCO ) UNIV COLUMBIA NEW YORK.
XX
XX Racaniello V, Ta, Tatem JM, Weekslevy CL;
XX
XX WPI; 1992-096882/12.
XX P-PSDB; AAR22210.
XX
XX New vaccine against infectious polio-virus comprises RNA virus - for
XX producing RNA virus cDNA and viable RNA virus.
XX
XX Claim 7; Fig 6; 110pp; English.
XX
XX The cDNA sequence is that of a true RNA virus, i.e. the cDNA directs the
XX prodn. of a viable RNA virus which is phenotypically similar to the
XX source virus. Viral RNA was isolated from a virus pellet obd. from a
XX culture of primary monkey kidney cells infected with an attenuated strain
XX 3 poliovirus. The RNA was sequenced and compared to the published
XX P3/Sabin cDNA sequence (Stanway et al., Proc. Natl. Acad. Sci. USA, 81;
XX 1539-43 (1984)). Two nucleotide differences were observed; at position
XX 2493 a T in the Stanway sequence was replaced by a C in the new sequence
XX and at position 6061 a C was replaced by a U(T). The viral DNA was then
XX used as a template for the synthesis of ds cDNA which was used to produce
XX a cDNA library in pUC9. A full length cDNA was determined from several
XX clones isolated from the library. On sequencing, three differences were
XX found in the cDNA, compared to the RNA sequence, at positions 198, 4466
XX and 6334. Site directed mutagenesis was used to correct the sequence at
XX each point. Fragments contg. the correct sequence were amplified by PCR
XX and then ligated to form a true P3/Sabin cDNA in a plasmid pVR318. On
XX sequencing, the plasmid was found to have a T at position 2493 instead of
XX a C. In order to change this, a SacI/HindIII fragment spanning a
XX nucleotides 1895-4241 from pVR318 was removed and replaced with a
XX corresp. fragment from a subclone pLL3-271. The resulting ligation prod.
XX pLLB3, represents a true full length type 3 polio- virus vaccine strain
XX cDNA. The RNA viruses are used in vaccines against polio. The screening
XX method can be used during amplification of the source virus for vaccine
XX prodn. to ensure maintenance of C at position 2493 in the viral genome
XX i.e. increasing the attenuation. The new prod. overcomes the problem of
XX errors introduced during replication of ss RNA, which is much higher than
XX for ds DNA. See also AAQ22966,7. (Updated on 25-MAR-2003 to correct PA
XX field.)
XX
XX Sequence 7432 BP; 2148 A; 1743 C; 1738 G; 1803 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 2; Length 7432;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
DB 568 AAGGAACACGGACACCCAA 549

RESULT 84
AAN20042/C
ID AAN20042 standard; cDNA; 7440 BP.
XX
XX AAN20042;
XX
XX 28-OCT-2003 (revised)
XX 27-AUG-2003 (revised)
XX 25-MAR-2003 (revised)
XX 05-AUG-1992 (first entry)
XX
XX Sequence of a full-length cDNA copy of the poliovirus genome in plasmid
XX pVR106.
XX
XX Poliovirus; picornavirus; vaccine; antigen; immunogen; ss.
XX
XX Homo sapiens; poliovirus.
XX

```

```
PH Key Location/Qualifiers
FT CDS 743..949
FT /*tag= a
FT /product= "P4"
FT CDS 950..1765
FT /*tag= b
FT /product= "VP2"
FT CDS 1766..2479
FT /*tag= c
FT /product= "VP3"
FT CDS 2480..3385
FT /*tag= d
FT /product= "VP1"
FT CDS 3386..3832
FT /*tag= e
FT /product= "3b"
FT CDS 3833..4123
FT /*tag= f
FT /product= "5b"
FT CDS 4124..5110
FT /*tag= g
FT /product= "X"
FT CDS 5111..5371
FT /*tag= h
FT /product= "1b"
FT CDS 5372..5986
FT /*tag= i
FT /product= "VPg"
FT CDS 5987..7375
FT /*tag= j
FT /product= "4 (p63)"
XX
XX W08203632-A.
XX
XX 28-OCT-1982.
XX
XX 20-APR-1981; 81US-00255879.
XX
XX 20-APR-1981; 81US-00255879.
XX 12-NOV-1981; 81US-00320525.
XX
XX (MASI ) MASSACHUSETTS INST TECHNOLOGY.
XX
XX Baltimore D, Racaniello VR;
XX
XX WPI; 1982-95059E/44.
XX P-PSDB; AAP20037.
XX
XX Prodn. of CDNA representing viral RNA sequences - by transcription,
XX insertion into vector and host cell transformation.
XX
XX Example; Table 1, pages 25-31; 50pp; English.
XX
XX Plasmid pVR106 was produced by combining plasmids pVR104 and pVR105. It
XX contains a full-length cDNA copy of the poliovirus genome. E.coli HB101
XX contg. this plasmid has been registered as ATCC 31844. The full-length
XX poliovirus cDNA molecule is itself infectious and can be introduced into
XX cells and these cultured to produce RNA virus. Alternatively, the
XX infectious cDNA can be treated with mutagens and the altered material
XX used to infect cells so that attenuated viral RNA is prod. and this used
XX to make vaccines. For antibody prodn., cDNA capable of directing antigen
XX prodn. is selected and isolated and incorporated into cells which are
XX incubated to produce RNA antigen. (Updated on 25-MAR-2003 to correct PA
XX field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 28-OCT-
XX 2003 to standardise OS field)
XX
XX Sequence 7440 BP; 2205 A; 1734 C; 1716 G; 1785 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 1; Length 7440;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAGGAAACACGGACACCCAA 20
XX
XX
```

```
Db 565 AAGGAAACACGGACACCCAA 546
|||||
RESULT 85
AAX26152/c
ID AAX26152 standard; DNA; 7441 BP.
XX
XX AAX26152;
AC
XX 21-MAY-1999 (first entry)
DT
XX
XX DNA sequence of human poliovirus 1.
XX
XX Replication-competent; Sabin type 1 poliovirus vector; cloning site;
XX 3C-protease cleavage site; mucosal vaccine; infectious disease; AIDS;
XX human immunodeficiency virus type 1; HIV-1; small pox; poliomyelitis;
XX Hepatitis C; acquired immunodeficiency syndrome; Mahoney vector; viral;
XX poliovirus; ss.
XX
XX Poliovirus.
XX
XX W09907859-A1.
FN
XX
XX 18-FEB-1999.
PD
XX
XX 07-AUG-1998; 98WO-KR000242.
PF
XX
XX 07-AUG-1997; 97KR-00037812.
PR
XX
XX (ALTW-) ALTWELL BIOTECH INC.
PA
XX
XX Bae YS, Jung HR;
PI
XX
XX WPI; 1999-167434/14.
DR
XX
XX New replication-competent recombinant Sabin type 1 poliovirus vector -
XX useful for developing mucosal vaccines against HIV-type 1, small pox,
XX poliomyelitis and hepatitis C.
XX
XX Disclosure; Page 51-55; 64pp; English.
XX
XX The invention relates to a replication-competent recombinant Sabin type 1
XX poliovirus vector encoding a multiple cloning site and 3C-protease
XX cleavage site between the two end N-terminal residues. This comprises a
XX vector containing an exogenous vaccine gene at the multiple cloning site.
XX A method of production of both vectors is also provided. The recombinant
XX vectors are useful for developing various mucosal vaccines against a
XX number of infectious diseases, including human immunodeficiency virus
XX type 1 (HIV-1) (which causes acquired immunodeficiency syndrome (AIDS)),
XX small pox, poliomyelitis and Hepatitis C. The poliovirus-mediated mucosal
XX vaccine vectors overcome the disadvantages exhibited by Mahoney vectors
XX by being safe to humans, replicable (having equal replication ability to
XX that of the wild type) vectors, where the introduced vaccine genes are
XX stably maintained during viral passages
XX
XX Sequence 7441 BP; 2210 A; 1730 C; 1715 G; 1786 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 2; Length 7441;
XX Best Local Similarity 100.0%; Pred. No. 13;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 AAGGAAACACGGACACCCAA 20
XX
XX 565 AAGGAAACACGGACACCCAA 546
|||||
RESULT 86
ACC43138/c
ID ACC43138 standard; DNA; 7873 BP.
XX
XX ACC43138;
AC
XX
```

DT 17-JUN-2003 (first entry)  
 XX Nucleotide sequence of gene expression vector pGFPstopneo.  
 DE Gene expression vector; beta-galactosidase; luciferase; pGFPstopneo; ss.  
 KW Synthetic.  
 XX WO2003014361-A1.  
 XX 20-FEB-2003.  
 XX 31-JUL-2002; 2002WO-EP008520.  
 XX 02-AUG-2001; 2001EP-00118632.  
 XX (ALTA-) ALTANA PHARMA AG.  
 XX Hauser H, Mueller PP, Schaefer KP, Steinhilber W;  
 XX WPI; 2003-268203/26.  
 XX New recombinant gene expression vector, useful for producing a host cell  
 PT clone highly expressing a gene of interest, comprises a promoter  
 PT sequence, gene of interest, translational stop signal and a selectable  
 PT marker gene.  
 XX  
 PS Example 1; Fig 12; 52pp; English.  
 XX The specification describes a recombinant gene expression vector, which  
 CC comprises a promoter sequence; a gene of interest encoding beta-  
 CC galactosidase; a TGA translational stop signal; and translationally  
 CC linked to the gene of interest a selectable marker gene encoding  
 CC luciferase. The recombinant gene expression vector is useful for  
 CC producing a host cell clone expressing a gene of interest. The vector is  
 CC also useful for the selection of transformed host cells that express a  
 CC gene of interest. The present sequence represents pGFPstopneo. It was  
 CC used during construction of vectors of the invention  
 XX  
 SQ Sequence 7873 BP; 1939 A; 2060 C; 2053 G; 1821 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 8; Length 7873;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 3286 AAGGAACACGACACCCAA 3267  
 |||||  
 RESULT 87  
 ADP74702/c  
 ID ADP74702 standard; DNA; 7925 BP.  
 XX ADP74702;  
 AC  
 XX 26-AUG-2004 (first entry)  
 XX Novel bicistronic retroviral vector related vector #4.  
 XX immunosuppressive; gene therapy; vector; bicistronic retroviral vector;  
 KW severe combined immune deficiency syndrome; protein expression;  
 KW antisense; ds; gene.  
 XX Synthetic.  
 OS Unidentified.  
 XX Location/Qualifiers  
 FH LTR 162..674  
 FT /\*tag= a  
 FT /standard name= "5'-LTR"  
 FT 675..1572  
 FT 5'UTR  
 FT /\*tag= b

CDS 1573..2700  
 FT /\*tag= c  
 FT /product= "HSV-TK"  
 FT misc RNA 2711..3335  
 FT /\*tag= d  
 FT /standard\_name= "IRES"  
 FT 3383..4183  
 FT /\*tag= e  
 FT /product= "neo"  
 FT 4478..5067  
 FT /\*tag= f  
 FT /standard\_name= "3'-LTR"  
 XX  
 PN EP1428886-A1.  
 XX 16-JUN-2004.  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX 09-DEC-2002; 2002EP-00027555.  
 XX (CELL-) CELLTECH GMBH BIOTECHNOLOGIE.  
 XX Heberlein C, Gindullis F, Hannemann J, Strathmann G;  
 XX WPI; 2004-452367/43.  
 XX Bicistronic retroviral vector, useful in gene therapy, particularly of  
 PT graft versus host disease, contains components of both murine embryonic  
 PT stem cell and myeloproliferative sarcoma viruses.  
 XX Disclosure; Page 66-68; 91pp; German.  
 PS The present invention relates to a new bicistronic retroviral vector.  
 CC These are used for (over)expression of proteins, suppressing expression  
 CC of (non-)viral RNA and/or proteins by the antisense technique, e.g. to  
 CC suppress a dominant-negative phenotype, also infectious viral particles  
 CC that contain the vectors, in gene therapy, particularly for control of  
 CC guest versus host disease, especially where haematopoietic cells are  
 CC transduced with the vector or where T cells are transduced, for adoptive  
 CC immunotherapy, but also for treating severe combined immune deficiency  
 CC syndrome, and for expression cloning of genes. The present sequence is a  
 CC vector sequence shown in the exemplification of the invention.  
 XX  
 SQ Sequence 7925 BP; 1714 A; 2242 C; 2135 G; 1834 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 12; Length 7925;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 3273 AAGGAACACGACACCCAA 3254  
 |||||  
 RESULT 88  
 ACC43139/c  
 ID ACC43139 standard; DNA; 7943 BP.  
 XX ACC43139;  
 AC  
 XX 17-JUN-2003 (first entry)  
 DT Nucleotide sequence of gene expression vector pGFPstopneoSECIS.  
 DE Gene expression vector; beta-galactosidase; luciferase; pGFPstopneoSECIS;  
 KW ss.  
 XX Synthetic.  
 OS WO2003014361-A1.  
 XX 20-FEB-2003.  
 PD

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XX 31-JUL-2002; 2002WO-EP008520.
PF
XX
XX 02-AUG-2001; 2001EP-00118632.
PR
XX
XX (ALTA-) ALTANA PHARMA AG.
PA
XX
XX Hauser H, Mueller PP, Schaefer KP, Steinhilber W;
PI
XX WPI; 2003-268203/26.
DR
XX
XX New recombinant gene expression vector, useful for producing a host cell
XX clone highly expressing a gene of interest, comprises a promoter
XX sequence, gene of interest, translational stop signal and a selectable
XX marker gene.
XX
XX Example 4; Fig 13; 52pp; English.
PS
XX
XX The specification describes a recombinant gene expression vector, which
XX comprises a promoter sequence; a gene of interest encoding beta-
XX galactosidase; a TGA translational stop signal; and translationally
XX linked to the gene of interest a selectable marker gene encoding
XX luciferase. The recombinant gene expression vector is useful for
XX producing a host cell clone expressing a gene of interest. The vector is
XX also useful for the selection of transformed host cells that express a
XX gene of interest. The present sequence represents pGFPstopneoSEClS. It
XX was used during construction of vectors of the invention
XX
XX Sequence 7943 BP; 1958 A; 2074 C; 2074 G; 1837 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 8; Length 7943;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 3286 AAGGAACACGGACACCCAA 3267

RESULT 89
ID AAV18096/C
XX
XX AAV18096 standard; DNA; 8298 BP.
AC
XX
XX AAV18096;
XX
XX 04-AUG-1998 (first entry)
XX
XX pMCLDHAP tricistronic vector for the expression of hmAb45-TNF alpha.
XX
XX Circular; antibody-cytokine fusion protein; tricistronic vector;
XX TNF alpha; IL-2; IRES; internal ribosome entry site; ds.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX promoter 1..904
XX /tag= a
XX /note= "CMV promoter with an upstream MPSV enhancer"
XX intron 905..976
XX /tag= b
XX /number= Intron 1
XX sig_peptide 977..1018
XX /tag= c
XX /note= "Partial leader sequence"
XX 5'UTR 1019..1106
XX /tag= d
XX /note= "5'UTR from poliovirus"
XX CDS 1107..1433
XX /tag= e
XX /product= "Light chain hmAb425, variable region"
XX sig_peptide 1107..1115
XX /tag= f
XX /note= "Rest of the leader sequence"
XX

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```

FT intron 1260..2581
FT /tag= k
FT /number= 3
FT intron 1434..1595
FT /tag= g
FT /number= Intron 2
FT CDS 1596..1913
FT /tag= h
FT /product= "Light chain hmAb425, constant region"
FT 5'UTR 1914..2028
FT /tag= i
FT /note= "5' UTR from poliovirus"
FT RBS 2029..2159
FT /tag= j
FT /note= "Poliovirus derived internal ribosome entry site"
FT CDS 2582..4537
FT /tag= l
FT /note= "Heavy chain hmAb425 fused to TNF alpha"
FT misc_feature 4565..5279
FT /tag= m
FT /note= "Comprises of a 5' UTR from poliovirus, an
FT internal ribosome entry site and intron 4"
FT CDS 5280..5876
FT /tag= n
FT /product= "Puromycin acetyl transferase"
FT /note= "Selection marker"
FT polyA_signal 5929..6181
FT /tag= o
FT /standard_name= "SV40 PolyA"
XX
XX WO9811241-A1.
XX
XX 19-MAR-1998.
XX
XX 02-SEP-1997; 97WO-EP004765.
XX
XX 16-SEP-1996; 96EP-00114820.
XX 30-SEP-1996; 96EP-00115635.
XX
XX (MERE ) MERCK PATENT GMBH.
XX
XX Von Hoegen I, Burge C, Bruemmer W, Dunker R, Rieke E, Welge T;
XX Hauser H, Mielke C;
XX
XX WPI; 1998-207400/18.
XX
XX P-PSDS; AAW48647, AAW48648, AAW48649, AAW48650, AAW48651.
XX
XX Oligo:cistronic expression vector - useful for production of, e.g.
XX MAb425/TNF--a or MAb425/IL-2 antibody fusion protein.
XX
XX Claim 11; Fig 15; 89pp; English.
XX
XX The present sequence represents a new pMCLDHAP tricistronic vector for
XX the expression of an antibody-cytokine fusion protein, hmAb425-TNF alpha.
XX hmAb425-TNF alpha comprises of the TNF alpha fused to the C-terminus of
XX the heavy chain of humanized by the IL-2 sequence. The TNF alpha
XX sequence can be substituted by the IL-2 sequence. The hmAb425 has
XX specificity for the human EGF receptor. The vector also contains a strong
XX promoter/enhancer unit, a selection marker gene and at least two
XX poliovirus derived internal ribosomal entry site (IRES) sequences. The
XX vector can be expressed in mammalian host cells for the production of
XX heteromeric fusion proteins. This expression system is claimed to produce
XX the heteromeric proteins in high yields
XX
XX Sequence 8298 BP; 1974 A; 2364 C; 2134 G; 1826 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 20; DB 2; Length 8298;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20
Db 5140 AAGGAACACGGACACCCAA 5121

```

OS	Synthetic.
OS	Unidentified.
XX	
XX	WO2004035799-A2.
XX	
XX	29-APR-2004.
PD	
XX	
XX	10-OCT-2003; 2003WO-EP011252.
PF	
XX	
XX	11-OCT-2002; 2002DE-01048141.
PR	
XX	
XX	(UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.
PA	
XX	
XX	Waehler R, Schnieders F;
PI	
XX	
XX	WPI; 2004-357221/33.
DR	
XX	
XX	Viral vector that expresses single-chain interleukin-12 and costimulator,
PT	useful for treatment of tumors, viral infections, e.g. human
PT	immunodeficiency virus, and prion diseases.
XX	
PS	Disclosure; Fig 25; 129pp; German.
XX	
CC	The present invention relates to a viral vector that includes a nucleic acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory protein. Viral vectors and virus particles derived from them are useful for treatment of tumours, infectious diseases (e.g. HIV, hepatitis A, B or C, cytomegalovirus or human papilloma virus), or prion diseases. The present sequence is a viral vector shuttle sequence used in the exemplification of the invention.
CC	
XX	
SQ	Sequence 10633 BP; 2627 A; 2749 C; 2779 G; 2427 T; 0 U; 51 Other;
	Query Match 100.0%; Score 20; DB 12; Length 10633;
	Best Local Similarity 100.0%; Pred.No. 14;
	Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AAGGAAACACGGACACCCAA 20 
Db	3244 AAGGAAACACGGACACCCAA 3225 
RESULT 92	
ID	ABK86536/c
ID	ABK86536 standard; DNA; 11058 BP.

XX ABK86536;  
 XX  
 XX  
 XX 07-AUG-2003 (revised)  
 XX 30-AUG-2002 (first entry)  
 XX  
 XX EIAV based retroviral vector pONY8-TRIC.  
 XX  
 XX Parkinson's disease; gene therapy; retroviral vector; ds; cyclic; EIAV;  
 KW neuroprotective; antiparkinsonian; NOI; IRES; lentiviral particle;  
 KW nucleotide site of interest; Internal Ribosome Entry Site; PONY8-TRIC;  
 KW tyrosine hydroxylase; GTP-cyclohydrolase 1; bicistronic cassette;  
 KW Aromatic Amino Acid Dopa Decarboxylase; tricistronic cassette;  
 KW Vesicular Monoamine Transporter 2; neurodegenerative disease.  
 XX  
 XX Equine infectious anemia virus.  
 OS Human cytomegalovirus.  
 OS Escherichia coli.  
 OS Aequorea victoria.  
 OS Homo sapiens.  
 OS Synthetic.  
 XX WO200229065-A2.  
 XX  
 XX 11-APR-2002.  
 XX  
 XX 05-OCT-2001; 2001WO-GB004433.  
 XX  
 XX 06-OCT-2000; 2000GB-00024550.  
 XX (OXFO-) OXFORD BIOMEDICA UK LTD.  
 XX  
 XX Kingsman AJ, Mazarakis ND, Martin-Rendon E, Azzouz M, Rohll J;  
 XX WPI; 2002-507885/54.  
 XX  
 XX A novel retroviral vector genome is useful in the treatment of  
 PT Parkinson's disease.  
 XX  
 XX Example 8; Page 70-72; 106pp; English.  
 XX  
 XX The invention relates to a retroviral vector genome (G1) comprising two  
 CC or more NOIs (nucleotide sites of interest), operably linked by one or  
 CC more Internal Ribosome Entry Site(s) (IRES). Also included are a vector  
 CC system (S1) comprising (G1), production (M1) of a lentiviral particle, a  
 CC viral particle (P1) produced by (M1) or by (S1), a pharmaceutical  
 CC composition comprising (G1), (S1) or (P1), a bicistronic cassette  
 CC comprising a nucleotide sequence which encodes: a) tyrosine hydroxylase  
 CC and a nucleotide sequence which encodes GTP-cyclohydrolase 1 operably  
 CC linked by one or more IRES(s); or b) Aromatic Amino Acid Dopa  
 CC Decarboxylase and a nucleotide sequence which encodes Vesicular Monoamine  
 CC Transporter 2 operably linked by one or more IRES(s), a tricistronic  
 CC cassette comprising a nucleotide sequence which encodes tyrosine  
 CC hydroxylase, a nucleotide sequence that encodes GTP-cyclohydrolase 1 and  
 CC a nucleotide sequence which encodes Aromatic Amino Acid Dopa  
 CC Decarboxylase, operably linked by one or more IRES(s) and a cell that has  
 CC been transduced with (S1). G1, the vector system (S1), and the viral  
 CC particle (P1) can all be used to treat and/or prevent (by gene therapy) a  
 CC neurodegenerative disease, especially Parkinson's disease in a subject,  
 CC and also in the manufacture of a pharmaceutical composition to treat the  
 CC above mentioned disease. Treatment with vectors capable of delivering  
 CC e.g., Tyrosine hydroxylase, GTP-cyclohydrolase 1, Aromatic Amino Acid  
 CC Dopa Decarboxylase and Vesicular Monoamine Transporter 2, are useful for  
 CC the last stages of treatment for sufferers of Parkinson's disease where  
 CC they do not respond significantly to L-dopa treatment by prior art  
 CC methodologies. The present sequence is retroviral vector of the  
 CC invention, pONY8-TRIC comprising elements of the EIAV (Equine infectious  
 CC anaemia virus) genome, human cytomegalovirus sequences, a plasmid  
 CC backbone, a green fluorescent protein sequence and the tricistronic  
 XX cassette. (Updated on 07-AUG-2003 to correct OS field.)  
 XX  
 XX Sequence 11058 BP; 2875 A; 2647 C; 2813 G; 2723 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 11058;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 3813 AAGGAAACACGGACACCCAA 3794  
 |||||  
 RESULT 93  
 AAV12373/c  
 ID AAV12373 standard; DNA; 11326 BP.  
 XX  
 XX  
 AC AAV12373;  
 XX  
 DT 17-OCT-2003 (revised)  
 DT 03-JUL-1998 (first entry)  
 XX  
 XX Chimeric protease NS3/poliiovirus gene NS3 delta-C-PV1.  
 XX  
 KW Chimeric; Hepatitis C virus; HCV; poliovirus; liver cirrhosis;  
 KW NS3 protease gene; NSSA/5B; hepatocellular carcinoma; anti-HCV drug; ss.  
 XX  
 OS Hepatitis C virus.  
 OS Poliovirus.  
 OS Chimeric.  
 XX  
 FN WO9800548-A1.  
 XX  
 XX 08-JAN-1998.  
 XX  
 XX 25-JUN-1997; 97WO-KR000120.  
 XX  
 XX 28-JUN-1996; 96KR-00024910.  
 XX (GLDS ) LG CHEM CO LTD.  
 XX (UYPO-) UNIV POHANG SCI & TECHNOLOGY.  
 PA  
 PA Jang SK, Hahn BS;  
 XX  
 XX WPI; 1998-086973/08.  
 XX  
 XX Recombinant gene encoding hepatitis C surrogate virus - comprises  
 PT picornavirus and hepatitis C virus protease NS3 genes and hepatitis C  
 PT virus protease NS3 target sites, useful for drug screening.  
 XX  
 XX Claim 1; Fig 6A-6E; 36pp; English.  
 XX  
 XX The present chimeric sequence comprises of a Hepatitis C Virus (HCV)  
 CC protease NS3 gene and its target site NS5A/5B gene inserted into the open  
 CC reading frame of the poliovirus gene. HCV is the major etiologic agent of  
 CC non-A, non-B hepatitis, and has been implicated in liver cirrhosis and  
 CC hepatocellular carcinoma. The invention provides a hepatitis C surrogate  
 CC virus comprising of the recombinant gene described. Upon expression, the  
 CC HCV NS3 protease would cleave its target site to become independent of  
 CC the poliovirus polyprotein. HCV NS3 protease contained within the  
 CC surrogate is a good therapeutic target molecule for the development of  
 CC anti-HCV drugs, since its activity is considered essential for viral  
 CC proliferation. The surrogate virus is claimed to be useful than the  
 CC existing in vitro systems for HCV culture for screening anti-HCV drugs  
 CC and testing for their efficacy. It is also considered to be useful for  
 CC studying HCV genes in viral replication. (Updated on 17-OCT-2003 to  
 CC standardise OS field)  
 XX  
 XX Sequence 11326 BP; 3169 A; 2751 C; 2737 G; 2669 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 20; DB 2; Length 11326;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 565 AAGGAAACACGGACACCCAA 546  
 |||||



RESULT 94  
ADO07659/c  
ID ADO07659 standard; DNA; 11746 BP.  
XX  
XX  
AC ADO07659;  
XX  
XX  
DT 15-JUL-2004 (first entry)  
XX  
XX  
DE Viral vector shuttle (CMV) IL12 (IRES) 4-1BBL (IRES) IL-2.  
XX  
XX  
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;  
KW immunostimulant; expression cassette; viral vector; interleukin-12;  
KW co-stimulatory protein; cancer; infection; ds; gene.  
XX  
XX  
OS Synthetic.  
OS Unidentified.  
XX  
XX  
FN WO2004035799-A2.  
XX  
XX  
PD 29-APR-2004.  
XX  
XX  
PF 10-OCT-2003; 2003WO-EP011252.  
XX  
XX  
PR 11-OCT-2002; 2002DE-01048141.  
XX  
XX  
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.  
XX  
XX  
PI Waehler R, Schnieders F;  
XX  
XX  
DR WPI; 2004-357221/33.  
XX  
XX  
SQ Sequence 11746 BP; 2920 A; 3037 C; 3055 G; 2683 T; 0 U; 51 Other;  
XX  
XX  
PT Viral vector that expresses single-chain interleukin-12 and costimulator,  
PT useful for treatment of tumors, viral infections, e.g. human  
PT immunodeficiency virus, and prion diseases.  
XX  
XX  
PS Disclosure; Fig 24; 129pp; German.  
XX  
XX  
CC The present invention relates to a viral vector that includes a nucleic  
CC acid encoding a single-chain interleukin-12 (IL-12) and a co-stimulatory  
CC protein. Viral vectors and virus particles derived from them are useful  
CC for treatment of tumors, infectious diseases (e.g. HIV, hepatitis A, B  
CC or C, cytomegalovirus or human papilloma virus), or prion diseases. The  
CC present sequence is a viral vector shuttle sequence used in the  
CC exemplification of the invention.  
XX  
XX  
SQ Sequence 11746 BP; 2920 A; 3037 C; 3055 G; 2683 T; 0 U; 51 Other;  
XX  
XX  
Query Match 100.0%; Score 20; DB 12; Length 11746;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGGAACACGACACCCAA 20  
DB 3244 AAGGAACACGACACCCAA 3225  
RESULT 95  
ADO07662/c  
ID ADO07662 standard; DNA; 38246 BP.  
XX  
XX  
AC ADO07662;  
XX  
XX  
DT 15-JUL-2004 (first entry)  
XX  
XX  
DE Viral vector pAd-3.  
XX  
XX  
KW cytostatic; virucide; anti-HIV; hepatotropic; neuroprotective;  
KW immunostimulant; expression cassette; viral vector; interleukin-12;  
KW co-stimulatory protein; cancer; infection; ds; gene.  
XX  
XX  
OS Synthetic.

OS Unidentified.  
XX  
XX  
FN WO2004035799-A2.  
XX  
XX  
PD 29-APR-2004.  
XX  
XX  
PF 10-OCT-2003; 2003WO-EP011252.  
XX  
XX  
PR 11-OCT-2002; 2002DE-01048141.  
XX  
XX  
PA (UYHA-) UNIV HAMBURG-EPPENDORF KLINIKUM.  
XX  
XX  
PI Waehler R, Schnieders F;  
XX  
XX  
DR WPI; 2004-357221/33.  
XX  
XX  
SQ Sequence 38246 BP; 8959 A; 10813 C; 10384 G; 8043 T; 0 U; 47 Other;  
XX  
XX  
Query Match 100.0%; Score 20; DB 12; Length 38246;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 AAGGAACACGACACCCAA 20  
DB 6097 AAGGAACACGACACCCAA 6078  
RESULT 96  
ADK66744/c  
ID ADK66744 standard; DNA; 62 BP.  
XX  
XX  
AC ADK66744;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
XX  
DE Picornaviridae DNA 5'-untranslated region specific probe.  
XX  
XX  
KW Gene expression; gene polymorphism; cross-species hybridisation; probe;  
KW ss.  
XX  
XX  
OS Picornaviridae.  
XX  
XX  
PN US2003211526-A1.  
XX  
XX  
PD 13-NOV-2003.  
XX  
XX  
PF 14-FEB-2003; 2003US-00366823.  
XX  
XX  
PR 15-FEB-2002; 2002US-0357541P.  
XX  
XX  
PA (JUAN/) JUANG J.  
PA (HSIU/) HSIUNG C A.  
PA (LINC/) LIN C.  
XX  
XX  
PI Juang J, Hsiung CA, Lin C;  
XX  
XX  
DR WPI; 2004-059849/06.  
XX  
XX  
PT Collection of at least four nucleic acid probes for analysis of gene

PT expression and of gene polymorphisms, comprises each probe including  
 PT segment and entirety of which hybridizes under low stringency conditions  
 PT to genes of two species.

XX Example; SEQ ID NO 5; 11pp; English.

XX The present invention relates to a collection of at least four nucleic  
 CC acid probes, each including a segment, the entirety of which hybridizes  
 CC under low stringency conditions to at least a first gene of first species  
 CC and a second gene of second species, where the hybridising probes  
 CC correspond to different genes of the two species and the genes are  
 CC orthologous to each other. The invention is useful for analysis of gene  
 CC expression and of gene polymorphisms. The probes are designed for cross-  
 CC species hybridisation, e.g. by identification of conserved segments among  
 CC orthologous genes. The present sequence is Picornaviridae DNA 5'-  
 CC untranslated region (UTR) specific probe. This sequence is used in the  
 CC exemplification of the invention.

XX Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;

Query Match 100.0%; Score 20; DB 12; Length 62;  
 Best Local Similarity 95.0%; Pred. No. 15;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 ||:|||||  
 Db 57 AAKGAACACGGACACCCAA 38

RESULT 97  
 AEC07516/c  
 ID AEC07516 standard; DNA; 62 BP.  
 XX  
 AC AEC07516;  
 XX  
 DT 20-OCT-2005 (first entry)  
 XX  
 DE Picornaviridae 5'UTR degenerate probe, SEQ ID NO:5.  
 XX  
 KW DNA detection; hybridization; 5'-UTR; probe; ss.  
 XX  
 OS Picornaviridae.  
 XX  
 TW200303921-A.  
 XX  
 PD 16-SEP-2003.

XX  
 XX  
 XX 14-FEB-2003; 2003TW-00103058.  
 XX  
 PR 15-FEB-2002; 2002US-00357541.  
 XX  
 FA (NAHE-) NAT HEALTH RES INST.  
 XX  
 PI Juang J, Shiung J, Lin J;  
 XX  
 DR WPI; 2005-579874/59.

XX Trans-species nucleic acid probe - for a probe collection having at least  
 PT four nucleic acid probes.

XX Example; SEQ ID NO 5; 46pp; Chinese.

XX The invention relates to a collection of at least four nucleic acid  
 CC probes comprising a segment able to hybridize to orthologous genes from  
 CC at least two different species. In the embodiments of the invention, the  
 CC probe segment is at least 60% identical to orthologous genes from two  
 CC different species. The present sequence represents a degenerate probe  
 CC used to detect 5' untranslated region (5'UTR) sequences from viruses of  
 CC the Picornaviridae family.

XX Sequence 62 BP; 9 A; 11 C; 15 G; 20 T; 0 U; 7 Other;

Query Match 100.0%; Score 20; DB 14; Length 62;

Best Local Similarity 95.0%; Pred. No. 15;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 ||:|||||  
 Db 57 AAKGAACACGGACACCCAA 38

RESULT 98  
 ACD26711/c  
 ID ACD26711 standard; DNA; 28 BP.  
 XX  
 AC ACD26711;  
 XX  
 DT 11-SEP-2003 (first entry)  
 XX  
 DE Enterovirus detection method associated primer #11.  
 XX  
 KW Enterovirus detection; primer; ss.  
 XX  
 OS Enterovirus.  
 XX  
 CN1366066-A.  
 XX  
 PD 28-AUG-2002.  
 XX  
 PF 15-JAN-2001; 2001CN-00100622.  
 XX  
 PR 15-JAN-2001; 2001CN-00100622.  
 XX  
 PA (JING-) JINGYU BIOLOGIC SCI TECHNOLOGY IND CO LT.  
 XX  
 PI Li G, Bai Q, Zeng Y;  
 XX  
 DR WPI; 2003-230558/23.

XX Process, primer and probe for detecting and discriminating enterovirus.  
 XX  
 PS Claim 5; Page 2; 33pp; Chinese.  
 XX  
 CC The invention describes the application of nucleotide primer to detecting  
 CC enterovirus. The detection method and the reagent kit are disclosed. This  
 CC sequence represents an enterovirus detection method associated primer  
 CC  
 XX Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other;

Query Match 100.0%; Score 20; DB 8; Length 28;  
 Best Local Similarity 95.0%; Pred. No. 22;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAACACGGACACCCAA 20  
 ||:|||||  
 Db 24 AADGAACACGGACACCCAA 5

RESULT 99  
 ADU47464/c  
 ID ADU47464 standard; DNA; 28 BP.  
 XX  
 AC ADU47464;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE p3 probe used to detect enterovirus type 71 (EV71) in a sample.  
 XX  
 KW Detection; enterovirus type 71; probe; ss.  
 XX  
 OS Enterovirus.  
 XX  
 US6818397-B1.  
 XX  
 PD 16-NOV-2004.

PP 28-NOV-2000; 2000US-00724678.  
 PR 28-NOV-2000; 2000US-00724678.  
 XX (CHIP-) CHIP BIOTECHNOLOGY INC.  
 XX Lee K, Bair C, Tseng Y, Wang Y, Wang S;  
 XX WPI; 2004-793563/78.  
 DR This invention provides a method and a kit for detecting and  
 XX differentiating an enterovirus type 71 (EV71) in a sample. The method  
 XX involves contacting nucleic acids in the sample with a pair of primers to  
 XX form an amplification product; contacting the amplification product with  
 XX at least one synthetic nucleotide sequence fixed on a solid substrate and  
 XX detecting hybridisation. The present sequence is a probe used to detect  
 XX and differentiate enterovirus type 71 (EV71) in a sample.  
 XX Sequence 28 BP; 2 A; 4 C; 6 G; 15 T; 0 U; 1 Other;  
 SQ Query Match 100.0%; Score 20; DB 13; Length 28;  
 Best Local Similarity 95.0%; Pred. No. 22;  
 Matches 19; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 AAGGAACACGACGACCCAA 20  
 ||:|||||  
 Db 24 AAGGAACACGACGACCCAA 5  
 RESULT 100  
 ID ADW75017/C  
 XX ADW75017 standard; DNA; 70 BP.  
 XX AC ADW75017;  
 XX 07-APR-2005 (first entry)  
 XX Human rhinovirus probe PBRH\_00006.  
 DE probe; ss; biochip; DNA chip; microorganism detection; diagnosis;  
 XX infection; adenovirus infection; coronavirus infection;  
 XX respiratory disease; Chlamydia pneumoniae infection;  
 XX SARS coronavirus infection; treponema pallidum infection; sialodentitis;  
 XX rubella virus infection; rhinovirus infection;  
 XX respiratory syncytial virus infection; influenza virus infection;  
 XX parainfluenza virus infection; mycoplasma infection;  
 XX measles virus infection; HIV infection; HIV1 infection;  
 XX hepatitis A virus infection; hepatitis B virus infection;  
 XX hepatitis C virus infection; hepatitis D virus infection;  
 XX hepatitis E virus infection; hepatitis G virus infection;  
 XX herpesvirus infection.  
 XX Human rhinovirus sp.  
 OS WO2005005658-A1.  
 XX 20-JAN-2005.  
 XX 14-JUL-2003; 2003WO-CN000561.  
 XX 14-JUL-2003; 2003WO-CN000561.  
 XX (CAP1-) CAPITAL BIOCHIP CO LTD.  
 XX (UYQ1) UNIV QINGHUA.  
 XX Li Z, Tao S, Cheng J;  
 XX Search completed: March 9, 2006, 00:30:11  
 XX Job time : 214.388 secs

DR WPI; 2005-122431/13.  
 XX New chip for assaying for a coronavirus causing the severe acute  
 PT respiratory syndrome (SARS-Cov) and a non-SARS-Cov infectious organism  
 PT comprising a support and oligonucleotide probes.  
 XX Disclosure; Page 34; 122pp; English.  
 XX This invention describes a novel chip used to detect a coronavirus  
 CC causing the severe acute respiratory syndrome (SARS-Cov) and a non-SARS-  
 CC Cov infectious organism. The chip comprises an oligonucleotide probe  
 CC complementary to a nucleotide sequence of SARS-Cov or non-SARS-Cov  
 CC infectious organism causing SARS-like symptoms which located within a  
 CC conserved region of the viral genome. The conserved region of SARS-Cov  
 CC genome is a region located within replicase 1A or 1B gene or the  
 CC nucleocapsid gene of SARS-Cov. The structural protein coding gene of SARS  
 CC -Cov genome is a gene encoding the spike glycoprotein, the small envelope  
 CC protein or nucleocapsid gene. The chip also comprises at least one of an  
 CC immobilization control probe labeled and not participating in any  
 CC hybridization reaction when a sample containing or suspected of  
 CC containing SARS-Cov or a non-SARS-Cov infectious organism. The detection  
 CC method also includes multiplex PCR using primers which amplify nucleotide  
 CC sequences from an influenza A and B virus, a human metapneumovirus, human  
 CC adenovirus and human coronavirus 229E or OC43. The presence of the SARS-  
 CC Cov is determined when a positive hybridization signal is detected using  
 CC at least one of two oligonucleotide probes complementary to two different  
 CC nucleotide sequences located within replicase 1A or 1B, spike  
 CC glycoprotein or nucleocapsid genes of the SARS-Cov, a positive signal is  
 CC detected from the immobilization control probe, a positive hybridization  
 CC signal is detected using the positive control probe and there is no  
 CC hybridization signal using the negative control probe. Detecting a  
 CC positive hybridization signal using at least one of the two  
 CC oligonucleotide probes while not detecting a positive hybridization  
 CC signal using the probe complementary to a nucleotide sequence located of  
 CC within the spike glycoprotein gene of the SARS-Cov indicates mutation of  
 CC the SARS-Cov. The non-SARS-Cov infectious organism causing SARS-like  
 CC symptoms is a human coronavirus 229E or OC43; human enteric coronavirus,  
 CC influenza A or B virus, parainfluenza virus 1, 2, 3 or 4, respiratory  
 CC syncytial virus, human metapneumovirus, rhinovirus, adenovirus,  
 CC mycoplasma pneumoniae, Chlamydia pneumoniae, measles virus or rubella  
 CC virus. Non-SARS-Cov infectious organisms capable of damaging an  
 CC infectious host's immune system include hepatitis A, B, C, D, E or G  
 CC virus, a transfusion transmitting virus (TTV), a human immunodeficiency  
 CC virus 1 (HIV1), a human cytomegalovirus (HCMV), an Epstein-Barr virus  
 CC (EBV) or Treponema pallidum, avian infectious bronchitis virus, avian  
 CC infectious laryngotracheitis virus, murine hepatitis virus, equine  
 CC coronavirus, canine coronavirus, feline coronavirus, porcine epidemic  
 CC diarrhoea virus, porcine transmissible gastroenteritis virus, bovine  
 CC coronavirus, feline infectious peritonitis virus, rat coronavirus,  
 CC neonatal calf diarrhoea coronavirus, porcine haemagglutinating  
 CC encephalomyelitis virus of rat. The methods and compositions of the  
 CC invention are useful in amplifying and detecting SARS-Cov nucleotide  
 CC sequences, in particular for diagnosing early-stage SARS patients  
 CC (infected less than one to three days) and determining whether a subject  
 CC is infected by SARS-Cov and/or a non-SARS-Cov infectious organism causing  
 CC SARS-like symptoms. This sequence represents a probe used in the method  
 CC of the invention.  
 XX Sequence 70 BP; 11 A; 12 C; 20 G; 27 T; 0 U; 0 Other;  
 SQ Query Match 95.0%; Score 19; DB 14; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 29;  
 Matches -19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 AGGAACACGACGACCCAA 20  
 ||:|||||  
 Db 52 AGGAACACGACGACCCAA 34

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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:12:30 ; Search time 1570.68 Seconds  
(without alignments)  
595.756 Million cell updates/sec

Title: US-10-829-474-2  
Perfect score: 20  
Sequence: 1 aaggaacacggacacccaa 20

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_est3:\*
- 4: gb\_hic:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_est7:\*
- 9: gb\_ges1:\*
- 10: gb\_ges2:\*
- 11: gb\_ges3:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	19	95.0	603	1	AL728550
2	18.4	92.0	676	7	CK751666
3	18.4	92.0	845	4	CNS0FP9W
4	18.4	92.0	908	4	CNS0FVC0
5	18.4	92.0	962	11	CNS03BCU
6	18.4	92.0	1042	3	BQ056756
7	18.4	92.0	1230	2	BG752980
8	18	90.0	924	3	BM359242
9	17.4	87.0	458	6	CB359607
10	17.4	87.0	520	9	AZ078930
11	17.4	87.0	682	10	CW118506
12	17.4	87.0	689	10	CW682736
13	17.4	87.0	717	7	CK028165
14	17.4	87.0	729	10	AG479585
15	17.4	87.0	750	7	CF998205
16	17.4	87.0	770	11	CNS03817
17	17.4	87.0	785	7	CV480587
18	17.4	87.0	794	2	BG985751
19	17.4	87.0	794	7	CV486670
20	17.4	87.0	798	7	CK026895
21	17.4	87.0	800	7	CV126404
22	17.4	87.0	819	10	CW117728

C 96	16.8	84.0	1251	9	B2576789	169	15.8	79.0	284	10	CZ594840	CZ594840 CMHD-GT_2
C 97	16.8	84.0	1338	4	CNS0G3AI	170	15.8	79.0	286	1	AV052597	AV052597 AV052597_
C 98	16.8	84.0	1490	4	CNS0RFXN	C 171	15.8	79.0	314	1	AV021413	AV021413 AV021413
C 99	16.8	84.0	1541	4	CNS0RFXW	C 172	15.8	79.0	314	6	CB684607	CB684607 OSNEFI4E
C 100	16.8	84.0	1559	4	CNS0GLAC	C 173	15.8	79.0	315	2	CB576337	CB576337 MBT3043
C 101	16.8	84.0	1577	4	CNS0GLDM	C 174	15.8	79.0	316	2	BB237888	BB237888 BB237888
C 102	16.8	84.0	1585	4	CNS0RQ1R	C 175	15.8	79.0	329	1	AA098537	AA098537 mo10h05.r
C 103	16.8	84.0	1813	2	BF144191	C 176	15.8	79.0	331	8	D60927	D60927 HUM139E06B
C 104	16.8	84.0	3872	4	AK031828	C 177	15.8	79.0	340	9	AQ948615	AQ948615 Sheared D
C 105	16.8	84.0	391	9	EH432447	C 178	15.8	79.0	341	10	CW765705	CW765705 OS_BBa007
C 106	16.4	82.0	451	9	AZ065501	C 179	15.8	79.0	343	3	BQ168857	BQ168857 WHE2471.D
C 107	16.4	82.0	453	7	CK564864	C 180	15.8	79.0	348	1	AA894125	AA894125 EST19728
C 108	16.4	82.0	496	9	AQ985003	C 181	15.8	79.0	352	4	AK206687	AK206687 Mus muscu
C 109	16.4	82.0	505	3	BI387931	C 182	15.8	79.0	355	1	AI170242	AI170242 EST216168
C 110	16.4	82.0	524	9	AZ025615	C 183	15.8	79.0	362	8	D60288	D60288 HUM037C01B
C 111	16.4	82.0	531	9	AQ633537	C 184	15.8	79.0	366	5	CI5565	CI5565 CI5565 Clon
C 112	16.4	82.0	542	9	AQ508060	C 185	15.8	79.0	369	2	BG072477	BG072477 H311A01-
C 113	16.4	82.0	566	2	BF904033	C 186	15.8	79.0	371	9	BZ229210	BZ229210 CH230-488
C 114	16.4	82.0	566	9	AZ036472	C 187	15.8	79.0	375	10	CW118176	CW118176 104_494_1
C 115	16.4	82.0	583	9	AQ544174	C 188	15.8	79.0	376	8	D60883	D60883 HUM135G07B_
C 116	16.4	82.0	600	5	BH236595	C 189	15.8	79.0	381	1	AI598789	AI598789 EST250492
C 117	16.4	82.0	616	1	AV728635	C 190	15.8	79.0	384	5	BY689987	BY689987 HUM037C01A
C 118	16.4	82.0	653	9	BH1998	C 191	15.8	79.0	387	8	D80679	D80679 HUM037C01A
C 119	16.4	82.0	668	8	DN637308	C 192	15.8	79.0	389	7	CV043810	CV043810 dba19f04.
C 120	16.4	82.0	674	9	AQ051998	C 193	15.8	79.0	397	5	BY001982	BY001982 BY001982
C 121	16.4	82.0	682	7	CK515348	C 194	15.8	79.0	401	2	BE177238	BE177238 RC6-HT059
C 122	16.4	82.0	710	9	BH951435	C 195	15.8	79.0	404	5	BY610270	BY610270 BY610270
C 123	16.4	82.0	730	9	BH214104	C 196	15.8	79.0	407	2	BE137277	BE137277 u61f07.Y
C 124	16.4	82.0	751	11	CR828818	C 197	15.8	79.0	407	6	CB979169	CB979169 CAB40007
C 125	16.4	82.0	751	11	CR828818	C 198	15.8	79.0	408	7	CN304454	CN304454 170006001
C 126	16.4	82.0	795	9	BZ604205	C 199	15.8	79.0	410	9	AQ404432	AQ404432 HS_5059_B
C 127	16.4	82.0	839	8	CK777270	C 200	15.8	79.0	411	10	CW107557	CW107557 104_477_1
C 128	16.4	82.0	875	8	DR547552	C 201	15.8	79.0	417	2	BG010402	BG010402 RC2-GN030
C 129	16.4	82.0	916	10	CU128207	C 202	15.8	79.0	418	2	BG010401	BG010401 RC2-GN030
C 130	16.4	82.0	930	2	BF316245	C 203	15.8	79.0	421	5	BY631755	BY631755 BY631755
C 131	16.4	82.0	938	2	BF316245	C 204	15.8	79.0	422	11	DE085040	DE085040 Oryzias 1
C 132	16.4	82.0	1080	10	CW931528	C 205	15.8	79.0	429	10	CZ669751	CZ669751 OM_Ba022
C 133	16.4	82.0	1210	8	DN688614	C 206	15.8	79.0	430	2	BG606657	BG606657 WHE2451.D
C 134	16.4	82.0	1507	1	AL932973	C 207	15.8	79.0	431	6	CD731564	CD731564 4041620_1
C 135	16	80.0	134	3	BF061196	C 208	15.8	79.0	435	9	AQ892575	AQ892575 HS_3158_A
C 136	16	80.0	188	8	T42425	C 209	15.8	79.0	436	2	BF547491	BF547491 UI-R-C2p-
C 137	16	80.0	361	9	CE0601279	C 210	15.8	79.0	439	1	AW823378	AW823378 uf60b04.x
C 138	16	80.0	416	5	BY635171	C 211	15.8	79.0	442	7	CN956808	CN956808 4308_5001
C 139	16	80.0	459	9	CE101574	C 212	15.8	79.0	447	9	AZ072114	AZ072114 RPTC-23-3
C 140	16	80.0	622	3	EN046383	C 213	15.8	79.0	450	9	AZ879853	AZ879853 RPTC-23-1
C 141	16	80.0	664	7	CV221612	C 214	15.8	79.0	459	9	BH772510	BH772510 tes9e01.b
C 142	16	80.0	714	2	BF583519	C 215	15.8	79.0	464	6	CD475142	CD475142 naQ03-1ms
C 143	16	80.0	716	7	CO050810	C 216	15.8	79.0	466	2	BG015617	BG015617 CM1-GN032
C 144	16	80.0	747	2	BF676532	C 217	15.8	79.0	467	2	BH776876	BH776876 BB776876
C 145	16	80.0	863	7	CK936037	C 218	15.8	79.0	468	9	CE202769	CE202769 tigr-g88-
C 146	16	80.0	867	10	CL079034	C 219	15.8	79.0	470	10	CE822376	CE822376 tigr-g88-
C 147	16	80.0	919	5	BK435422	C 220	15.8	79.0	476	9	BH296102	BH296102 CH230-44P
C 148	16	80.0	927	7	CK934596	C 221	15.8	79.0	476	10	CE682954	CE682954 tigr-g88-
C 149	16	80.0	985	5	BK411195	C 222	15.8	79.0	483	9	AZ454435	AZ454435 1M0256G20
C 150	16	80.0	1052	5	BH412566	C 223	15.8	79.0	484	1	AW435409	AW435409 UI-R-BJ0P
C 151	16	80.0	1101	10	CNS00H11	C 224	15.8	79.0	494	2	BF418582	BF418582 UI-R-BJ2-
C 152	16	80.0	1509	8	DN723376	C 225	15.8	79.0	498	5	BK519475	BK519475 nm_9_n16
C 153	16	80.0	1545	7	CK403600	C 226	15.8	79.0	525	7	CN041963	CN041963 nm_9_n16
C 154	15.8	79.0	73	7	CK725626	C 227	15.8	79.0	526	2	BE850866	BE850866 uw89f08.Y
C 155	15.8	79.0	145	7	CV068770	C 228	15.8	79.0	526	9	AQ660324	AQ660324 Sheared D
C 156	15.8	79.0	150	9	AZ053463	C 229	15.8	79.0	528	2	BE198402	BE198402 ug78b12.Y
C 157	15.8	79.0	156	6	CB979101	C 230	15.8	79.0	539	10	CW408585	CW408585 fdbb001f1
C 158	15.8	79.0	161	3	BQ361776	C 231	15.8	79.0	540	9	AZ561040	AZ561040 RPTC-23-2
C 159	15.8	79.0	214	1	AI170319	C 232	15.8	79.0	540	9	AQ507216	AQ507216 RPTC-11-3
C 160	15.8	79.0	221	1	AI136451	C 233	15.8	79.0	542	8	DN867810	DN867810 nac30b08.
C 161	15.8	79.0	235	1	BI100454	C 234	15.8	79.0	543	3	BM506856	BM506856 ih31c07.Y
C 162	15.8	79.0	236	8	D80694	C 235	15.8	79.0	544	9	AZ559864	AZ559864 RPTC-23-2
C 163	15.8	79.0	253	1	AI013680	C 236	15.8	79.0	545	9	CC896516	CC896516 ZMWB022
C 164	15.8	79.0	253	3	EM422604	C 237	15.8	79.0	550	7	CN033182	CN033182 Mach_10_K
C 165	15.8	79.0	261	1	AV373306	C 238	15.8	79.0	550	7	CO748634	CO748634 SnSTbaa4
C 166	15.8	79.0	277	1	AV210353	C 239	15.8	79.0	552	6	CF341045	CF341045 TgSTZyJ3
C 167	15.8	79.0	279	1	AJ778950	C 240	15.8	79.0	553	11	CR107466	CR107466 Reverse 8
C 168	15.8	79.0	281	2	BF849741	C 241	15.8	79.0	553	11	CR107466	CR107466 Reverse 8

C 242	15.8	79.0	554	6	CD210985	CD210985	HS1_58_D0
C 243	15.8	79.0	563	6	CB547866	AMGNUC:N	
C 244	15.8	79.0	564	9	B58842	CIT-HSP-201	
C 245	15.8	79.0	566	10	AG962387	Drosophila	
C 246	15.8	79.0	568	1	AUI59437	AUI59437	
C 247	15.8	79.0	571	1	AUI11294	AUI11294	
C 248	15.8	79.0	573	3	BI961817	MONO1_7_A	
C 249	15.8	79.0	573	10	CW758775	OG_BBA006	
C 250	15.8	79.0	573	10	CW764566	OG_BBA007	
C 251	15.8	79.0	575	9	CC488592	CH240_320	
C 252	15.8	79.0	577	3	BI834934	603088808	
C 253	15.8	79.0	580	7	CF885358	tric081x	
C 254	15.8	79.0	580	9	AZ034756	RPCI-23-2	
C 255	15.8	79.0	586	10	AG977843	Drosophila	
C 256	15.8	79.0	587	6	CF622727	ih43e04.x	
C 257	15.8	79.0	590	10	CL538864	OB_BA004	
C 258	15.8	79.0	591	11	CR101159	Reverse_8	
C 259	15.8	79.0	592	9	BZ870876	CH240_226	
C 260	15.8	79.0	593	10	CW165929	104_574_1	
C 261	15.8	79.0	594	3	BM651695	170006873	
C 262	15.8	79.0	596	8	DR947456	EST113899	
C 263	15.8	79.0	598	7	CN041994	nm_36h.f1	
C 264	15.8	79.0	599	5	BO416153	GA_Ed010	
C 265	15.8	79.0	600	5	BU457823	60375861	
C 266	15.8	79.0	603	9	AQ387125	RPCI11-14	
C 267	15.8	79.0	604	5	BD783230	UI-R-PFO-	
C 268	15.8	79.0	606	6	CD740184	4028969_1	
C 269	15.8	79.0	607	10	CW213232	104_644_1	
C 270	15.8	79.0	608	10	CW213047	104_644_1	
C 271	15.8	79.0	615	10	EX959231	Forward_8	
C 272	15.8	79.0	626	5	BR868351	EX959231	
C 273	15.8	79.0	626	9	BZ143662	EX868351	
C 274	15.8	79.0	629	10	CW213231	104_644_1	
C 275	15.8	79.0	629	10	CW435965	fb5b001f1	
C 276	15.8	79.0	632	9	AO644444	RPCI93-EC	
C 277	15.8	79.0	633	10	CW763950	OG_BBA007	
C 278	15.8	79.0	634	2	BI295909	UI-R-DKO-	
C 279	15.8	79.0	635	6	CA966114	CCLL03a11	
C 280	15.8	79.0	638	10	CW063252	104_308_1	
C 281	15.8	79.0	640	2	BF538777	602050709	
C 282	15.8	79.0	640	3	BM440217	pg2rin.pk0	
C 283	15.8	79.0	640	10	CW092513	104_455_1	
C 284	15.8	79.0	642	10	CE815541	tigr-gss-	
C 285	15.8	79.0	647	9	AZ367385	1M0117G04	
C 286	15.8	79.0	648	10	CW843379	ET13709.D	
C 287	15.8	79.0	649	10	CL859570	OR_CBA009	
C 288	15.8	79.0	651	10	CW406991	fb5b001f1	
C 289	15.8	79.0	654	9	AZ086758	RPCI-23-4	
C 290	15.8	79.0	656	1	AM027103	AM027103	
C 291	15.8	79.0	660	7	CV504864	71437.1.M	
C 292	15.8	79.0	660	10	CW664103	OG_BBA001	
C 293	15.8	79.0	664	1	AV658301	AV658301	
C 294	15.8	79.0	669	5	BM446460	BM446460	
C 295	15.8	79.0	671	3	BI387900	BF226_002	
C 296	15.8	79.0	672	6	CF361053	827360.MA	
C 297	15.8	79.0	674	1	AW914884	EST346188	
C 298	15.8	79.0	676	7	CN304450	170004252	
C 299	15.8	79.0	676	10	CE378039	tigr-gss-	
C 300	15.8	79.0	677	6	CB421329	594989.MA	
C 301	15.8	79.0	681	7	CN734746	25RDBN.U	
C 302	15.8	79.0	681	8	CM660197	PO01019C0	
C 303	15.8	79.0	681	10	CZ411861	104_631_1	
C 304	15.8	79.0	682	3	BI696522	603347477	
C 305	15.8	79.0	692	7	CK842307	UI-R-AD0-	
C 306	15.8	79.0	694	5	BM446261	BM446261	
C 307	15.8	79.0	694	9	CC519770	CH240_366	
C 308	15.8	79.0	695	10	CW203965	104_631_1	
C 309	15.8	79.0	696	6	CB422283	595373.MA	
C 310	15.8	79.0	697	7	CN788698	4123060.B	
C 311	15.8	79.0	697	8	CX772410	UI-EH-HG0	
C 312	15.8	79.0	697	9	AZ869893	2M0182109	
C 313	15.8	79.0	700	7	CN842112	AGENCOURT	
C 314	15.8	79.0	704	5	BY702935	BY702935	
C 315	15.8	79.0	706	9	BZ990015	BZ990015	
C 316	15.8	79.0	707	10	CW408584	CW408584	
C 317	15.8	79.0	709	5	BU349121	BU349121	
C 318	15.8	79.0	709	5	EX467744	EX467744	
C 319	15.8	79.0	713	10	CW235675	104_691_1	
C 320	15.8	79.0	717	6	CA504021	UI-R-FJ0-	
C 321	15.8	79.0	720	10	CNS000FE	AL090920	
C 322	15.8	79.0	737	8	CK660004	Arabidops	
C 323	15.8	79.0	738	7	CN403178	PO01016G1	
C 324	15.8	79.0	738	8	DN870210	vll_P45_n	
C 325	15.8	79.0	739	5	BU958431	DN870210	
C 326	15.8	79.0	743	11	CR134716	na05b03	
C 327	15.8	79.0	744	9	BI188697	AGENCOURT	
C 328	15.8	79.0	744	11	CNS07SNM	BU958431	
C 329	15.8	79.0	747	5	BU334634	CR134716	
C 330	15.8	79.0	750	9	BZ672480	Forward_8	
C 331	15.8	79.0	752	5	BZ666985	AL625636	
C 332	15.8	79.0	755	10	AG572296	T7_end_of	
C 333	15.8	79.0	757	2	BG497439	BU334634	
C 334	15.8	79.0	759	7	CV126842	603496920	
C 335	15.8	79.0	765	6	CD100163	BZ672480	
C 336	15.8	79.0	765	7	CO120323	BU2666985	
C 337	15.8	79.0	771	5	BU432376	603817877	
C 338	15.8	79.0	771	9	CK915049	AG572296	
C 339	15.8	79.0	774	2	BI261132	BG497439	
C 340	15.8	79.0	777	11	CR042909	CV126842	
C 341	15.8	79.0	780	9	CE963638	AGENCOURT	
C 342	15.8	79.0	780	6	CB573559	CD100163	
C 343	15.8	79.0	783	6	CB573559	CO120323	
C 344	15.8	79.0	791	10	CZ134998	GR_Eb023	
C 345	15.8	79.0	796	9	BZ810168	BU432376	
C 346	15.8	79.0	805	1	AL525208	603220605	
C 347	15.8	79.0	807	10	AG446231	CK915049	
C 348	15.8	79.0	808	2	BF278041	C08613ba	
C 349	15.8	79.0	810	2	BG494062	BI261132	
C 350	15.8	79.0	819	10	EX176133	CR335725	
C 351	15.8	79.0	820	6	CB663429	CR042909	
C 352	15.8	79.0	821	11	CR147047	Forward_8	
C 353	15.8	79.0	823	11	CR197183	BO1BR46TR	
C 354	15.8	79.0	827	7	CO120324	CE963638	
C 355	15.8	79.0	828	10	CG015394	CB573559	
C 356	15.8	79.0	830	2	BF209067	AGENCOURT	
C 357	15.8	79.0	839	10	CG448216	CZ134998	
C 358	15.8	79.0	843	7	CK243139	BZ810168	
C 359	15.8	79.0	849	9	AQ741350	PUGAX03TB	
C 360	15.8	79.0	850	2	BG678112	AL525208	
C 361	15.8	79.0	850	8	DN981327	AG446231	
C 362	15.8	79.0	851	2	BI152566	GA_Eb003	
C 363	15.8	79.0	851	10	CNS01SE9	BP278041	
C 364	15.8	79.0	862	6	CD519427	GA_Eb003	
C 365	15.8	79.0	865	7	CK396760	BG494062	
C 366	15.8	79.0	882	7	CK246257	EX176133	
C 367	15.8	79.0	882	2	BG566405	CB663429	
C 368	15.8	79.0	885	5	BU542166	OSJNE08G	
C 369	15.8	79.0	886	9	CK243138	CR147047	
C 370	15.8	79.0	888	9	AQ444504	CR197183	
C 371	15.8	79.0	891	5	BX899502	CR197183	
C 372	15.8	79.0	891	8	DR949226	CO120324	
C 373	15.8	79.0	894	7	CK271572	CG015394	
C 374	15.8	79.0	896	8	DR732700	ZUAB678TV	
C 375	15.8	79.0	898	10	CG133608	BF209067	
C 376	15.8	79.0	904	5	BG192231	601872946	
C 377	15.8	79.0	905	2	BG192231	OGTBF56TV	
C 378	15.8	79.0	906	5	BU359063	CK243139	
C 379	15.8	79.0	906	6	CF586659	CK243139	
C 380	15.8	79.0	917	2	BI255411	ES7729894	
C 381	15.8	79.0	917	6	CD759635	BG566405	
C 382	15.8	79.0	923	10	CG284176	BU542166	
C 383	15.8	79.0	926	10	CG974398	AGENCOURT	
C 384	15.8	79.0	929	9	BI163074	AGENCOURT	
C 385	15.8	79.0	930	10	CZ502302	AGENCOURT	
C 386	15.8	79.0	932	9	CC302560	AGENCOURT	
C 387	15.8	79.0	932	11	CNS04H4X	AGENCOURT	

388	15.8	79.0	939	7	CO583484	CO583484	ILLUMIGEN	461	15.4	77.0	242	1	BB019730	BB019730
389	15.8	79.0	943	5	BX455797	BX455797	ILLUMIGEN	462	15.4	77.0	244	2	BB443255	BB443255
390	15.8	79.0	945	7	CO583780	CO583780	ILLUMIGEN	463	15.4	77.0	245	2	BB215147	BB215147
391	15.8	79.0	953	10	CL990070	CL990070	ZMMBRe000	464	15.4	77.0	249	1	BB045234	BB045234
392	15.8	79.0	953	11	CNS04DY3	AL286356	Tetradon	465	15.4	77.0	261	1	BB045234	BB045234
393	15.8	79.0	954	2	CG032761	CG032761	602298416	466	15.4	77.0	262	1	AV372672	AV372672
394	15.8	79.0	956	10	CL495291	CL495291	SAIL_607	467	15.4	77.0	262	1	BB403471	BB403471
395	15.8	79.0	960	10	CNS01S4F	AL164760	Tetradon	468	15.4	77.0	272	1	BB157553	BB157553
396	15.8	79.0	965	1	AJ513593	AJ513593		469	15.4	77.0	273	2	BB351685	BB351685
397	15.8	79.0	969	2	BG250063	BG250063	602362151	470	15.4	77.0	274	1	BB128463	BB128463
398	15.8	79.0	974	10	CG180690	PUPPQ29TD		471	15.4	77.0	275	1	BB086964	BB086964
399	15.8	79.0	978	10	CL867573	CL867573	Gna_01_F0	472	15.4	77.0	275	2	BB439732	BB439732
400	15.8	79.0	998	5	BU432548	BU432548	603221445	473	15.4	77.0	276	2	BB258922	BB258922
401	15.8	79.0	1004	2	BF532238	BF532238	602073140	474	15.4	77.0	277	2	BB399952	BB399952
402	15.8	79.0	1004	3	BI803125	BI803125	AV048340	475	15.4	77.0	282	1	BB156233	BB156233
403	15.8	79.0	1017	1	AV048340	AV048340	HI01C10_E	476	15.4	77.0	285	2	BB526488	BB526488
404	15.8	79.0	1017	2	BG484563	BG484563	602505727	477	15.4	77.0	287	1	BB039699	BB039699
405	15.8	79.0	1019	10	CG180687	PUPPQ29TB		478	15.4	77.0	289	1	BB069297	BB069297
406	15.8	79.0	1026	11	CNS05C82	AL130779	Tetradon	479	15.4	77.0	291	2	BB472380	BB472380
407	15.8	79.0	1031	2	BF688846	BF688846	602185444	480	15.4	77.0	292	10	CL217275	CL217275
408	15.8	79.0	1040	11	CNS05QDP	AL349126	Tetradon	481	15.4	77.0	294	1	AV139376	AV139376
409	15.8	79.0	1046	3	BQ070097	BQ070097	AGENCOURT	482	15.4	77.0	296	3	BI529097	BI529097
410	15.8	79.0	1063	10	AG044635	AG044635	Pan trogl	483	15.4	77.0	297	2	BB228039	BB228039
411	15.8	79.0	1095	10	AG522776	Mus muscu		484	15.4	77.0	297	2	BB516781	BB516781
412	15.8	79.0	1098	10	CW934549	EDCC086TR		485	15.4	77.0	299	1	BB071614	BB071614
413	15.8	79.0	1119	3	BM918421	BM918421	AGENCOURT	486	15.4	77.0	299	2	BG308663	BG308663
414	15.8	79.0	1119	5	BU509189	BU509189	AGENCOURT	487	15.4	77.0	301	2	BG305123	BG305123
415	15.8	79.0	1123	9	BZ699302	BZ699302	SP_Ba006	488	15.4	77.0	303	8	DN339676	DN339676
416	15.8	79.0	1141	2	BG764367	BG764367	602736257	489	15.4	77.0	309	2	BG305897	BG305897
417	15.8	79.0	1158	8	DN731985	DN731985	CNB61-G06	490	15.4	77.0	310	3	BM469821	BM469821
418	15.8	79.0	1187	4	AK002400	Mus muscu		491	15.4	77.0	311	3	BM496945	BM496945
419	15.8	79.0	1214	5	BU161845	BU161845	AGENCOURT	492	15.4	77.0	316	2	BB395942	BB395942
420	15.8	79.0	1214	10	AG346583	AG346583	Mus muscu	493	15.4	77.0	316	5	EX866463	EX866463
421	15.8	79.0	1217	10	AG361173	AG361173	Mus muscu	494	15.4	77.0	319	1	AW826769	AW826769
422	15.8	79.0	1255	8	DN681077	DN681077	CGX16-B03	495	15.4	77.0	321	2	BB207613	BB207613
423	15.8	79.0	1272	9	AQ0899307	AQ0899307	HS_2055_B	496	15.4	77.0	324	2	BB297636	BB297636
424	15.8	79.0	1295	3	BM007491	BM007491	603616760	497	15.4	77.0	325	1	BB138210	BB138210
425	15.8	79.0	1310	2	BG117422	BG117422	602347435	498	15.4	77.0	331	9	BB084601	BB084601
426	15.8	79.0	1318	8	DN681772	DN681772	CGX20-B12	499	15.4	77.0	336	8	D61283	D61283
427	15.8	79.0	1374	10	AJ859431	AJ859431	Braselia	500	15.4	77.0	367	7	CO307251	CO307251
428	15.8	79.0	1434	8	DN720125	DN720125	CNB132-A0	501	15.4	77.0	387	6	CA633556	CA633556
429	15.8	79.0	1630	2	BG110241	BG110241	602279895	502	15.4	77.0	387	6	CA633556	CA633556
430	15.8	79.0	1652	5	BZ48702	BZ48702	603593633	503	15.4	77.0	387	6	CA633556	CA633556
431	15.8	79.0	1700	3	BI523064	BI523064	603175589	504	15.4	77.0	387	6	CA633556	CA633556
432	15.8	79.0	2058	10	CL973526	CL973526	OsIFCC024	505	15.4	77.0	387	6	CA633556	CA633556
433	15.8	79.0	2522	4	AK075788	AK075788	Mus muscu	506	15.4	77.0	387	6	CA633556	CA633556
434	15.8	79.0	2538	4	AK007732	AK007732	Mus muscu	507	15.4	77.0	387	6	CA633556	CA633556
435	15.8	79.0	2619	4	AK028990	AK028990	Mus muscu	508	15.4	77.0	387	6	CA633556	CA633556
436	15.8	79.0	4403	4	HS0806618	HS0806618		509	15.4	77.0	387	6	CA633556	CA633556
437	15.8	79.0	4676	4	AK038558	AK038558	Mus muscu	510	15.4	77.0	387	6	CA633556	CA633556
438	15.6	78.0	4676	4	AK038558	AK038558	Mus muscu	511	15.4	77.0	387	6	CA633556	CA633556
439	15.4	77.0	154	6	CD783027	CD783027	Drosophila	512	15.4	77.0	387	6	CA633556	CA633556
440	15.4	77.0	156	10	CE680180	CE680180	tigr-gss-	513	15.4	77.0	387	6	CA633556	CA633556
441	15.4	77.0	177	9	BI100335	BI100335	RPCT-24-3	514	15.4	77.0	387	6	CA633556	CA633556
442	15.4	77.0	179	1	AW853711	AW853711	RC3-C7025	515	15.4	77.0	387	6	CA633556	CA633556
443	15.4	77.0	192	1	AV073591	AV073591	AV073591	516	15.4	77.0	387	6	CA633556	CA633556
444	15.4	77.0	198	2	BF334324	BF334324	RC3-C7025	517	15.4	77.0	387	6	CA633556	CA633556
445	15.4	77.0	199	1	AV322081	AV322081	AV322081	518	15.4	77.0	387	6	CA633556	CA633556
446	15.4	77.0	206	1	AV171862	AV171862	AV171862	519	15.4	77.0	387	6	CA633556	CA633556
447	15.4	77.0	211	1	BB147938	BB147938	BB147938	520	15.4	77.0	387	6	CA633556	CA633556
448	15.4	77.0	212	1	AA286472	AA286472	va28a12.x	521	15.4	77.0	387	6	CA633556	CA633556
449	15.4	77.0	212	1	BB132774	BB132774	BB132774	522	15.4	77.0	387	6	CA633556	CA633556
450	15.4	77.0	229	1	AV272840	AV272840	AV272840	523	15.4	77.0	387	6	CA633556	CA633556
451	15.4	77.0	229	2	BB535680	BB535680	BB535680	524	15.4	77.0	387	6	CA633556	CA633556
452	15.4	77.0	231	1	AV251995	AV251995	AV251995	525	15.4	77.0	387	6	CA633556	CA633556
453	15.4	77.0	231	2	BB210922	BB210922	BB210922	526	15.4	77.0	387	6	CA633556	CA633556
454	15.4	77.0	232	1	AV250808	AV250808	AV250808	527	15.4	77.0	387	6	CA633556	CA633556
455	15.4	77.0	232	1	BB148115	BB148115	BB148115	528	15.4	77.0	387	6	CA633556	CA633556
456	15.4	77.0	232	2	BB478667	BB478667	BB478667	529	15.4	77.0	387	6	CA633556	CA633556
457	15.4	77.0	236	1	AV355045	AV355045	AV355045	530	15.4	77.0	387	6	CA633556	CA633556
458	15.4	77.0	236	2	BB378536	BB378536	BB378536	531	15.4	77.0	387	6	CA633556	CA633556
459	15.4	77.0	239	1	BB160907	BB160907	BB160907	532	15.4	77.0	387	6	CA633556	CA633556
460	15.4	77.0	240	1	BB017168	BB017168	BB017168	533	15.4	77.0	387	6	CA633556	CA633556

## ALIGNMENTS

RESULT 1	AL728550	603 bp	mRNA	linear	EST 18-APR-2002
LOCUS	AL728550	Danio rerio embryonic inner ear subtracted cDNA Danio			
DEFINITION	AL728550	Danio rerio embryonic inner ear subtracted cDNA Danio			
ACCESSION	AL728550.1	GI:20193154			
VERSION	AL728550.1	GI:20193154			
KEYWORDS	EST.				
SOURCE	Danio rerio (zebrafish)				
ORGANISM	Danio rerio				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Actinopterygii; Neopterygii; Teleostei; Ostariophysi;				
	Cypriniformes; Cyprinidae; Danio.				
REFERENCE	1 (bases 1 to 603)				
AUTHORS	Coimbrin, R., Weil, D., Brottier, P., Blanchard, S., Levi, M.,				
	Hardelin, J. P., Weissenbach, J., and Petit, C.				
TITLE	A subtracted cDNA library from the zebrafish (Danio rerio)				
	embryonic inner ear				
JOURNAL	Unpublished (2002)				
COMMENT	Contact: Genoscope				
	Genoscope - Centre National de Sequencage				
	2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE				
FEATURES	Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.				
source	Location/Qualifiers				
	1..603				
	/organism="Danio rerio"				
	/mol_type="mRNA"				
	/db_xref="taxon:7955"				



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/clone="BNOAA1002B08"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subtracted
cDNA"
/note="subtracted cDNA library"

ORIGIN
Query Match          95.0%; Score 19; DB 1; Length 603;
Best Local Similarity 100.0%; Pred. No. 2.6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
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Db 31 AAGGAAACACGGACACCA 49
    |||||

RESULT 2
LOCUS          CK751666          676 bp      mRNA      linear      EST 09-JUN-2005
DEFINITION    atr02-9msl-b08 Amborella trichopoda cDNA clone atr02-9msl-b08
              5', mRNA sequence.
ACCESSION     CK751666
VERSION       CK751666.1 GI:42642089
KEYWORDS      EST.
SOURCE        Amborella trichopoda
ORGANISM      Amborella trichopoda
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Basal Magnoliophyta; Amborellales;
              Amborellaceae; Amborella.
              1 (bases 1 to 676)
REFERENCE     1 depamphilis, C., Carlson, J., Ma, H., Soltis, D., Soltis, P.,
AUTHORS       Oppenheimer, D., Frohlich, M., Doyle, J., Tanksley, S., Webb, M.,
              Leebens-Mack, J., Landherr, L., Ilut, D. and Wall, K.
              Generation of ESTs from early female flower buds of Amborella
              trichopoda
              Unpublished (2003)
JOURNAL
COMMENT       Contact: Claude depamphilis or James Leebens-Mack
              Mueller Laboratory
              Penn State University
              208 Mueller Laboratory, Department of Biology, ATTN Rm212, Penn
              State University, University Park, PA 16802, USA
              Tel: 814 863 6413
              Fax: 814 865 9131
              Email: cw33@psu.edu or jhl10@psu.edu
              The sequence provided is trimmed of vector and low quality regions.
              Full sequence and original trace file are available from the Plant
              Genome Network website (http://pgn.cornell.edu)
              Plate: atr02-9msl row: b column: 08
              Seq primer: M13F.
              Location/Qualifiers
                1..676
                /organism="Amborella trichopoda"
                /mol_type="mRNA"
                /db_xref="PGN:atr02-9msl-b08"
                /db_xref="taxon:13333"
                /clone="atr02-9msl-b08"
                /tissue_type="female flower buds"
                /dev_stage="4mm buds"
                /lab_host="SOLR"
                /clone_lib="Atr02"
                /note="Vector: pBluescript SK (+/-); Site 1: EcoRI;
                Site 2: XhoI; This is a directionally cloned,
                non-normalized library. This library has been generated by
                the Floral Genome Project (FGP). The Floral Genome Project
                is funded by NSF's Plant Genome Research Program
                (DBI-0115684). More information about the project can be
                obtained at http://fgp.bio.psu.edu"

ORIGIN
Query Match          92.0%; Score 18.4; DB 7; Length 676;
Best Local Similarity 95.0%; Pred. No. 5.1e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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Qy 1 AAGGAAACACGGACACCA 20
    |||||
Db 47 AAGGAAACATGGACACCA 66
    |||||

RESULT 3
CNSOFFP9W/c      845 bp      mRNA      linear      HTC 05-JUL-2005
LOCUS            Tetraodon nigroviridis full-length cDNA.
DEFINITION       CG682120
ACCESSION        CG682120.2 GI:56281159
VERSION          HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
KEYWORDS         Tetraodon nigroviridis
SOURCE           Tetraodon nigroviridis
ORGANISM         Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
                  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                  Tetraodontidae; Tetraodon.
REFERENCE        1
AUTHORS          Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
                  Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
                  Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
                  Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
                  Castellano, S., Anthonard, V., Jubin, C., Castelli, V., Katinka, M.,
                  Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
                  Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P.,
                  Gouzy, J., Parra, G., Lardier, G., Chappelle, C., McKernan, K.J.,
                  McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
                  Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
                  Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
                  Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J.
                  and Roest Crolius, H.
                  Genome duplication in the teleost fish Tetraodon nigroviridis
                  reveals the early vertebrate proto-karyotype
                  Nature 431 (7011), 946-957 (2004)
JOURNAL          PUBMED 15496914
COMMENT          2 (bases 1 to 845)
AUTHORS          Genoscope.
TITLE            Direct Submission
JOURNAL          Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
                  : 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
                  (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                  On Dec 3, 2004 this sequence version replaced gi:51180027.
                  The sequences are based on single pass reads.
                  More information available at
                  http://www.genoscope.cns.fr/tetraodon.
FEATURES         Location/Qualifiers
                  1..845
                  /organism="Tetraodon nigroviridis"
                  /mol_type="mRNA"
                  /db_xref="taxon:99883"
                  /tissue_type="Eyes"

ORIGIN
Query Match          92.0%; Score 18.4; DB 4; Length 845;
Best Local Similarity 95.0%; Pred. No. 5.2e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 20
    |||||
Db 510 AAGGAAACACGGAAACCA 491
    |||||

RESULT 4
CNSOFFVC0/c      908 bp      mRNA      linear      HTC 05-JUL-2005
LOCUS            Tetraodon nigroviridis full-length cDNA.
DEFINITION       CG689972
ACCESSION        CG689972
VERSION          HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
KEYWORDS         Tetraodon nigroviridis
SOURCE           Tetraodon nigroviridis
ORGANISM         Tetraodon nigroviridis

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

1  
**REFERENCE**  
**AUTHORS**  
 Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N., Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A., Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C., Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N., Castellano, S., Anthonard, V., Jubin, C., Castelli, V., Katinka, M., Vacherie, B., Bieumont, C., Skalli, Z., Cattolico, L., Poulain, J., De Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P., Couzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C., Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D., Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F., Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissenbach, J. and Roest Crolius, H.

**TITLE**  
 Genome duplication in the teleost fish Tetraodon nigroviridis reveals the early vertebrate proto-karyotype

**JOURNAL**  
 Nature 431 (7011), 946-957 (2004)

**PUBMED**  
 15496914

**REFERENCE**  
 2 (bases 1 to 908)

**AUTHORS**  
 Genoscope.

**TITLE**  
 Direct Submission

**JOURNAL**  
 Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage - 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

**COMMENT**  
 On Dec 3, 2004 this sequence version replaced gi:51187879.  
 The sequences are based on single pass reads.  
 More information available at  
<http://www.genoscope.cns.fr/tetraodon>.

**FEATURES**  
 source  
 Location/Qualifiers  
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 /organism="Tetraodon nigroviridis"  
 /mol\_type="mRNA"  
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 /tissue\_type="Eyes"

**ORIGIN**  
 Query Match 92.0%; Score 18.4; DB 4; Length 908;  
 Best Local Similarity 95.0%; Pred. No. 5.2e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy**  
 1 AAGGAACACGACCCAA 20  
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 573 AAGGAACACGACCCAA 554

**Db**

**RESULT 5**  
**CNS03BCU/c**  
**LOCUS**  
**DEFINITION**  
 Tetraodon nigroviridis genome survey sequence T7 end of clone 011J14 of library G from Tetraodon nigroviridis, genomic survey sequence.

**ACCESSION**  
 AL236343.1 GI:7895478

**VERSION**  
 GSS; genome survey sequence.

**KEYWORDS**  
 Tetraodon nigroviridis

**SOURCE**  
 Tetraodon nigroviridis

**ORGANISM**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Tetraodon.

1  
**REFERENCE**  
**AUTHORS**  
 Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fzames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.

**TITLE**  
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence

**JOURNAL**  
 Nat. Genet. 25 (2), 235-238 (2000)

**PUBMED**  
 10835645

**REFERENCE**  
 2

**AUTHORS**  
 Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fzames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

**TITLE**  
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

**JOURNAL**  
 Genome Res. 10 (7), 939-949 (2000)

**PUBMED**  
 10899143

**REFERENCE**  
 3 (bases 1 to 962)

**AUTHORS**  
 Genoscope.

**TITLE**  
 Direct Submission

**JOURNAL**  
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage - BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

**COMMENT**  
 - Web : [www.genoscope.cns.fr](http://www.genoscope.cns.fr)  
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at  
<http://www.genoscope.cns.fr/Tetraodon>.

**FEATURES**  
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 Location/Qualifiers  
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 /clone="011J14"  
 /clone\_lib="G"  
 /notes="Genoscope sequence ID : COBG011DE07LP1  
 end : T7"

**ORIGIN**  
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 Best Local Similarity 95.0%; Pred. No. 5.3e+02;  
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

**Qy**  
 1 AAGGAACACGACCCAA 20  
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 731 AAGGAACACGACCCAA 712

**Db**

**RESULT 6**  
**LOCUS**  
**DEFINITION**  
 AGENCOURT\_6940541 NIH\_MGC\_99 Homo sapiens cDNA clone IMAGE:5809184 5', mRNA sequence.

**ACCESSION**  
 BQ056756

**VERSION**  
 BQ056756.1 GI:19816096

**KEYWORDS**  
 EST.

**SOURCE**  
 Homo sapiens (human)

**ORGANISM**  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

**REFERENCE**  
 1 (bases 1 to 1042)

**AUTHORS**  
 NIH-MGC <http://mgc.nci.nih.gov/>.

**TITLE**  
 National Institutes of Health, Mammalian Gene Collection (MGC)

**JOURNAL**  
 Unpublished (1999)

**COMMENT**  
 Contact: Robert Strausberg, Ph.D.  
 Email: [cgabs-r@mail.nih.gov](mailto:cgabs-r@mail.nih.gov)  
 Tissue Procurement: Lou Staudt  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LICM2054 row: 9 column: 09  
 High quality sequence stop: 587.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5809184"  
 /tissue\_type="lymphoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"

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/clone lib="NIH_MGC_99"
/note="Organ: lymph; Vector: POTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

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## ORIGIN

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Query Match          92.0%; Score 18.4; DB 3; Length 1042;
Best Local Similarity 95.0%; Pred. No. 5.3e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 AAGGAAACACGGACCCCAA 20
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Db 841 AAGGAAACACGGACCCCAA 860
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## RESULT 7

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BG752980/c
LOCUS      602732438F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4876160 5',
DEFINITION mRNA sequence.

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ACCESSION  BG752980
VERSION     BG752980.1 GI:14063633

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KEYWORDS   EST.

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SOURCE     Homo sapiens (human)

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## ORGANISM

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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.

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## REFERENCE

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1 (bases 1 to 1230)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

```

## AUTHORS

```

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

```

## JOURNAL

```

Tissue procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```

```

Plate: LCM1758 row: k column: 09

```

```

High quality sequence start: 23
High quality sequence stop: 98.

```

```

Location/Qualifiers

```

## FEATURES

```

source

```

```

1..1230

```

```

/organism="Homo sapiens"

```

```

/mol_type="mRNA"

```

```

/db_xref="taxon:9606"

```

```

/clone="IMAGE:4876160"

```

```

/tissue_type="normal pigmented retinal epithelium"

```

```

/lab_host="DH10B (phage-resistant)"

```

```

/clone_lib="NIH_MGC_43"

```

```

/note="Organ: eye; Vector: POTB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCAGCAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

```

## ORIGIN

```

Query Match          92.0%; Score 18.4; DB 2; Length 1230;
Best Local Similarity 95.0%; Pred. No. 5.4e+02;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 AAGGAAACACGGACCCCAA 20
|||||
Db 1123 AAGGAAACACGGACCCCAA 1104
|||||

```

## RESULT 8

```

BM359242/c

```

```

LOCUS      924 bp mRNA linear EST 09-JAN-2002
DEFINITION GA_BA0018E15r Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_BA0018E15r, mRNA sequence.

```

```

ACCESSION  BM359242
VERSION     BM359242.1 GI:18099988

```

## KEYWORDS

```

EST.

```

## ORGANISM

```

Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium...

```

## REFERENCE

```

1 (bases 1 to 924)
Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J.,

```

```

Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

```

```

An integrated analysis of the genetics, development, and evolution
of the cotton fiber

```

## JOURNAL

```

Unpublished (2000)

```

## COMMENT

```

Contact: Wing RA

```

```

Clemson University Genomics Institute

```

```

Clemson University

```

```

100 Jordan Hall, Clemson, SC 29634, USA

```

```

Tel: 864 656 7288

```

```

Fax: 864 656 4293

```

```

Email: rwing@clemson.edu

```

```

Total High Quality bases = 150

```

```

Seq primer: TAATACGACTCACTATAGGG

```

```

High quality sequence start: 4

```

```

High quality sequence stop: 900.

```

```

Location/Qualifiers

```

```

1..924

```

```

/organism="Gossypium arboreum"

```

```

/mol_type="mRNA"

```

```

/strain="AKA"

```

```

/cultivar="8400"

```

```

/db_xref="taxon:29729"

```

```

/clone="GA_BA0018E15r"

```

```

/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"

```

```

/lab_host="E. coli"

```

```

/clone_lib="Gossypium arboreum 7-10 dpa fiber library"

```

```

/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

```

```

Query Match          90.0%; Score 18; DB 3; Length 924;
Best Local Similarity 100.0%; Pred. No. 8.2e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 AAGGAAACACGGACCC 18
|||||

```

```

Db 417 AAGGAAACACGGACCC 400
|||||

```

## RESULT 9

```

CB359607

```

## LOCUS

```

DEFINITION CB359607 458 bp mRNA linear EST 10-NOV-2003
IMAGE:6901841 5' similar to (NM_002231) kangai 1, mRNA sequence.

```

## ACCESSION

```

CB359607

```

## VERSION

```

CB359607.1 GI:29003418

```

## KEYWORDS

```

EST.

```

## SOURCE

```

Danio rerio (zebrafish)

```

## ORGANISM

```

Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.

```

## REFERENCE

```

1 (bases 1 to 458)

```

AUTHORS Mathavan,S., Wei,C., Thoreau,H., Chia,J.M. and Ruan,Y.  
 TITLE Genome Institute of Singapore, Zebrafish EST Collection  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Ruan Y

Cloning and Sequencing  
 Genome Institute of Singapore  
 60 Biopolis Street, #02-01, Genome, Singapore 138672  
 Tel: +65 6478 8073  
 Fax: +65 6478 9059  
 Email: ruanyj@gis.a-star.edu.sg  
 GSS-Clone ID: ZF001-P00027-PP\_J16  
 PCR Primers  
 FORWARD: M13  
 BACKWARD: M13

Plate: ZF001-P00027-DPE-F-D  
 Seq primer: CCGCATACTGTATAGCA  
 High quality sequence stop: 458.

#### FEATURES

source  
 Location/Qualifiers  
 1. 458  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:6901841"  
 /tissue\_type="Embryo"  
 /dev stage="7 Different embryonic stages (From just fertilized embryos to 72 hours just hatched baby fish)"  
 /lab\_host="DH10B"  
 /clone\_lib="GISZF001"  
 /note="Vector: pDNR-LIB; Site\_1: Sfi A (GGCATTACGGCC); Site\_2: Sfi B (GGCGCTCGGCC); Priming method: Sfi-(dt)30 Primed ; Priming sequence: 5.ATTCTAGA GCGCAGGCGGCC GACATG(T)30VN ; Directionally cloned. 5' cloning site: Sfi A site GGCATTACGGCC ; 5' linker/adaptor sequence: 5.AAGCAGTGATCAACGACGAGTGGCC ; 3' cloning site: Sfi B site GGCGCTCGGCC ; 3' linker/adaptor sequence: same as the priming sequence ; Average insert size: 2kb ; For PCR insert analysis: Use M13 Forward and reverse primers ; Library Amplified Recombinants (inserts): 98 ; Library complexity: 5x10<sup>6</sup> ; Full-length construction (method): SMART, a Clontech method ; Library constructed by: S. Mathavan, Chia-Lin Wei, and Yijun Ruan Genome Institute of Singapore"

#### ORIGIN

Query Match 87.0%; Score 17.4; DB 6; Length 458;  
 Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCA 19  
 |||||  
 Db 188 AAGGAAACACGACACTCA 206

#### RESULT 10

AZ078930/c  
 LOCUS AZ078930 520 bp DNA linear GSS 31-MAR-2000  
 DEFINITION RPCI-23-410F20-TV RPCI-23 Mus musculus genomic clone  
 RPCI-23-410F20, genomic survey sequence.

ACCESSION AZ078930  
 VERSION AZ078930.1 GI:7371829  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 520)

Akinret,B., Levins,M., McGann,S., Teegaye,G., Geer,K., Krol,M., de Jong,P. and Frazer,C.M.  
 Mouse BAC End Sequences from Library RPCI-23  
 Unpublished (1999)

Other\_GSSs: RPCI-23-410F20.TJ  
 COMMENT

Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208

Email: szhao@tigr.org  
 Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/orderingframe.htm>) or from Resea ch Genetics ([info@resgen.com](mailto:info@resgen.com)). BAC end page: [http://www.tigr.org/tdb/bac ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html)  
 Plate: 410 row: F column: 20

Seq primer: T7

Class: BAC ends.

#### FEATURES

Location/Qualifiers  
 1. 520  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-410F20"  
 /sex="Female"  
 /lab host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

#### ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 520;  
 Best Local Similarity 94.7%; Pred. No. 1.5e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 AGGAAACACGACACCA 20  
 |||||  
 Db 79 AGGAAACACGACACCA 61

#### RESULT 11

CW718506/c  
 LOCUS CW718506 682 bp DNA linear GSS 05-NOV-2004  
 DEFINITION MARC 1010385 CHORI-240-397C5 Bos taurus genomic clone 1C6, genomic survey sequence.

ACCESSION CW718506  
 VERSION CW718506.1 GI:55422216  
 KEYWORDS GSS.

SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

REFERENCE 1 (bases 1 to 682)  
 Smith,T.F.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.  
 SNP discovery in cattle based on low coverage sequencing of BAC clones

Unpublished (2004)  
 Other\_GSSs: MARC\_1009233

COMMENT Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390

Email: [smith@email.marc.usda.gov](mailto:smith@email.marc.usda.gov)  
 Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim\_alt option. Vector identified with cross match v0.990329.

Seq primer: GTAATACGACTCACTATAGG

```

FEATURES
  source
    Class: BAC subclone.
    Location/Qualifiers
      1..682
        /organism="Bos taurus"
        /mol_type="genomic DNA"
        /db_xref="taxon:9913"
        /clone="1C6"
        /sex="Male"
        /tissue_type="blood"
        /clone_lib="CHORI-240-397C5"
        /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
        BamHI; BAC DNA was digested with Sau3A. Fragments were
        sized to 800-1200 bases and subcloned into pBLUESCRIPT
        SK-."
ORIGIN
  Query Match      87.0%; Score 17.4; DB 10; Length 682;
  Best Local Similarity 94.7%; Pred. No. 1.5e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCCA 19
   |||||||
DB 300 AAGGAACACGACACCCCA 282

RESULT 12
LOCUS CW682736
DEFINITION OG_BB0039K22.r OG_BBA Oryza glaberrima genomic clone OG_BB0039K22
3'- genomic survey_sequence.
ACCESSION CW682736
VERSION CW682736.1 GI:55150750
KEYWORDS GSS.
SOURCE Oryza glaberrima (African rice)
ORGANISM Oryza glaberrima
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoidae; Oryzaceae; Oryza.
REFERENCE 1 (bases 1 to 689)
AUTHORS Kim, H., Yu, Y., Wissotski, M., Byrne, M., Stum, D., Smart, D., Rao, K.,
Luo, M., Jetty, R., Kudrna, D., Muller, C., Hatfield, J., Soderlund, C.
and Wing, R.
MAP
  Unpublished (2004)
  Contact: Rod A. Wing
  Arizona Genomics Institute
  University of Arizona
  Forbes Building Room 303, Tucson, AZ 85721-0036, USA
  Tel: 520 626 9595
  Fax: 520 621 1259
  Email: rwing@genome.arizona.edu
PCR Primers
  FORWARD: TAA TAC GAC TCA CTA TAG GG
  BACKWARD: CAC TCA TTA GGC ACC CCA
Plate: 0039 row: K column: 22
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
FEATURES
  source
    Location/Qualifiers
      1..689
        /organism="Oryza glaberrima"
        /mol_type="genomic DNA"
        /db_xref="taxon:4538"
        /clone="OG_BB0039K22"
        /tissue_type="young leaves"
        /lab_host="DH10B T1 phage resistant"
        /clone_lib="OG_BBA"
        /note="Vector: pGIBAC1; Site 1: HindIII; Site 2: HindIII"
ORIGIN
  Query Match      87.0%; Score 17.4; DB 10; Length 689;
  Best Local Similarity 94.7%; Pred. No. 1.5e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 AAGGAACACGACACCCCA 19
   |||||||
DB 506 AAGGAACACGACACCCCA 524

RESULT 13
LOCUS CK028165
DEFINITION AGENCOURT 16626291 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7052495
5', mRNA sequence.
ACCESSION CK028165
VERSION CK028165.1 GI:38554089
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 717)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics / NIH
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LIA014826 row: k column: 21
High quality sequence stop: 686.
FEATURES
  source
    Location/Qualifiers
      1..717
        /organism="Danio rerio"
        /mol_type="mRNA"
        /db_xref="taxon:7955"
        /clone="IMAGE:7052495"
        /tissue_type="whole body"
        /lab_host="DH10B"
        /clone_lib="NIH_ZGC_7"
        /note="Vector: pExpress; Site 1: NotI; Site 2: EcoRV;
        Bulk tissue was collected from a whole adult individual
        from the Tuebingen strain. 1st strand cDNA was primed with
        a Not I - oligo(dT) primer, double-stranded cDNA was
        cloned into the Not I and EcoRV sites of pExpress-1.
        Library was size-selected for >1 kb fragments and
        normalized. A non-normalized version of this library is
        also available (NIH_ZGC_10). Library was constructed by
        Open Biosystems (Huntsville, AL)"
ORIGIN
  Query Match      87.0%; Score 17.4; DB 7; Length 717;
  Best Local Similarity 94.7%; Pred. No. 1.5e+03;
  Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAACACGACACCCCA 19
   |||||||
DB 335 AAGGAACACGACACCCCA 353

RESULT 14
LOCUS AG479585
DEFINITION Mus musculus molossinus DNA, clone:MSMG01-373J11.T7, genomic survey
sequence.
ACCESSION AG479585
VERSION AG479585.1 GI:48186815
KEYWORDS GSS.

```

**SOURCE**  
**ORGANISM** Mus musculus molossinus (Japanese wild mouse)  
 Mus musculus molossinus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

**REFERENCE**  
**AUTHORS** 1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T., Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and Shiroishi, T.  
**TITLE** Contribution of Asian mouse subspecies *Mus musculus molossinus* to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis  
**JOURNAL** Genome Res. 14 (12), 2439-2447 (2004)  
**PUBMED** 15574823  
**REFERENCE** 2 (bases 1 to 729)  
**AUTHORS** Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.  
**TITLE** Direct Submission  
**JOURNAL** Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail: hattori@psc.riken.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
**COMMENT** Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp).  
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Tsukuba Institute, Bio Resource Center.  
 Tsukuba, Tsukuba, 305-0074 Japan  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@rtc.riken.jp  
**PRIMERS**  
 Sequencing : T7  
**LIBRARY**  
 Vector : pBACe3.6  
 R.Site 1 : ECoRI.  
 R.Site 2 : ECoRI.

**FEATURES**  
**source**  
 Location/Qualifiers  
 1..729  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-373J11.T7"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_libs="MSMg01 Mouse Male BAC Library"

**ORIGIN**  
 Query Match 87.0%; Score 17.4; DB 10; Length 729;  
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 AAGGAACACGACACCA 19  
 |||||  
 Db 629 AAGGAACACGACACCA 611  
 |||||

**RESULT 15**  
**LOCUS** CF998205  
**DEFINITION** AGNCOURT 16393924 NIH\_ZGC\_7 Danio rerio cDNA clone IMAGE:7038534 5', mRNA sequence.  
**ACCESSION** CF998205  
**VERSION** CF998205.1 GI:38519056  
**KEYWORDS** EST.  
**SOURCE** Danio rerio (zebrafish)  
**ORGANISM** Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
**REFERENCE** 1 (bases 1 to 750)  
**AUTHORS** NIH-MGC http://mgc.nci.nih.gov/.  
**TITLE** National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)

**COMMENT**  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Len Zon, Harvard  
 cDNA Library Preparation: Open Biosystems  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LLAM14790 row: f column: 04  
 High quality sequence stop: 698.  
**FEATURES**  
**source**  
 Location/Qualifiers  
 1..750  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:7038534"  
 /tissue\_type="whole body"  
 /lab\_host="DHI0B"  
 /clone\_lib="NIH\_ZGC\_7"  
 /notes="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;  
 Bulk tissue was collected from a whole adult individual from the Tuebingen strain. 1st strand cDNA was primed with a Not I - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1. Library was size-selected for >1 kb fragments and normalized. A non-normalized version of this library is also available (NIH\_ZGC 10). Library was constructed by Open Biosystems (Huntsville, AL)"

**ORIGIN**  
 Query Match 87.0%; Score 17.4; DB 7; Length 750;  
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Oy 1 AAGGAACACGACACCA 19  
 |||||  
 Db 259 AAGGAACACGACACTCA 277  
 |||||

**RESULT 16**  
**LOCUS** CNS03817/c  
**DEFINITION** Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 004G16 of library G from Tetraodon nigroviridis, genomic survey sequence.  
**ACCESSION** AL232036  
**VERSION** AL232036.1 GI:7891040  
**KEYWORDS** GSS; genome survey sequence.  
**SOURCE** Tetraodon nigroviridis  
**ORGANISM** Tetraodon nigroviridis  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 Tetraodontidae; Tetraodontidae; Tetraodon.  
**REFERENCE** 1  
**AUTHORS** Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.  
**TITLE** Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence  
**JOURNAL** Nat. Genet. 25 (2), 235-238 (2000)  
**PUBMED** 10835645  
**REFERENCE** 2  
**AUTHORS** Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.  
**TITLE** Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis  
**JOURNAL** Genome Res. 10 (7), 939-949 (2000)

10899143  
PUBMED  
REFERENCE: 3 (bases 1 to 770)  
Genoscope.  
Direct Submission  
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
This sequence is a single read and was generated as part of a large  
scale clone-end and sequencing project of the tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.  
Location/Qualifiers  
1..770  
/organism="Tetraodon nigroviridis"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:99883"  
/clone="004G16"  
/clone\_lib="G"  
/note="Genoscope sequence ID : COBG004BD08XE1  
end : PUC-ori"

ORIGIN  
source  
Query Match 87.0%; Score 17.4; DB 11; Length 770;  
Best Local Similarity 94.7%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AAGGAACACGACACCCA 19  
Db 303 AAGGAACACGACACCCA 285  
|||||  
|||||

RESULT 17  
CV480587/c  
LOCUS  
DEFINITION AGNCOURT 33240879 NIH\_ZGC\_19 Danio rerio cDNA clone IMAGE:7452402  
3', mRNA sequence.  
ACCESSION CV480587  
VERSION CV480587.1 GI:53736629  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: William S. Talbot, Stanford University  
cDNA Library Preparation: Dr. Sumio Sugano  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLNL15709 row: j column: 16  
High quality sequence start: 8  
High quality sequence stop: 673.  
Location/Qualifiers  
1..785  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:7452402"  
/tissue type="5 day old whole larvae"  
/lab host="DH10B Tona"  
/clone\_lib="NIH\_ZGC\_19"  
/note="Organ: mixed; Vector: pME18S-FL3; Site\_1: DralII;

Site\_2: DralII; 1st strand cDNA was primed with an  
oligo(dT) primer  
[GGCGCTGAGACGGCTATGCGCTTTTTTTTTTTTTTTT];  
double-stranded cDNA was ligated to a DraIII adaptor  
[GGCUACUGG], digested and directionally cloned into  
distinct DraIII sites of the pME18S-FL3. Library was size  
selected for 1.0 kb, with an average insert size of ~1.2kb.  
Library constructed by Yutaka Suzuki (University of Tokyo  
Institute of Medical Science). Custom primers recommended  
for sequencing: 5' end primer 5'-GGATGTGCTTTACTTCA-3',  
and 3' end primer 5'-CGACCTGCAGCTCGACACA-3'. Note: This  
is a Zebrafish Gene Collection (ZGC) library"

ORIGIN  
source  
Query Match 87.0%; Score 17.4; DB 7; Length 785;  
Best Local Similarity 94.7%; Pred. No. 1.6e+03;  
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 AAGGAACACGACACCCA 19  
Db 77 AAGGAACACGACACTCA 59  
|||||  
|||||

RESULT 18  
BG985751  
LOCUS  
DEFINITION 2867 NICHD\_Zebrafish\_normalized\_I Danio rerio cDNA clone 2867, mRNA  
sequence.  
ACCESSION BG985751  
VERSION BG985751.1 GI:14389831  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
REFERENCE 1 (bases 1 to 794)  
AUTHORS Kudoh, T., Teang, M., Hukriede, N.A., Chen, X., Dedekian, M.,  
Clarke, C.J., Kiang, A., Schultz, S., Epstein, J.A., Toyama, R. and  
David, I.B.  
A gene expression screen in zebrafish embryogenesis  
Genome Res. 11 (12), 1979-1987 (2001)  
11731487  
Contact: David IB  
Laboratory of Molecular Genetics  
National Institute of Child Health and Human Development, NIH  
Bldg. 6B, Room 413, 9000 Rockville Pike, Bethesda, MD 20892 USA  
Tel: 301 496 4448  
Fax: 301 496 0243  
Email: idavid@nih.gov  
Seq primer: T3.  
Location/Qualifiers  
1..794  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="2867"  
/dev stage="bud to 10 somite stage embryos"  
/clone\_lib="NICHD\_Zebrafish\_normalized\_I"  
/note="vector: pBluescript KS+; Site\_1: NotI; Site\_2:  
Sall; RNA was reverse-transcribed to first strand cDNA  
using SuperScriptII reverse-transcriptase and tagged  
oligo-dT primer which contains several restriction sites  
including a NotI site:  
gactagtctagatcgatcgagcgagcgccgcccccttttttttttt. Second  
strand DNA was synthesized by E. coli DNA polymerase I in  
combination with E. coli RNase H and E. coli DNA ligase.  
Double stranded cDNA was ligated with Sall adaptor. These  
cDNAs were cloned into the Sall/NotI site of pBluescript  
KS+ and transformed into E. coli Electromax DH10B by  
electroporation."

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Query Match      87.0%; Score 17.4; DB 2; Length 794;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
    |||||
Db 460 AAGGAAACACGGACACTCA 478

RESULT 19
CV486670/c
LOCUS
DEFINITION AGNCOURT 33240863 NIH_ZGC_19 Danio rerio cDNA clone IMAGE:7452401
3', mRNA sequence.
ACCESSION CV486670.1 GI:53742712
VERSION
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 794)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM15709 row: j column: 15
High quality sequence start: 6
High quality sequence stop: 710.
Location/Qualifiers
FEATURES
    source
    1..794
        /organism="Danio rerio"
        /mol_type="mRNA"
        /db_xref="taxon:7955"
        /clone="IMAGE:7452401"
        /tissue_type="5 day old whole larvae"
        /lab_host="DH10B Tona"
        /clone_lib="NIH_ZGC_19"
        /note="Organ: mixed; Vector: pME18S-FL3; Site 1: DraIII;
        Site 2: DraIII; 1st strand cDNA was primed with an
        oligo(dT) primer
        [GCGCTGACAGCGCTATGTGGCTTTTCTTTTCTTTT];
        double-stranded cDNA was ligated to a DraIII adaptor
        [GGCUACUG], digested and directionally cloned into
        distinct DraIII sites of the pME18S-FL3. Library was size
        selected for 1.0 kb, with a average insert size of ~1.2kb.
        Library constructed by Yutaka Suzuki (University of Tokyo
        Institute of Medical Science). Custom primers recommended
        for sequencing: 5' end primer 5'-GGATGTTGCTTTACTTCTA-3'
        and 3' end primer 5'-CGACTTCGACCTCGACACA-3'. Note: This
        is a Zebrafish Gene Collection (ZGC) library"

Query Match      87.0%; Score 17.4; DB 7; Length 794;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
    |||||
Db 79 AAGGAAACACGGACACTCA 61

RESULT 21
CV126404
LOCUS
DEFINITION AGNCOURT 32003381 NIH_ZGC_17 Danio rerio cDNA clone IMAGE:7416843
5', mRNA sequence.
ACCESSION CV126404
VERSION CV126404.1 GI:51861239
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

```

```

RESULT 20
CV026895
LOCUS
DEFINITION AGNCOURT_16619433 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7054646
5', mRNA sequence.
ACCESSION CV026895
VERSION CV026895.1 GI:38552819
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 798)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Biosystems
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHAM14832 row: e column: 12
High quality sequence stop: 720.
Location/Qualifiers
FEATURES
    source
    1..798
        /organism="Danio rerio"
        /mol_type="mRNA"
        /db_xref="taxon:7955"
        /clone="IMAGE:7054646"
        /tissue_type="whole body"
        /lab_host="DH10B"
        /clone_lib="NIH_ZGC_7"
        /note="Vector: pExpress1; Site 1: NotI; Site 2: EcoRV;
        Bulk tissue was collected from a whole adult individual
        from the Tuebingen strain. 1st strand cDNA was primed with
        a Not I- oligo(dT) primer, double-stranded cDNA was
        cloned into the Not I and EcoRV sites of pExpress-1.
        Library was size-selected for >1 kb fragments and
        normalized. A non-normalized version of this library is
        also available (NIH_ZGC 10). Library was constructed by
        Open Biosystems (Huntsville, AL)"

Query Match      87.0%; Score 17.4; DB 7; Length 798;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCA 19
    |||||
Db 467 AAGGAAACACGGACACTCA 485

RESULT 21
CV126404
LOCUS
DEFINITION AGNCOURT 32003381 NIH_ZGC_17 Danio rerio cDNA clone IMAGE:7416843
5', mRNA sequence.
ACCESSION CV126404
VERSION CV126404.1 GI:51861239
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

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/lab host="DH10B Tona"
/clone lib="NIH ZGC 4"
/note="Organ: brain/CNS; Vector: PME18S-FL3; Site_1:
DraIII; Site_2: DraIII"

ORIGIN
Query Match      87.0%; Score 17.4; DB 7; Length 848;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
Db 218 AAGGAAACACGGACACT 236

RESULT 24
CW718544/c
LOCUS
DEFINITION MARC_1010456 CHORI-240-397C5 Bos taurus genomic clone 1F5, genomic
survey sequence.
ACCESSION CW718544
VERSION CW718544.1 GI:55422254
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 891)
Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.
SNP discovery in cattle based on low coverage sequencing of BAC
clones
Unpublished (2004)
Other_GSSs: MARC_1009304
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Seq primer: GTAATACGACTCACTATAGGG
Class: BAC subclone.
Location/Qualifiers
    source
    1..891
    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /db_xref="taxon:9913"
    /clone="1F5"
    /sex="Male"
    /tissue type="Blood"
    /clone lib="CHORI-240-397C5"
    /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
    BamHI; BAC DNA was digested with Sau3A. Fragments were
    sized to 800-1200 bases and subcloned into pBLUESCRIPT
    SK-."

FEATURES
    source
    1..891
    AAGGAAACACGGACACCCA 19
    |||||
    300 AAGGAAACACGGACACCCA 282

ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 891;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
Db 300 AAGGAAACACGGACACCCA 282

RESULT 25
CW717765
LOCUS
DEFINITION MARC_1009304 CHORI-240-397C5 Bos taurus genomic clone 1F5, genomic
survey sequence.
ACCESSION CW717765
VERSION CW717765.1 GI:55421475
KEYWORDS GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Pecora; Bovidae; Bovinae; Bos.
1 (bases 1 to 905)
Smith,T.P.L., Stone,R.T., Keele,J.W., Snelling,W.M. and Harhay,G.P.
SNP discovery in cattle based on low coverage sequencing of BAC
clones
Unpublished (2004)
Other_GSSs: MARC_1010456
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@mail.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Seq primer: AATTAACTCTCACTAAAGGG
Class: BAC subclone.
Location/Qualifiers
    source
    1..905
    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /db_xref="taxon:9913"
    /clone="1F5"
    /sex="Male"
    /tissue type="Blood"
    /clone lib="CHORI-240-397C5"
    /note="Vector: pBLUESCRIPT SK-; Site 1: BamHI; Site 2:
    BamHI; BAC DNA was digested with Sau3A. Fragments were
    sized to 800-1200 bases and subcloned into pBLUESCRIPT
    SK-."

ORIGIN
Query Match      87.0%; Score 17.4; DB 10; Length 905;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCA 19
    |||||
    651 AAGGAAACACGGACACCCA 669

RESULT 26
CW717765/c
LOCUS
DEFINITION AUF_IpHdk 47 p20 Head kidney cDNA library Ictalurus punctatus cDNA
5' similar to Autosomal Highly Conserved Protein, mRNA sequence.
ACCESSION CK412195
VERSION CK412195.1 GI:40572779
KEYWORDS EST.
SOURCE Ictalurus punctatus (channel catfish)
ORGANISM Ictalurus punctatus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 961)
Liu,Z., Li,P., Liu,L., He,C., Kucuktas,H., Feng,J., Chen,L.,
Peatman,R., Baoprasertkul,P., Simmons,M., Muir,W., Grizzle,J.,
Dunham,R. and Brady,Y.
30,000 new catfish ESTs: new resources for functional analysis of
genes involved in aquaculture performance traits
Unpublished (2004)
Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell

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* and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: T7.

FEATURES             Location/Qualifiers
  source             1..961
    /organism="Ictalurus punctatus"
    /mol_type="mRNA"
    /db_xref="taxon:7998"
    /clone_lib="Head kidney cDNA library"
    /note="Organ: Head kidney; Vector: pSport1; Site_1: NotI;
    Site_2: SalI"

ORIGIN
Query Match          87.0%; Score 17.4; DB 7; Length 961;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AAGGAACACCGACACCCA 19
    |||||
Db 270 AAGGAACACCGTCACCCA 252

RESULT 27
LOCUS             BM415978                963 bp mRNA linear EST 28-JAN-2002
DEFINITION       OP21060 Mixed Stage EST's from Globodera pallida, the potato cyst
ACCESSION        BM415978
VERSION          BM415978.1 GI:18382777
KEYWORDS
SOURCE
ORGANISM         Globodera pallida
                  Globodera pallida
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
                  Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

REFERENCE
AUTHORS          Heer, J., Sosinski, B., Pokrzywa, R.M., Wairy, A. and Opperman, C.
TITLE            Mixed Stage EST's from Globodera pallida, the potato cyst nematode
JOURNAL          Unpublished (2001)
COMMENT          Contact: Opperman, C
                  Center for the Biology of Nematode Parasitism
                  NC State University; IACR-Rothamsted
                  Campus Box 7616; Raleigh, NC 27695, USA
                  Tel: 919.515.6699
                  Fax: 919.515.9500
                  Email: warthog@unity.ncsu.edu
                  GT11-9PCN F A05 GT11-9 F 033.ab1.

FEATURES             Location/Qualifiers
  source             1..963
    /organism="Globodera pallida"
    /mol_type="mRNA"
    /db_xref="taxon:36090"
    /clone_lib="Mixed Stage EST's from Globodera pallida, the
    potato cyst nematode"
    /note="Vector: lambda GT11; This is a collaborative effort
    between IACR-Rothamsted and North Carolina State
    University. The library was constructed from mixed stage
    G. pallida in lambda GT11 by Paul Burroughs,
    IACR-Rothamsted."

ORIGIN
Query Match          87.0%; Score 17.4; DB 3; Length 963;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AAGGAACACCGACACCCA 19
    |||||
Db 572 AAGGTACACCGACACCCA 590

* and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
Fax: 334 844 9208
Email: zliu@acesag.auburn.edu
Seq primer: T7.

FEATURES             Location/Qualifiers
  source             1..961
    /organism="Ictalurus punctatus"
    /mol_type="mRNA"
    /db_xref="taxon:7998"
    /clone_lib="Head kidney cDNA library"
    /note="Organ: Head kidney; Vector: pSport1; Site_1: NotI;
    Site_2: SalI"

ORIGIN
Query Match          87.0%; Score 17.4; DB 7; Length 961;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AAGGAACACCGACACCCA 19
    |||||
Db 270 AAGGAACACCGTCACCCA 252

RESULT 27
LOCUS             BM415978                963 bp mRNA linear EST 28-JAN-2002
DEFINITION       OP21060 Mixed Stage EST's from Globodera pallida, the potato cyst
ACCESSION        BM415978
VERSION          BM415978.1 GI:18382777
KEYWORDS
SOURCE
ORGANISM         Globodera pallida
                  Globodera pallida
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina;
                  Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.

REFERENCE
AUTHORS          Heer, J., Sosinski, B., Pokrzywa, R.M., Wairy, A. and Opperman, C.
TITLE            Mixed Stage EST's from Globodera pallida, the potato cyst nematode
JOURNAL          Unpublished (2001)
COMMENT          Contact: Opperman, C
                  Center for the Biology of Nematode Parasitism
                  NC State University; IACR-Rothamsted
                  Campus Box 7616; Raleigh, NC 27695, USA
                  Tel: 919.515.6699
                  Fax: 919.515.9500
                  Email: warthog@unity.ncsu.edu
                  GT11-9PCN F A05 GT11-9 F 033.ab1.

FEATURES             Location/Qualifiers
  source             1..963
    /organism="Globodera pallida"
    /mol_type="mRNA"
    /db_xref="taxon:36090"
    /clone_lib="Mixed Stage EST's from Globodera pallida, the
    potato cyst nematode"
    /note="Vector: lambda GT11; This is a collaborative effort
    between IACR-Rothamsted and North Carolina State
    University. The library was constructed from mixed stage
    G. pallida in lambda GT11 by Paul Burroughs,
    IACR-Rothamsted."

ORIGIN
Query Match          87.0%; Score 17.4; DB 3; Length 963;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 AAGGAACACCGACACCCA 19
    |||||
Db 572 AAGGTACACCGACACCCA 590

```

```

RESULT 28
LOCUS             CG745203                1121 bp DNA linear GSS 24-OCT-2003
DEFINITION       P038-1-B12.ya Ppa EcoRI BAC Library Pristionchus pacificus genomic,
ACCESSION        CG745203
VERSION          CG745203.1 GI:37966129
KEYWORDS          GSS.
SOURCE            Pristionchus pacificus
ORGANISM         Pristionchus pacificus
                  Pristionchus pacificus
                  Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
                  Neodiplogasteridae; Pristionchus.
REFERENCE
AUTHORS          Srinivasan, J., Sinz, W., Jesse, T., Wiggers-Perbolte, L., Jansen, K.,
                  Buntjer, J., van der Meulen, M. and Sommer, R.J.
                  An integrated physical and genetic map of the nematode Pristionchus
                  pacificus
                  Mol. Genet. Genomics 269 (5), 715-722 (2003)
                  12884007
                  Contact: Sommer RJ
                  Evolutionary Biology
                  Max-Planck-Institute for Developmental Biology
                  Spemannstr. 37-39, Tuebingen D-72076, Germany
                  Tel: 00497071601371
                  Fax: 00497071601498
                  Email: ralf.sommer@tuebingen.mpg.de
                  Class: BAC ends.
FEATURES             Location/Qualifiers
  source             1..1121
    /organism="Pristionchus pacificus"
    /mol_type="genomic DNA"
    /strain="California"
    /db_xref="taxon:54126"
    /clone_lib="Ppa EcoRI BAC Library"
    /note="The library was generated by a partial digest of
    the genomic DNA with EcoRI and cloning into the BAC
    vector."

ORIGIN
Query Match          87.0%; Score 17.4; DB 10; Length 1121;
Best Local Similarity 94.7%; Pred. No. 1.6e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 AGGAACACCGACACCCA 20
    |||||
Db 1098 AGGAACACCGACACCCA 1116

RESULT 29
LOCUS             CK027487                1134 bp mRNA linear EST 26-NOV-2003
DEFINITION       AGENCOURT_16624073 NIH_ZGC_7 Danio rerio cDNA clone IMAGE:7053855
ACCESSION        CK027487
VERSION          CK027487.1 GI:38553411
KEYWORDS          EST.
SOURCE            Danio rerio (zebrafish)
ORGANISM         Danio rerio
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                  Cypriniformes; Cyprinidae; Danio.
                  1 (bases 1 to 1134)
                  NIH-MGC http://mgs.nci.nih.gov/.
                  National Institutes of Health, Mammalian Gene Collection (MGC)
                  Unpublished (1999)
                  Contact: Daniela S. Gerhard, Ph.D.
                  Office of Cancer Genomics
                  National Cancer Institute / NIH
                  Bldg. 31 Rm10A07 Bethesda, MD 20892
                  Email: cgapbs-r@mail.nih.gov
                  Tissue procurement: Len Zon, Harvard
                  cDNA Library Preparation: Open Biosystems
                  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

```

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

Plate: LRAM14830 row: d column: 13

High quality sequence stop: 832.

#### FEATURES

Location/Qualifiers  
 1..1134  
 /organism="Danio rerio"  
 /mol\_type="mrna"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:7053855"  
 /tissue\_type="whole body"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_ZGC\_7"

/note="vector: pExpress1; Site 1: NotI; Site 2: EcoRV;  
 Bulk tissue was collected from a whole adult individual  
 from the Tuebingen strain. 1st strand cDNA was primed with  
 a Not I - oligo(dT) primer, double-stranded cDNA was  
 cloned into the Not I and EcoRV sites of pExpress-1.  
 Library was size-selected for >1 kb fragments and  
 normalized. A non-normalized version of this library is  
 also available (NIH\_ZGC\_10). Library was constructed by  
 Open Biosystems (Huntsville, AL)"

#### ORIGIN

Query Match 87.0%; Score 17.4; DB 7; Length 1134;  
 Best Local Similarity 94.7%; Pred. No. 1.6e+03;  
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAGGAAACACGGACACCCA 19

Db 861 AAGGAAACACGGACACTCA 879

#### RESULT 30

C2679560 683 bp DNA linear GSS 07-JUL-2005  
 LOCUS OM\_Ba0237005.r OM\_Ba Oryza minuta genomic clone OM\_Ba0237005 3',  
 DEFINITION genomic survey sequence.

ACCESSION C2679560

VERSION C2679560.1 GI:70291142

KEYWORDS GSS.

SOURCE Oryza minuta

ORGANISM Oryza minuta

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzeae; Oryza.

REFERENCE 1 (bases 1 to 683)

AUTHORS Kim, H., Collura, K., Wissotski, M., Byrne, M., Stum, D., Smart, D.,  
 Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and  
 Wang, R.

TITLE OMAP (Oryza Map Alignment Project)- Arizona Genomics Institute

JOURNAL Unpublished (2005)

COMMENT Contact: Rod A. Wing

Arizona Genomics Institute

University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: 520 626 9595

Fax: 520 621 1259

Email: [rwing@genome.arizona.edu](mailto:rwing@genome.arizona.edu)

Plate: 0237 row: 0 column: 05

Class: BAC ends.

Location/Qualifiers

1..683

/organism="Oryza minuta"

/mol\_type="genomic DNA"

/db\_xref="taxon:63629"

/clone="OM\_Ba0237005"

/tissue\_type="leaves"

/lab\_host="DH10B"

/clone\_lib="OM\_Ba"

/note="vector: pCUGIBAC1; Site\_1: HindIII; Site\_2:

#### FEATURES

source

#### RESULT 32

BH693975

LOCUS BH693975

DEFINITION BOMI227TF BO 2.3 KB Brassica oleracea genomic clone BOMI227,

genomic survey sequence.

ACCESSION BH693975

VERSION BH693975.1 GI:18764555

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

#### ORIGIN

Query Match 85.0%; Score 17; DB 10; Length 683;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGAACACGGACACCCA 19

Db 653 GGAACACGGACACCCA 669

#### RESULT 31

BZ020345/c

LOCUS BZ020345

DEFINITION osh04a08.b1 B.oleracea002 Brassica oleracea genomic, genomic survey

sequence.

ACCESSION BZ020345

VERSION BZ020345.1 GI:23580078

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 712)

AUTHORS Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T.,

Nash, W., Rabinowicz, P.D. and Wilson, R.K.

Whole genome shotgun reads from Brassica oleracea

Unpublished (2002)

COMMENT Contact: Richard K. Wilson

Genome Sequencing Center

Washington University School of Medicine

Email: [submissions@watson.wustl.edu](mailto:submissions@watson.wustl.edu)

Plate: osh04 row: a column: 08

Seq primer: -21UPPOT forward

Class: shotgun

High quality sequence start: 28

High quality sequence stop: 551.

Location/Qualifiers

1..712

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/db\_xref="taxon:3712"

/clone\_lib="B.oleracea002"

/note="vector: P0TW13; Whole genome shotgun library from

flowering buds. DNA was purified from a crude nuclear

prep using Brassica oleracea T0100DH3 buds provided by

Thomas Osborn at the University of Wisconsin. Genomic

DNA was provided by Pablo Rabinowicz (CSHL) and the

shotgun library prepared at Washington University Genome

Sequencing Center."

#### ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 712;  
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 AGGAACACGGACACCC 18

Db 497 AGGAACACGGACACCC 481

#### RESULT 32

BH693975

LOCUS BH693975

DEFINITION BOMI227TF BO 2.3 KB Brassica oleracea genomic clone BOMI227,

genomic survey sequence.

ACCESSION BH693975

VERSION BH693975.1 GI:18764555

KEYWORDS GSS.

SOURCE Brassica oleracea

ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica;

# REFERENCE AUTHORS

1 (bases 1 to 751)

Ayele, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,

Utterback, T.R., Wortman, J.R., White, O.R. and Town, C.D.

Whole genome shotgun sequencing of *Brassica oleracea* and its

application to gene discovery and annotation in Arabidopsis

Genome Res. 15 (4), 487-495 (2005)

# JOURNAL PUBMED

15805490

Other GSSs: BOMIZ27TR

Contact: Chris Town

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TF

Class: sheared ends.

# FEATURES source

Location/Qualifiers

1..751

/organism="Brassica oleracea"

/mol\_type="genomic DNA"

/strain="TO100DH3"

/db\_xref="taxon:3712"

/clone="BOMIZ27"

/clone\_lib="BO 2.3 KB"

/note="Vector: pHOsl; Site 1: BstXI; 2-3 kb sheared

genomic DNA inserted into pHOsl using BstXI linkers"

# ORIGIN

Query Match 85.0%; Score 17; DB 9; Length 751;  
Best Local Similarity 100.0%; Pred. No. 2.4e+03;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

# Qy Db

2 AGGAACACGACACCC 18

80 AGGAACACGACACCC 96

# RESULT 33 LOCUS

CW176116 108 bp DNA linear GSS 29-OCT-2004  
104 588 11158315 116 36578 066 Sorghum methylation filtered library  
(LibID: 104) Sorghum bicolor genomic clone 11158315, genomic survey  
sequence.

# ACCESSION VERSION

CW176116.1 GI:54868683

GSS.

# KEYWORDS SOURCE

Sorghum bicolor (sorghum)

# ORGANISM

Sorghum bicolor

# REFERENCE AUTHORS

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCD clade; Panicoideae; Andropogoneae; Sorghum.

# REFERENCE AUTHORS

1 (bases 1 to 108)

Bedell, J.A., Budiman, M.A., Nurnberg, A., Citek, R.W., Robbins, D.,

Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,

McMenamy, J., Smith, M., Huleman, H., Roe, B.A., Wiley, G., Korff, I.F.,

Rabinowitz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and

Martenssen, R.A.

Sorghum genome sequencing by methylation filtration

# JOURNAL PUBMED

PLoS Biol. 3 (1), e13 (2005)

15660154

# COMMENT

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: 588 row: p column: 19

Seq primer: T3 Reverse

Class: methylation filtered

# FEATURES source

High quality sequence stop: 108.

Location/Qualifiers

1..108

/organism="Sorghum bicolor"

/mol\_type="genomic DNA"

/cultivar="ATx623"

/db\_xref="taxon:4558"

/clones="11158315"

/clone\_lib="Sorghum methylation filtered library (LibID: 104)"

/note="Organ: leaf; Vector: pBCKS(-); Site 1: HincII; DNA

prepared from purified nuclei was randomly sheared, end-

repaired, size fractionated to enrich for the 0.5 to 5

kb fraction, ligated into HincII-digested pBCKS(-) vector

and electroporated into E. coli cells. This is a

methylation filtered library."

# ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 108;  
Best Local Similarity 90.0%; Pred. No. 2.5e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

# Qy

1 AAGGAACACGACACCAA 20

# Db

81 AAGGAGACGACACCAA 100

# RESULT 34 LOCUS

CW290195 209 bp mRNA linear EST 16-SEP-2003  
StrPus38.003354 Sea urchin embryo 7hr cleavage stage cDNA library  
MPMGp538 Strongylocentrotus purpuratus cDNA clone  
CALTP538J242;MPI\_538\_2J24\_3', mRNA sequence.

# ACCESSION VERSION

CW290195.1 GI:34741272

# KEYWORDS SOURCE

EST.

# ORGANISM

Strongylocentrotus purpuratus  
Strongylocentrotus purpuratus  
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;  
Echinoidea; Euechinoidea; Echinacea; Echinoidea;  
Strongylocentrotidae; Strongylocentrotus.

# REFERENCE AUTHORS

1 (bases 1 to 209)

Poustka, A.J., Groth, D., Hennig, S., Thamm, S., Cameron, A., Beck, A.,

Reinhardt, R., Herwig, R., Panopoulou, G. and Lehrach, H.

Generation, annotation, evolutionary analysis, and database

integration of 20,000 unique sea urchin EST clusters

Genome Res. 13 (12), 2736-2746 (2003)

# JOURNAL COMMENT

Contact: Poustka AJ

Laboratory 145, dept. Lehrach

Max-Planck-Institut fuer Molekulare Genetik

Inhestr. 63-73, D-14195 Berlin, Germany

Tel: +49 30 8413 1235

Fax: +49 30 8413 1128

Email: poustka@molgen.mpg.de

The library was characterised by oligonucleotide fingerprinting

(ONF) to reduce sequencing redundancy. According to the ONF

procedure, clones that display the same hybridisation matrix with a

battery of 200 8mer oligonucleotides are grouped into clusters. One

clone per ONF cluster is selected for sequencing. The size of each

cluster is an indicator of the frequency of a transcript in the

analysed library. The cluster size as well as the coordinates of

the other clones assigned to the same ONF cluster as the clone from

which the above EST is generated is available at the sea urchin

project web site at: [http://www.molgen.mpg.de/ag\\_seaurchin/](http://www.molgen.mpg.de/ag_seaurchin/). cDNA

clones and filters are distributed via the Resource Center/Primary

Database of the German Human Genome Project (<http://www.rzpd.de>)

PCR Primers

FORWARD: 5' CCCAGGCTTACACTTATGCTCCGGCTCG 3' (M13RSP) 5'-seq

BACKWARD: 5' GCTATTACCGAGCTGCCAAGGGGATGTG 3' (M13FSP) 3'-seq

Seq primer: 5' GCTATTACCGAGCTGCCAAGGGGATGTG 3' (M13FSP)

High quality sequence stop: 209.

# FEATURES source

Location/Qualifiers

1..209

```
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="CALTp538J242,MPI_538_2J24"
/tissue_type="whole embryo"
/dev_stage="embryonic 7hr"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin embryo 7hr cleavage stage cDNA library MPMPp538"
/notes="Vector: pSport1; Site 1: NotI; Site 2: SalI; Random primed and directionally cloned in pSport1 vector using a NotI (5'-PGACTAGTTCGATCGAGCGGCCGC (T)15-3' and a SalI 5'-TCGACCCACGGCTCG-3'adapters (Gibco BRL)"

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 209;
Best Local Similarity 90.0%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 20 AAGGAAACCCAGACACCCAA 39
    |||||

RESULT 35
CD319193/c
LOCUS
DEFINITION StrP538.000555 Sea urchin embryo 7hr cleavage stage cDNA library
MPMPp538 Strongylocentrotus purpuratus cDNA clone
CALTp538J242,MPI_538_2J24 5', mRNA sequence.
CD319193
CD319193.1 GI:34791254
EST.
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 210)
Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A.,
Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
Laboraty 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel.: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
PCR Primers
FORWARD: 5' CCCAGGCTTTACTTTTANGCTTCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTGCGCAGTTCGGAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCCGGAATTCGGGT-3' pSport3/86
High quality sequence stop: 210.
Location/Qualifiers
1. .210
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"

/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
/clone="CALTp538J242,MPI_538_2J24"
/tissue_type="whole embryo"
/dev_stage="embryonic 7hr"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin embryo 7hr cleavage stage cDNA library MPMPp538"
/notes="Vector: pSport1; Site 1: NotI; Site 2: SalI; Random primed and directionally cloned in pSport1 vector using a NotI (5'-PGACTAGTTCGATCGAGCGGCCGC (T)15-3' and a SalI 5'-TCGACCCACGGCTCG-3'adapters (Gibco BRL)"

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 209;
Best Local Similarity 90.0%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 20 AAGGAAACCCAGACACCCAA 39
    |||||

RESULT 35
CD319193/c
LOCUS
DEFINITION StrP538.000555 Sea urchin embryo 7hr cleavage stage cDNA library
MPMPp538 Strongylocentrotus purpuratus cDNA clone
CALTp538J242,MPI_538_2J24 5', mRNA sequence.
CD319193
CD319193.1 GI:34791254
EST.
Strongylocentrotus purpuratus
Strongylocentrotus purpuratus
Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoidea;
Strongylocentrotidae; Strongylocentrotus.
1 (bases 1 to 210)
Poustka,A.J., Groth,D., Hennig,S., Thamm,S., Cameron,A., Beck,A.,
Reinhardt,R., Herwig,R., Panopoulou,G. and Lehrach,H.
Generation, annotation, evolutionary analysis, and database
integration of 20,000 unique sea urchin EST clusters
Genome Res. 13 (12), 2736-2746 (2003)
Contact: Poustka AJ
Laboraty 145, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Innestr.63-73, D-14195 Berlin, Germany
Tel.: +49 30 8413 1235
Fax: +49 30 8413 1128
Email: poustka@molgen.mpg.de
The library was characterised by oligonucleotide fingerprinting
(ONF) to reduce sequencing redundancy. According to the ONF
procedure, clones that display the same hybridisation matrix with a
battery of 200 8mer oligonucleotides are grouped into clusters. One
clone per ONF cluster is selected for sequencing. The size of each
cluster is an indicator of the frequency of a transcript in the
analysed library. The cluster size as well as the coordinates of
the other clones assigned to the same ONF cluster as the clone from
which the above EST is generated is available at the sea urchin
project web site at: http://www.molgen.mpg.de/ag_seaurchin/. cDNA
clones and filters are distributed via the Resource Center/Primary
Database of the German Human Genome Project (http://www.rzpd.de)
PCR Primers
FORWARD: 5' CCCAGGCTTTACTTTTANGCTTCGGCTCG 3' (M13RSP) 5'-seq
BACKWARD: 5' GCTATTGCGCAGTTCGGAAGGGGATGTG 3' (M13FSP) 3'-seq
Seq primer: 5'-CCGGTCCGGAATTCGGGT-3' pSport3/86
High quality sequence stop: 210.
Location/Qualifiers
1. .210
/organism="Strongylocentrotus purpuratus"
/mol_type="mRNA"
/db_xref="taxon:7668"
```

```
/clone="CALTp538J242,MPI_538_2J24"
/tissue_type="whole embryo"
/dev_stage="embryonic 7hr"
/lab_host="E.coli, XLI blue"
/clone_lib="Sea urchin embryo 7hr cleavage stage cDNA library MPMPp538"
/notes="Vector: pSport1; Site 1: NotI; Site 2: SalI; Random primed and directionally cloned in pSport1 vector using a NotI (5'-PGACTAGTTCGATCGAGCGGCCGC (T)15-3' and a SalI 5'-TCGACCCACGGCTCG-3'adapters (Gibco BRL)"

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 210;
Best Local Similarity 90.0%; Pred. No. 2.7e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 192 AAGGAAACCCAGACACCCAA 173
    |||||

RESULT 36
DN493639/c
LOCUS
DEFINITION G079P41.5pr Populus tremula wood cDNA library Populus tremula x
Populus tremuloides cDNA clone G079P41 5', mRNA sequence.
DN493639
DN493639.1 GI:60703829
EST.
Populus tremula x Populus tremuloides
Populus tremula x Populus tremuloides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Malpighiales; Salicaceae; Salicaceae; Populus.
1 (bases 1 to 351)
Sterky,F., Bhallerao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,
Brunner,A.M., Charbonnel-Campaa,L., Lindvall,J.J., Tandref,K.,
Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhallerao,R.P.,
Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.
A Populus EST resource for plant functional genomics
Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
15353603
Other ESTs: G079P41
Contact: Bo Segerman
Umea Plant Science Center, Department of Plant Physiology
Umea University
901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@plantphys.umu.se.

FEATURES
source
1. .351
/organism="Populus tremula x Populus tremuloides"
/mol_type="mRNA"
/db_xref="taxon:47664"
/clone="G079P41"
/tissue_type="Tension wood"
/clone_lib="Populus tension wood cDNA library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 351;
Best Local Similarity 90.0%; Pred. No. 2.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20
    |||||
Db 242 AAGGAAACCCAGACACCCAA 223
    |||||

RESULT 37
CW585488/c
LOCUS
DEFINITION OA_ABa0117123.r OA_ABa Oryza australiensis genomic clone
CW585488
OA_ABa0117123.r 363 bp DNA linear GSS 22-OCT-2004
```

OA\_ABA0117123 3', genomic survey sequence.  
 CW585488  
 VERSION GI:54477247  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Oryza australiensis  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 1 (bases 1 to 363)  
 Kim.H., Yu.Y., Stum.D., Yost.D., Rao.K., Luo.M., Jetty.R.,  
 Kudrna.D., Muller.C., Hatfield.J., Soderlund.C. and Wing.R.  
 OMAP Project  
 Unpublished (2004)  
 Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0117 row: I column: 23  
 Seq primer: CAC TCA TTA GGC ACC CCA  
 Class: BAC ends.  
 Location/Qualifiers  
 1..363  
 /organism="Oryza australiensis"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:4532"  
 /clone="OA\_ABA0117123"  
 /tissue\_type="young leaves"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_lib="OA\_ABA"  
 /note="Vector: pAGIBAC1; Site\_1: HindIII; Site\_2: HindIII"

Query Match 84.0%; Score 16.8; DB 10; Length 363;  
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 |||||  
 Db 129 AAGGAAATCGCGACACCCAA 110  
 |||||

RESULT 38  
 AI618550/c  
 LOCUS  
 DEFINITION zewp0061.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio  
 CDNA 5', mRNA sequence.  
 ACCESSION AI618550  
 VERSION AI618550.1 GI:4627717  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Danio rerio (zebrafish)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 370)  
 Ton,C., Mably,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and  
 Liew,C.C.  
 Identification and Characterization of Expressed Sequence Tags from  
 an Embryonic Zebrafish Heart cDNA Library  
 Unpublished (1999)  
 Contact: Liew CC  
 Brigham and Women's Hospital  
 Harvard Medical School  
 75 Francis St. Boston, MA 02115, USA  
 Tel: 617/328915  
 Fax: 617/9750995

Query Match 84.0%; Score 16.8; DB 1; Length 370;  
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 |||||  
 Db 193 AAGGAAACACGACACCCAA 174  
 |||||

RESULT 39  
 BP813540/c  
 LOCUS  
 DEFINITION BP813540 RAF119 Arabidopsis thaliana cDNA clone RAFL22-06-L22 5',  
 mRNA sequence.  
 ACCESSION BP813540  
 VERSION BP813540.1 GI:59849619  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Arabidopsis thaliana (thale cress)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 1 (bases 1 to 391)  
 Seki,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Akiyama,K.,  
 Iida,K., Enju,A., Sakurai,T., Arakawa,T., Carninci,P., Fukuda,S.,  
 Iida,J., Kawai,J., Sasaki,D., Shiraki,T., Hayashizaki,Y. and  
 Shinozaki,K.  
 Large-Scale Analysis of RIKEN Arabidopsis Full-length cDNAs  
 Unpublished (2005)  
 Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-3060  
 Email: meki@rtc.riken.go.jp  
 An Arabidopsis full-length cDNA library was constructed essentially  
 as reported previously (Seki et al., 1998, 2002). This clone is in a  
 modified pBluescript vector.  
 Please visit our web site (<http://pfgweb.gsc.riken.jp>) and  
<http://rage.gsc.riken.jp> for further details.  
 Location/Qualifiers  
 1..391  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAFL22-06-L22"  
 /tissue\_type="mixture of silique and flower"  
 /lab\_host="DH10B"  
 /clone\_lib="RAFL19"  
 /note="Site\_1: BamHI; Site\_2: SalI; Subtraction Library"

Email: cliew@rics.bwh.harvard.edu  
 PCR Primers  
 FORWARD: 5' GCCAAGCTCGAAATTAACCTCACTAAAGG 3'  
 BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTAAGGCG 3'  
 Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.  
 Location/Qualifiers  
 1..370  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /dev\_stage="embryonic day 3 post-fertilization"  
 /lab\_host="E.coli XL1-Blue mrf"  
 /clone\_lib="Zebrafish Embryonic Heart cDNA Library"  
 /note="Organ: heart; Vector: Lambda ZAP Express; Site\_1:  
 EcoRI; Site\_2: XhoI; mRNA was purified from embryonic  
 zebrafish hearts (3 day post-fertilization). cDNA was  
 synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI  
 adaptors were ligated, followed by digestion with XhoI,  
 for directional cloning into pre-digested lambda ZAP  
 Express vector."  
 Location/Qualifiers  
 1..391  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAFL22-06-L22"  
 /tissue\_type="mixture of silique and flower"  
 /lab\_host="DH10B"  
 /clone\_lib="RAFL19"  
 /note="Site\_1: BamHI; Site\_2: SalI; Subtraction Library"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 3; Length 391;  
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 346 AAGGAAACACGACACACCA 327

RESULT 40  
 BP664023 397 bp mRNA linear EST 27-JUN-2004  
 LOCUS BP664023 Arabidopsis thaliana cDNA clone RAFL21-50-E09 3',  
 DEFINITION mRNA sequence.

ACCESSION BP664023  
 VERSION BP664023  
 KEYWORDS EST.  
 SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

AUTHORS Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,  
 Nakajima, M., Enju, A., Akiyama, K., Ono, Y., Muramatsu, M.,  
 Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,  
 Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.

TITLE Functional annotation of a full-length Arabidopsis cDNA collection  
 JOURNAL Science 296 (5565), 141-145 (2002)  
 PUBMED 11910074

COMMENT Contact: Motoaki Seki  
 Plant Functional Genomics Research Group  
 RIKEN Genomic Sciences Center  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-4359  
 Fax: 81-298-36-3060

Email: msekio@tc.riken.go.jp  
 reversed clone; Please visit our web site  
 (<http://pfgweb.gsc.riken.go.jp/>) for further details.

## FEATURES

source  
 1..397  
 /organism="Arabidopsis thaliana"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:3702"  
 /clone="RAFL21-50-E09"  
 /lab\_host="DH10B"  
 /clone\_lib="RAFL21"  
 /note="Site 1: BamHI; Site 2: SalI; Subtraction Library.  
 The sequence was obtained from samples subjected to  
 various stress and plant hormones-treated"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 3; Length 397;  
 Best Local Similarity 90.0%; Pred. No. 2.8e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 37 AAGGAAACACGACACACCA 56

RESULT 41  
 CA730096 412 bp mRNA linear EST 26-NOV-2002  
 LOCUS CA730096 wipic.pk002.e2 wipic Arabidopsis thaliana cDNA clone wipic.pk002.e2 5',  
 DEFINITION end, mRNA sequence.

ACCESSION CA730096  
 VERSION CA730096.1 GI:25452099  
 KEYWORDS EST.  
 SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum

## REFERENCE

AUTHORS

TITLE  
 JOURNAL  
 COMMENT

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

1 (bases 1 to 412)  
 Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
 Miao, G., Caraher, N. and Hanafey, M.K.  
 DuPont Wheat cDNA Sequence  
 Unpublished (2002)

Contact: Scott V. Tingey  
 Crop Genetics

E. I. DuPont de Nemours and Company  
 1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
 Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com  
 Seq primer: M13.

FEATURES  
 source

1..412  
 Location/Qualifiers  
 /organism="Triticum aestivum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4565"  
 /clone="wipic.pk002.e2"  
 /tissue\_types="pistils"  
 /lab\_host="DH10B"  
 /clone\_lib="wipic"  
 /note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
 XhoI; Wheat (Triticum aestivum, Hi Line) immature pistils"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 412;  
 Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 Db 141 AAGGAAACCGGACACCCAA 160

RESULT 42  
 BU237703/c  
 LOCUS BU237703 427 bp mRNA linear EST 26-NOV-2002

DEFINITION 603410683F1 CSEQCHN24 Gallus gallus cDNA clone CHEST327e22 5', mRNA  
 sequence.

ACCESSION BU237703  
 VERSION BU237703.1 GI:25484495  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)

ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 427)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)

TITLE  
 JOURNAL  
 COMMENT

Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612089930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

FEATURES  
 source

1..427  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9031"  
 /clone="CHEST327e22"  
 /dev\_stage="22"



```

/lab_host="DH10B"
/clone_lib="CSQCHN24"
/notes="Organ: heads; Vector: pBluescript II KS(+); Site_1:
EcoRI; Site_2: NotI; This normalized library was
constructed from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."

```

## ORIGIN

```

Query Match      84.0%; Score 16.8; DB 5; Length 427;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 96 AAGGAAACACGACACCCAA 77

```

## RESULT 43

```

AG224508/c
LOCUS      444 bp DNA linear GSS 19-JUL-2003
DEFINITION Lotus corniculatus var. japonicus DNA, clone: LJ10118_r, genomic
survey sequence.

```

```

ACCESSION   AG224508
VERSION     AG224508.1 GI:26534354
KEYWORDS    GSS.
SOURCE      Lotus

```

```

ORGANISM    Lotus corniculatus var. japonicus (Lotus japonicus)

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
Lotus.

```

## REFERENCE

```

1 Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
JOURNAL Published Only in Database (2002)
2 (bases 1 to 444)
AUTHORS Sato, S.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)

```

## FEATURES

```

source
1..444
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjB10118_r"
/clone_lib="genomic BAC library"
/notes="VECTOR:pBelOBAC11
synonym: Lotus japonicus"

```

## ORIGIN

```

Query Match      84.0%; Score 16.8; DB 10; Length 444;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 345 AAGTAAACACGGAACCCAA 326

```

## RESULT 44

```

BP616001
LOCUS      447 bp mRNA linear EST 26-JUN-2004
DEFINITION BP616001 RAFL16 Arabidopsis thaliana cDNA clone RAFL16-18-B08 3',
mRNA sequence.

```

```

ACCESSION   BP616001
VERSION     BP616001.1 GI:49267183
KEYWORDS    EST.
SOURCE      Arabidopsis thaliana (thale cress)

```

```

ORGANISM    Arabidopsis thaliana

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

```

## REFERENCE

```

1 (bases 1 to 447)
Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
11910074

```

## COMMENT

```

Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
Fax: 81-298-36-3060
Email: msek@rtc.riken.go.jp
reversed clone; Please visit our web site
(http://pfgw.gen.go.jp/) for further details.
Location/Qualifiers
1..447
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL16-18-B08"
/lab_host="DH10B"
/clone_lib="RAFL16"
/notes="Site_1: BamHI; Site_2: SalI; dark-grown"

```

## FEATURES

```

source
1..447
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/clone="RAFL16-18-B08"
/lab_host="DH10B"
/clone_lib="RAFL16"
/notes="Site_1: BamHI; Site_2: SalI; dark-grown"

```

## ORIGIN

```

Query Match      84.0%; Score 16.8; DB 3; Length 447;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 AAGGAAACACGACACCCAA 20
    |||||
Db 37 AAGGAAACACGACACCCAA 56

```

## RESULT 45

```

BQ803856
LOCUS      475 bp mRNA linear EST 30-JUL-2002
DEFINITION WHE2842 H02_004ZS Triticum monococcum vernalized apex cDNA library
Triticum monococcum cDNA clone WHE2842_H02_004, mRNA sequence.

```

```

ACCESSION   BQ803856
VERSION     BQ803856.1 GI:22018825
KEYWORDS    EST.
SOURCE      Triticum monococcum

```

```

ORGANISM    Triticum monococcum

```

```

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.

```

## REFERENCE

```

1 (bases 1 to 475)
Anderson, O.D., Chao, S., Crossman, C., Dubcovsky, J., Echenique, V.,
Lazo, G.R., Pham, J., Rausch, C.J., Stamova, B., Wilson, C. and Woo, J.
The structure and function of the expressed portion of the wheat
genomes - Vernalized apex cDNA library from Triticum monococcum
Unpublished (2002)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific

```

## JOURNAL

## COMMENT

West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 510595773  
Fax: 510595818

Email: andersn@pw.usda.gov  
Sequences have been trimmed to remove vector sequence and low  
quality sequence with phred score less than 20

Seq primer: SK primer.

Location/Qualifiers

## FEATURES

source

1. .475  
/organism="Triticum monococcum"  
/mol\_type="mRNA"  
/cultivar="G3116"  
/db\_xref="taxon:4568"  
/clone="WHE2842\_H02\_004"  
/tissue\_type="Vernalized apex"  
/dev\_stage="One month old plants"  
/lab\_host="E. coli XL0LR"  
/clone\_lib="Triticum monococcum vernalized apex cDNA  
library"  
/note="Vector: Lambda Uni-ZAP XR, excised phagemid;  
Site 1: EcoRI; Site 2: XhoI; One-month old plants were  
subjected to vernalization treatment by placing them in  
the cold room at 6 C, under 15hr light/9hr dark condition.  
Total RNA was prepared from apex tissue extracted from  
plants with no cold treatment; and from plants with  
2-week, 4-week and 6-week cold treatment separately. Equal  
amount of total RNA was pooled from all four samples, a  
cDNA library was made using pooled polyA RNA and cDNA  
clones were in vivo excised at the University of  
California, Davis (V. Echenique, B. Stanova, J.  
Dubcovsky). Plasmid DNA preparations and DNA sequencing  
were performed in the OD Anderson lab (all other  
authors)."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 475;  
Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 10 AAGAAACACGACACCCAA 29

## RESULT 46

CA728920/c

LOCUS

DEFINITION wdilc.pk005.e10 wdilc Triticum aestivum cDNA clone wdilc.pk005.e10  
5' end, mRNA sequence.

ACCESSION CA728920.1 GI:25450920

VERSION

KEYWORDS

SOURCE

ORGANISM

Triticum aestivum (bread wheat)  
Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooideae; Triticeae; Triticum.

1 (bases 1 to 484)

Ingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,

Miao, G., Caraher, N. and Hanafey, M.K.

DuPont Wheat CDNA Sequence

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

## FEATURES

source

Location/Qualifiers

1. .484

## ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 485;  
Best Local Similarity 90.0%; Pred. No. 2.9e+03;

/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4568"  
/clone="wdilc.pk005.e10"  
/tissue\_type="inflorescence"  
/lab\_host="DH10B"  
/clone\_lib="wdilc"  
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2:  
XhoI; Wheat (Triticum aestivum, Hi Line) developing  
inflorescence +/- 4 cm"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 484;  
Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 219 AAGAAACACGACACCCAA 200

## RESULT 47

CW445890/c

LOCUS

DEFINITION fabb001f171e14f0 Sorghum methylation filtered library (LibID: 104)  
Sorghum bicolor genomic clone fabb001f171e14, genomic survey  
sequence.

ACCESSION CW445890

VERSION CW445890.1 GI:55193851

KEYWORDS

SOURCE

ORGANISM

Sorghum bicolor (sorghum)  
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
Clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 485)

Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,

Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K., Korf, I.F.,

McMenamy, J., Smith, M., Holsman, H., Roe, B.A., Wiley, G., Korf, I.F.,

Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddleloh, J.A. and

Martenssen, R.A.

Sorghum genome sequencing by methylation filtration

PLoS Biol. 3 (1), e13 (2005)

15660154

Contact: Bedell JA

Orion Genomics, LLC

4041 Forest Park Ave, St. Louis, MO 63108, USA

Tel: 314 615 6979

Fax: 314 615 5975

Email: jbedell@oriongenomics.com

Plate: fabb001f171 row: e column: 14

Seq primer: f Forward

Class: methylation filtered

High quality sequence stop: 485.

## FEATURES

source

1. .485  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="ATx623"  
/db\_xref="taxon:4558"  
/clone="fabb001f171e14"  
/clone\_lib="Sorghum methylation filtered library (LibID:  
104)"  
/note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBSK(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

```

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 342 AAGGAACACGGACACCCAA 323

RESULT 48
LOCUS BU229997
DEFINITION 603947773F1 CSEQCHN23 Gallus gallus cDNA clone CHEST903a19 5', mRNA
sequence.
ACCESSION BU229997
VERSION BU229997.1
KEYWORDS GI:25470352
SOURCE EST.
ORGANISM Gallus gallus (chicken)
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 514)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES
    source
    1..514
        /organism="Gallus gallus"
        /mol_type="mRNA"
        /strain="White Leghorn, Hisex"
        /db_xref="taxon:9031"
        /clone="CHEST903a19"
        /dev_stage="22"
        /lab_host="DH10B"
        /clone_lib="CSEQCHN23"
        /note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
        EcoRI; Site_2: NotI; This normalized library was
        constructed from 1 million independent clones. cDNA
        synthesis was initiated using an oligo(dT) primer, using
        methylated C in the first strand synthesis reaction.
        Following this first strand reaction, double-stranded cDNA
        was bluntended, ligated to NotI adapters, digested with
        EcoRI, size-selected, and cloned into the NotI and EcoRI
        compatible sites of a custom modified MCS of the
        pBluescript (KS+) vector. The library was normalized in 2
        rounds using conditions adapted from Soares et al., PNAS
        (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
        (1996): 791, except that a significantly longer
        reannealing hybridization was used."

ORIGIN
Query Match 84.0%; Score 16.8; DB 5; Length 514;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 344 AAGGAACACGGACACCCAA 363

RESULT 49
LOCUS CA013161
DEFINITION HT07J07: HT Hordeum vulgare subsp. vulgare cDNA clone HT07J07

ORIGIN
Query Match 84.0%; Score 16.8; DB 5; Length 514;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 344 AAGGAACACGGACACCCAA 363

RESULT 49
LOCUS CA013161
DEFINITION HT07J07: HT Hordeum vulgare subsp. vulgare cDNA clone HT07J07

```

```

5-PRIME, mRNA sequence.
CA013161
VERSION CA013161.1
KEYWORDS GI:24290505
SOURCE EST.
ORGANISM Hordeum vulgare subsp. vulgare
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 519)
AUTHORS Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
Graner,A.
TITLE Barley ESTs from germinating seeds
JOURNAL Unpublished (2002)
COMMENT Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 519 Std Error: 0.00
Plate: 7 row: J column: 7
Seq primer: M13rev.
Location/Qualifiers
    1..519
        /organism="Hordeum vulgare subsp. vulgare"
        /mol_type="mRNA"
        /cultivar="Barke"
        /sub_species="vulgare"
        /db_xref="GABI:261687"
        /db_xref="taxon:112509"
        /clone="HT07J07"
        /tissue_type="endosperm early"
        /dev_stage="0-16 hours after imbibition"
        /lab_host="XL10-Gold"
        /clone_lib="HT"
        /note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
        cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
        artefact caused by the kit, in most cases the EcoRI site
        is NOT present, as well as the EcoRI adapter used for
        cloning. To excise the insert, restriction sites upstream
        EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
        due to the cloning system used Blue/white selection for
        recombinants is not 100% reliable."

ORIGIN
Query Match 84.0%; Score 16.8; DB 5; Length 519;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAGGAACACGGACACCCAA 20
    ||||| ||||| ||||| |||||
Db 125 AAGGAACACGGACACCCAA 144

RESULT 50
LOCUS CF352554
DEFINITION lac30C03.y1 SiEP Mus musculus cDNA 5', mRNA sequence.
ACCESSION CF352554
VERSION CF352554.1
KEYWORDS GI:33956646
SOURCE EST.
ORGANISM Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 525)
AUTHORS Tidwell,R., Clifton,S., Marra,M., Hillier,L., Pape,D., Martin,J.,
Wylie,T., Theising,B., Bowers,Y., Gibbons,M., Ritter,E., Bennet,J.,
Ronko,I., Teagareishvili,R., Belaygorod,L., Grow,A., Maguire,L.,
Waterston,R. and Wilson,R.

```

TITLE WashU Stem cell EST Project  
JOURNAL Unpublished (2002)  
COMMENT Contact: Jeff Gordon and Mike Lovett  
WashU, Human Genetics Division  
Washington University School of Medicine  
Library materials provided by: Stappenbeck Th.S. and Gordon J.I.  
Library constructed by: Korshunova Y. and Lovett M. DNA sequencing  
by: Washington University Genome Sequencing Center For information  
on obtaining a clone please contact: Rose Tidwell  
(rtidwell@genetics.wustl.edu)  
Seq primer: -40RP from Gibco  
High quality sequence stop: 525.  
Location/Qualifiers  
1. 525  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/tissue\_type="small intestinal epithelial progenitors"  
/lab\_host="DH5alpha Ultra Max cells (Invitrogen)"  
/clone\_lib="SIEP"  
/note="Vector: pMP1; The library was synthesized with  
modified SMART primers with dntp at the end. After  
treatment with UDG the cDNA was cloned in pMP1 vector by  
annealing."

## FEATURES

source  
1. 525

## ORIGIN

Query Match 84.0%; Score 16.8; DB 6; Length 525;  
Best Local Similarity 90.0%; Pred. No. 2.9e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20

Db 488 AAGGAACACGGACACCCAA 507

## RESULT 51

CA637743/c  
LOCUS CA637743 544 bp mRNA linear EST 23-NOV-2002  
DEFINITION wrain.pk0002.c4 wrain Triticum aestivum cDNA clone wrain.pk0002.c4  
5' end, mRNA sequence.  
CA637743  
VERSION CA637743.1 GI:25216039  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 544)

## AUTHORS

Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
Miao, G., Caraher, N. and Hanafey, M.K.  
Miao, G., Caraher, N. and Hanafey, M.K.  
DuPont Wheat cDNA Sequence  
Unpublished (2002)

## TITLE

Contact: Scott V. Tingey

## JOURNAL

Crop Genetics

## COMMENT

E. I. DuPont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.

## FEATURES

source  
1..544

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone="wrain.pk0002.c4"

/tissue\_type="root"

/clone\_lib="wrain"

/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site 2:

XhoI; Wheat (Triticum aestivum L.) root; normalized from

## ORIGIN

wre1 library"

## Query Match

84.0%; Score 16.8; DB 6; Length 544;

## Best Local Similarity

90.0%; Pred. No. 2.9e+03; Mismatches 2; Indels 0; Gaps 0;

## Matches

18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20

Db 292 AATGAACACGGACACCCAA 273

## RESULT 52

BG727965/c

## LOCUS

BG727965 546 bp mRNA linear EST 09-MAY-2001

fp08e03.xl zebrafish gridded kidney Danio rerio cDNA clone

IMAGE:4729037 3' similar to TR:095624 095624 CPLA2 INTERACTING

PROTEIN. ; mRNA sequence.

## ACCESSION

BG727965

## VERSION

BG727965.1 GI:14013040

## KEYWORDS

EST.

## SOURCE

Danio rerio (zebrafish)

## ORGANISM

Danio rerio

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi;

Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 546)

REFERENCE

AUTHORS

Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, P., Marra, M.,

Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,

Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,

Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R.,

Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,

Waterston, R. and Wilson, R.

WashU Zebrafish EST Project 1998

Unpublished (1998)

CONTACT: Stephen L. Johnson

Washington University School

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA

Tel: 314 286 1800

Fax: 314 286 1810

Email: zbrfish@watson.wustl.edu

cDNA Library Preparation: Leonard Ira Zon DNA Sequencing by:

Washington University Genome Sequencing Center Clone distribution:

Genome Systems, St. Louis, Missouri (web address:

www.genomesystems.com) (email contact: info@genomesystems.com) and

Research Genetics, Huntsville, Alabama (web address:

www.resgen.com) (email contact: info@resgen.com) and

RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:

www.rzpd.de)

zebrafish identity (p-value greater than 1e-99) found to:

GI|2289384|gb|AA542449|AA542449 fa07a11.s1 Zebrafish ICRFzfls Danio

rerio cDNA

Seq primer: T7 from Gibco

High quality sequence stop: 353.

Location/Qualifiers

1..546

/organism="Danio rerio"

/mol\_type="mRNA"

/db\_xref="taxon:7955"

/clone="IMAGE:4729037"

/sex="mixed"

/tissue\_type="kidney pooled from 300 wild type adults"

/lab\_host="XL0LR"

/clone\_lib="zebrafish gridded kidney"

/note="Organ: kidney; Vector: pBK-CMV; Site\_1: EcoRI;

Site\_2: XhoI; Oligo dt cDNA library constructed from mRNA

pooled from pooled kidney tissue from 300 adult

zebrafish."

## ORIGIN

## Query Match

84.0%; Score 16.8; DB 2; Length 546;

## Best Local Similarity

90.0%; Pred. No. 2.9e+03; Mismatches 2; Indels 0; Gaps 0;

## Matches

18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20



```

Query Match      84.0%; Score 16.8; DB 2; Length 580;
Best Local Similarity 90.0%; Pred. No. 2.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   |||||
Db 396 AAGCAACACGACACCCAA 415

RESULT 55
LOCUS DE001557/c
DEFINITION Branchiostoma floridae DNA, clone: CH302-004F04.R, genomic survey
sequence.
ACCESSION DE001557
VERSION DE001557.1 GI:62243906
KEYWORDS GSS.
SOURCE Branchiostoma floridae (Florida lancelet)
ORGANISM Branchiostoma floridae
          Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
          Branchiostoma.
REFERENCE 1
AUTHORS Fujiyama A., Toyoda A., Hattori M. and Sakaki Y.
TITLE BAC end sequences of CH01-302 Amphioxus Library
JOURNAL Published Only in Database (2005)
REFERENCE 2 (bases 1 to 607)
AUTHORS Fujiyama A.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2005) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail: afujiyama@gsc.riken.jp, URL: http://hgp.gsc.riken.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
PRIMERS
Sequencing : TJ
LIBRARY
Vector : PTAREAC2.1
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1. .607
/organism="Branchiostoma floridae"
/mol_type="genomic DNA"
/db_xref="taxon:7739"
/clone="CH302-004F04.R"
/sex="male"
/tissue type="sperm"
/clone_lib="CH010302 Amphioxus genomic BAC library"
/note="Common name: amphioxus"

ORIGIN
Query Match      84.0%; Score 16.8; DB 11; Length 607;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   |||||
Db 32 AAGGAAACACGACACTAAA 13

RESULT 56
LOCUS CL773304/c
DEFINITION OR_BB0086D16.r OR_BB01 Ryza nivara genomic clone OR_BB0086D16 3',
genomic survey sequence.
ACCESSION CL773304
VERSION CL773304.1 GI:50847690
KEYWORDS GSS.
SOURCE Ryza nivara
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Query Match      84.0%; Score 16.8; DB 10; Length 608;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   |||||
Db 129 AAGGAAATGCGACACCCAA 110

RESULT 57
LOCUS CG099060/c
DEFINITION PUIHL20TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB7a0584C16,
genomic survey sequence.
ACCESSION CG099060
VERSION CG099060.1 GI:33981354
KEYWORDS GSS.
SOURCE Zea mays
          Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 628)
          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
          Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and
          Bennetzen, J.
          Maize Genomics Consortium
          Unpublished (2003)
          Other GSSs: PUIHL20TB
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TP
          Class: sheared ends.
          Location/Qualifiers
          1. .628
          /organism="Zea mays"
          /mol_type="genomic DNA"

```

```

Ehrhartoideae; Oryzeae; Oryza.
1 (bases 1 to 608)
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0086 row: D column: 16
Seq primer: CAC TCA TTA GGC ACC CCA
Class: BAC ends.
Location/Qualifiers
1. .608
/organism="Oryza nivara"
/mol_type="genomic DNA"
/db_xref="taxon:4536"
/clone="OR_BB0086D16"
/tissue_type="young leaves"
/lab_host="DH10B-T1 phage resistant"
/clone_lib="OR_BB0"
/note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 608;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
   |||||
Db 129 AAGGAAATGCGACACCCAA 110

RESULT 57
LOCUS CG099060/c
DEFINITION PUIHL20TD ZM 0.6 1.0 KB Zea mays genomic clone ZMMB7a0584C16,
genomic survey sequence.
ACCESSION CG099060
VERSION CG099060.1 GI:33981354
KEYWORDS GSS.
SOURCE Zea mays
          Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
          PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
          1 (bases 1 to 628)
          Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
          Resnick, A., Frazer, C.M., Yuan, Y., San Miguel, P., Ma, J. and
          Bennetzen, J.
          Maize Genomics Consortium
          Unpublished (2003)
          Other GSSs: PUIHL20TB
          Contact: Cathy Whitelaw
          TIGR
          9712 Medical Center Drive, Rockville, MD 20850, USA
          Tel: 301-838-5843
          Fax: 301-838-0208
          Email: whitelaw@tigr.org
          Seq primer: TP
          Class: sheared ends.
          Location/Qualifiers
          1. .628
          /organism="Zea mays"
          /mol_type="genomic DNA"

```

```

/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBTA0584C16"
/clone_lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cot selected genomic DNA library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 628;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 80 AAGGAACGACGACACCCAA 61

RESULT 58
CN206088
LOCUS Tor6515 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
DEFINITION Tor6515 Gametophyte rehydration Library Tortula ruralis cDNA, mRNA
ACCESSION CN206088
VERSION CN206088.1 GI:46902819
KEYWORDS EST.
SOURCE Tortula ruralis
ORGANISM Tortula ruralis
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
AUTHORS Bryopsida; Dicranidae; Pottiales; Pottiaceae; Tortula.
TITLE 1 (bases 1 to 632)
JOURNAL Oliver, M.J., Dowd, S.E., Zaragosa, J., Mauger, S.A. and Payton, P.R.
PUBMED The rehydration transcriptome of the desiccation-tolerant bryophyte
15546486 Tortula ruralis: transcript classification and analysis
COMMENT BMC Genomics 5 (1), 89 (2004)
Contact: Oliver Melvin J
Plant Stress Lab
USDA-ARS
3810 4th St, Lubbock, TX 79415, USA
Tel: 806-749-5560
Fax: 806-723-5272
Email: moliver@lbr.ars.usda.gov
PCR Primers
FORWARD: GTTTTCCAGTCACGAC
BACKWARD: CAGGAACAGCTATGAC.
Location/Qualifiers
1. 632
/organism="Tortula ruralis"
/mol_type="mRNA"
/db_xref="taxon:38588"
/clone_lib="Gametophyte rehydration Library"
/note="Organ: Green Gametophyte; Vector: pSport1; Site_1:
SalI; Site_2: NotI"

ORIGIN
Query Match      84.0%; Score 16.8; DB 7; Length 632;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 605 AAGGAACACGACACCCAA 624

RESULT 59
BU992244
LOCUS HD09102r HD Hordeum vulgare cDNA clone HD09102 5-PRIME, mRNA
DEFINITION HD09102r HD Hordeum vulgare cDNA clone HD09102 5-PRIME, mRNA
ACCESSION BU992244
VERSION BU992244
KEYWORDS EST.
SOURCE Hordeum vulgare

ORIGIN
Query Match      84.0%; Score 16.8; DB 5; Length 637;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 123 AAGGAACACGACACCCAA 142

RESULT 60
CL768700/c
LOCUS CL768700
DEFINITION OR BBa0140P17.f OR BBa Oryza nivara genomic clone OR_BBa0140P17 5',
genomic survey sequence.
ACCESSION CL768700
VERSION CL768700.1 GI:50815109
KEYWORDS GSS.
SOURCE Oryza nivara
ORGANISM Oryza nivara
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Ehrhartoideae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 643)
COMMENT Kim, H., Yu, Y., Stum, D., Vost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595

```

```

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 637)
AUTHORS Zhang, H., Weschke, W., Michalek, W., Stein, N. and Graner, A.
JOURNAL EST sequencing and analysis in barley (2002)
COMMENT Unpublished (2002)
Contact: Stein Nils
Molecular Markers Group, Department Genbank
Institute of Plant Genetics and Crop Plant Research (IPK)
Corrensstr. 3, 06466, Gatersleben, Germany
Tel: 039482-5522
Fax: 039482-5595
Email: stein@ipk-gatersleben.de
Insert Length: 637 Std Error: 0.00
Plate: 9 row: 1 column: 2
Seq primer: M13rev.
Location/Qualifiers
1. 637
/organism="Hordeum vulgare"
/mol_type="mRNA"
/cultivar="Golden Promise"
/db_xref="GABI:242352"
/db_xref="taxon:4513"
/clone="HD09102"
/tissue_type="callus"
/dev_stage="callus (5-10 mm in diameter)"
/lab_host="Xu10-Gold"
/clone_lib="HD"
/note="Vector: pBluescript SK+; Site_1: EcoRI (5'-end of
cDNA); Site_2: XhoI (3'-end of cDNA); Due to a cloning
artefact caused by the kit, in most cases the EcoRI site
is NOT present, as well as the EcoRI adapter used for
cloning. To excise the insert, restriction sites upstream
EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
due to the cloning system used Blue/white selection for
recombinants is not 100% reliable. Average insert size is 1
kb"

ORIGIN
Query Match      84.0%; Score 16.8; DB 5; Length 637;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
Db 123 AAGGAACACGACACCCAA 142

RESULT 60
CL768700/c
LOCUS CL768700
DEFINITION OR BBa0140P17.f OR BBa Oryza nivara genomic clone OR_BBa0140P17 5',
genomic survey sequence.
ACCESSION CL768700
VERSION CL768700.1 GI:50815109
KEYWORDS GSS.
SOURCE Oryza nivara
ORGANISM Oryza nivara
REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
AUTHORS Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
TITLE Ehrhartoideae; Oryzaceae; Oryza.
JOURNAL 1 (bases 1 to 643)
COMMENT Kim, H., Yu, Y., Stum, D., Vost, D., Rao, K., Luo, M., Jetty, R.,
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.
OMAP Project
Unpublished (2004)
Contact: Rod A. Wing
Arizona Genomics Institute
University of Arizona
Forbes Building Room 303, Tucson, AZ 85721-0036, USA
Tel: 520 626 9595

```

```

Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0140 row: P column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
  1..643
  /organism="Oryza nivara"
  /mol_type="genomic DNA"
  /db_xref="taxon:4536"
  /clone="OR_BB0140P17"
  /tissue_type="young leaves"
  /lab_host="DH10B-T1 phage resistant"
  /clone_lib="OR Bba"
  /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 643;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||||| ||||| ||||| |||||
Db 129 AAGGAATGCGACACCCAA 110

RESULT 61
CD893867      556 bp  mRNA  linear  EST 14-JUL-2003
LOCUS      G118.124L19F010828 G118 Triticum aestivum cDNA clone G118124L19,
DEFINITION      mRNA sequence.
ACCESSION      CD893867
VERSION      CD893867.1 GI:32664800
KEYWORDS      EST.
SOURCE      Triticum aestivum (bread wheat)
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                Pooideae; Triticeae; Triticum.
REFERENCE      1 (bases 1 to 556)
AUTHORS      Genoplante.
JOURNAL      Genoplante, a major partnership french program in plant genomics
COMMENT      Unpublished (2003)
                Contact: Genoplante
                Genoplante
                93, rue Henri Rochefort 91025 EVRY CEDEX France
                Tel: 33 1 69 47 54 00
                Fax: 33 1 69 47 54 10
                This sequence has been generated in the framework of the french
                plant genomics programme 'Genoplante' (http://www.genoplante.com
                and http://genoplante-info.infobiogen.fr).

FEATURES             source
  location/Qualifiers
    1..656
    /organism="Triticum aestivum"
    /mol_type="mRNA"
    /culturivar="recital"
    /db_xref="taxon:4565"
    /clone="G118124L19"
    /tissue_type="grain (118 degrees per day after
    pollination)"
    /clone_lib="G118"

ORIGIN
Query Match      84.0%; Score 16.8; DB 6; Length 656;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||||| ||||| ||||| |||||

Fax: 520 621 1259
Email: rwing@genome.arizona.edu
PCR Primers
FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Insert Length: 161 Std Error: 0.00
Plate: 0140 row: P column: 17
Seq primer: TAA TAC GAC TCA CTA TAG GG
Class: BAC ends.
Location/Qualifiers
  1..643
  /organism="Oryza nivara"
  /mol_type="genomic DNA"
  /db_xref="taxon:4536"
  /clone="OR_BB0140P17"
  /tissue_type="young leaves"
  /lab_host="DH10B-T1 phage resistant"
  /clone_lib="OR Bba"
  /note="Vector: pAGIBAC1; Site_1: HindIII; Site_2: HindIII"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 643;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||||| ||||| ||||| |||||
Db 129 AAGGAATGCGACACCCAA 110

RESULT 62
CG046335/c    661 bp  DNA  linear  GSS 19-AUG-2003
LOCUS      PUIFW42TB ZM 0.6.1.0_KB Zea mays genomic clone ZMMBTa0574G11,
DEFINITION      genomic survey sequence.
ACCESSION      CG046335
VERSION      CG046335.1 GI:33918515
KEYWORDS      GSS.
SOURCE      Zea mays
ORGANISM      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
                clade; Panicoideae; Andropogoneae; Zea.
REFERENCE      1 (bases 1 to 661)
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
                Resnick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
                Bennetzen,J.
TITLE      Maize Genomics Consortium
JOURNAL      Unpublished (2003)
COMMENT      Other GSSs: PUIFW42TD
                Contact: Cathy Whitelaw
                TIGR
                9712 Medical Center Drive, Rockville, MD 20850, USA
                Tel: 301-838-5843
                Fax: 301-838-0208
                Email: whitelaw@tigr.org
                Seq primer: TR
                Class: sheared ends.
                Location/Qualifiers
                  1..661
                  /organism="Zea mays"
                  /mol_type="genomic DNA"
                  /strain="B73"
                  /db_xref="taxon:4577"
                  /clone="ZMMBTa0574G11"
                  /notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
                  Cot selected genomic DNA library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 661;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20
||||| ||||| ||||| ||||| |||||
Db 121 AAGGAACACGACACCCAA 102

RESULT 63
BZ274036      666 bp  DNA  linear  GSS 15-OCT-2002
LOCUS      CH230-403G9.TJ CHORI-230 Segment 2 Rattus norvegicus genomic clone
DEFINITION      genomic survey sequence.
ACCESSION      BZ274036
VERSION      BZ274036.1 GI:23994788
KEYWORDS      GSS.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM      Rattus norvegicus
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE      1 (bases 1 to 666)
AUTHORS      Zhao S., Shetty,J., Shatsman,S., Teegaye,G., Geer,K.,
                Sivartsbeyn,A., Gebregorgis,S., Overton,L., Russell,D., Chen,D.,
                Riggs,F., de Jong,P. and Fraser,C.M.
                Rat BAC End Sequences from Library CHORI-230 MboI segment
                Unpublished (1999)
                Other GSSs: CH230-403G9.TV
                Contact: Shaying Zhao

```



availability, please contact Pieter de Jong (pdejong@mail.choi.org).  
Clones may be purchased from BACPAC Resources  
([http://www.choi.org/bacpac/orering\\_information.htm](http://www.choi.org/bacpac/orering_information.htm)). BAC end  
page: [http://www.tigr.org/tdb/bac\\_ends/rat/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html)  
Plate: 403 row: G column: 9  
Seq primer: SP6  
Class: BAC ends.

```
Query Match      84.0%; Score 16.8; DB 8; Length 673;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

QY 1 AAGGAAACACGGACACCAA 20  
|||  
239 AAGGAAACCCAGACACCAA 258  
DB

RESULT 65	BU476293/c				
LOCUS	BU476293	678 bp	mRNA	linear	EST 30-NOV-2002
DEFINITION	503471630F1 CSEQRN22	Gallus gallus	cDNA clone	ChEST34817	5', mRNA sequence.

ACCESSION	BU476293	
VERSION	BU476293.1	GI:25969870
KEYWORDS	EST.	
SOURCE	Gallus gallus (chicken)	
ORGANISM	Gallus gallus	
	Gallus gallus	

## SOURCE ORGANISM

Euryzoa; Metazoa; Chordata; Craniata; vertebrata; Sarcostomata;  
 Archosauia; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 678).  
 REFERENCE

AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

CONTACT  
Contact: Simon Hubbard  
Department of Biomolecular Sciences  
University of Manchester Institute of Science and Technology  
(UMIST)  
PO Box 88, Manchester, M60 1QD, UK  
Tel: 01612008930  
Fax: 01612360409  
Email: Simon.Hubbard@umist.ac.uk.

## FEATURES

```

source
1. .678
/organism="Gallus gallus",
/mol_type="mrna"
/strain="Layer and broiler"
/db_xref="taxon:9031"
/clone="ChEST34817"
/sex="Male and female"
/tissue_type="Chondrocytes isolated from growth plate
cartilage"
/dev_stage="adult"

```

```

/dev_stages-adult
/lab_host="DH10B"
/clone_lib="CSEQRN22"
/Note="Vector: pBluescript II KS(+); Site 1: EcoRI;
Site 2: NotI; This normalized library was constructed from
1 million independent clones. cDNA synthesis was initiated
using an oligo(dT) primer, using methylated C in the first
strand synthesis reaction. Following this first strand
reaction, double-stranded cDNA was blunted, ligated to
NotI adapters, digested with EcoRI, size-selected, and
cloned into the NotI and EcoRI compatible sites of a
custom modified MCS of the pBluescript (KS+) vector. The
library was normalized in 2 rounds using conditions
adapted from Soares et al., PNAS (1994) 91: 9228-9232 and
Bonaldo et al., Genome Research 6 (1996): 791, except that
a significantly longer reannealing hybridization was
used."

```

**Site 2:** NotI; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunt-ended, ligated to NotI adaptors, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCF of the pLucescript (KG+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 3228-3232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 678;  
 Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 ||||| ||||| ||||| ||||| |||||  
 Db 29 AAGGCCACACGGACACCCAA 10

## RESULT 66

BZ510687  
 LOCUS BZ510687 683 bp DNA linear GSS 16-DEC-2002  
 DEFINITION BOMQH50TF BO\_2\_3\_KB Brassica oleracea genomic clone BOMQH50,  
 genomic survey sequence.

ACCESSION BZ510687  
 VERSION BZ510687.1 GI:27035294  
 KEYWORDS GSS.

SOURCE Brassica oleracea  
 ORGANISM Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

## REFERENCE

1 (bases 1 to 683)  
 Avele M., Haas B.J., Kumar N., Wu H., Xiao Y., Van Aken S.,  
 Utterback T.R., Wortman J.R., White O.R. and Town C.D.  
 Whole genome shotgun sequencing of Brassica oleracea and its  
 application to gene discovery and annotation in Arabidopsis  
 Genome Res. 15 (4), 487-495 (2005)

## JOURNAL

PUBMED 15805490

COMMENT Other GSSs: BOMQH50TF

Contact: Chris Town

TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: Tg

Class: sheared ends.

Location/Qualifiers

## FEATURES

source

1. .683  
 /organism="Brassica oleracea"  
 /mol\_type="genomic DNA"  
 /strain="TO1000DH3"  
 /db\_xref="taxon:3712"  
 /clone="BOMQH50"  
 /clone\_lib="BO 2\_3 KB"  
 /note="Vector: pHO51, Site 1: BstXI; 2-3 kb sheared  
 genomic DNA inserted into pHO51 using BstXI linkers"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 683;  
 Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0;

Qy 1 AAGGAAACACGGACACCCAA 20  
 ||||| ||||| ||||| ||||| |||||  
 Db 6 AAGGAAACACGGACACCCAA 25

## RESULT 67

AG311675/c  
 LOCUS AG311675 686 bp DNA linear GSS 18-DEC-2004  
 DEFINITION Mus musculus molossinus DNA, clone:MSMg01-094110.TJ, genomic survey  
 sequence.

ACCESSION AG311675

VERSION AG311675.1 GI:47884629

KEYWORDS GSS.

SOURCE Mus musculus molossinus (Japanese wild mouse)

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

## REFERENCE

## AUTHORS

## TITLE

Contribution of Asian mouse subspecies Mus musculus molossinus to  
 genomic constitution of strain C57BL/6J, as defined by BAC-end  
 sequence-SNP analysis  
 Genome Res. 14 (12), 2439-2447 (2004)  
 15574823

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## COMMENT

Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kuniya Abe (abe@cric.riken.jp).  
 Teikoku Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@cric.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

source

1. .686  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-094110.TJ"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 686;  
 Best Local Similarity 90.0%; Pred. No. 3e+03; Mismatches 0; Indels 0; Gaps 0;  
 Matches 18; Conservative 0;

Qy 1 AAGGAAACACGGACACCCAA 20

||||| ||||| ||||| ||||| |||||

Db 674 AAGGAAACACGGACACCCAA 655

## RESULT 68

## LOCUS

## DEFINITION

Mus musculus molossinus DNA, clone:MSMg01-419D11.T7, genomic survey  
 sequence.

ACCESSION AG514370

VERSION AG514370.1 GI:48221783

KEYWORDS GSS.

SOURCE Mus musculus molossinus (Japanese wild mouse)

ORGANISM Mus musculus molossinus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

## TITLE

Contribution of Asian mouse subspecies Mus musculus molossinus to  
 genomic constitution of strain C57BL/6J, as defined by BAC-end  
 sequence-SNP analysis

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.

1 Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,  
 Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriwaiki, K. and  
 Shiroishi, T.

Contribution of Asian mouse subspecies Mus musculus molossinus to  
 genomic constitution of strain C57BL/6J, as defined by BAC-end  
 sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

15574823

2 (bases 1 to 686)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Suehiro-chou, Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan  
 (E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/,  
 Tel: 81-45-503-9111, Fax: 81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC  
 library availability, please contact Kuniya Abe (abe@cric.riken.jp).  
 Teikoku Institute of Physical and Chemical Research (RIKEN) 3-1-1  
 Koyadai, Tsukuba, 305-0074 Japan  
 phone: 81-298-36-9189, fax: 81-298-36-9199  
 e-mail: abe@cric.riken.jp

PRIMERS

Sequencing : TJ

LIBRARY

Vector : pBACE3.6

R.Site 1 : EcoRI

R.Site 2 : EcoRI

Location/Qualifiers

source

1. .686  
 /organism="Mus musculus molossinus"  
 /mol\_type="genomic DNA"  
 /sub\_species="molossinus"  
 /db\_xref="taxon:57486"  
 /clone="MSMg01-094110.TJ"  
 /sex="male"  
 /tissue\_type="mixture of kidney and spleen"  
 /clone\_lib="MSMg01 Mouse Male BAC Library"

```

JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 709)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY : pBACe3.6
Vector : EcoRI
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES Location/Qualifiers
source 1..709
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-419D11.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 709;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
|||||
Db 69 AAGGAACCTGACACCCAA 88
|||||

RESULT 69
AG442384/c
LOCUS 715 bp DNA linear GSS 22-DEC-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-324C12.T7, genomic survey
sequence.
ACCESSION AG442384
VERSION AG442384.1 GI:48085447
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T.,
Ezawa,K., Saicou,N., Hattori,M., Sakaki,Y., Moriaki,K. and
Shiroishi,T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 715)
AUTHORS Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC),
1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan
(E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY : pBACe3.6
Vector : EcoRI
R.Site 1 : EcoRI
R.Site 2 : EcoRI
FEATURES Location/Qualifiers
source 1..709
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-419D11.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
ORIGIN
Query Match 84.0%; Score 16.8; DB 10; Length 715;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 AAGGAACACGACACCCAA 20
|||||
Db 141 AAGGAACACGACACACAA 122
|||||

RESULT 70
DT057597/c
LOCUS 729 bp mRNA linear EST 11-AUG-2005
DEFINITION AGENCOURT 55704374 NIH_ZGC_21 Danio rerio cDNA clone IMAGE:7919645
5', mRNA sequence.
ACCESSION DT057597
VERSION DT057597.1 GI:72356846
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 729)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Chung-Der Hsiao, Ming-Yi Chou and Pung-Pung
Hwang
CDNA Library Preparation: Dr. Yutaka Suzuki
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
CDNA Sequencing by: Agencourt Bioscience Corporation
CDNA distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: LLAM16325 row: g column: 03
High quality sequence start: 24
High quality sequence stop: 287.
FEATURES Location/Qualifiers
source 1..729
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"

```

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/clone="IMAGE:7919645"
/tissue_type="40 pooled samples"
/lab_host="DH10B Tona"
/clone_lib="NIH_ZGC_21"
/note="Organ: skin; Vector: pME18S-FL3; Site 1: DraIII;
Site 2: DraII; 1st strand cDNA was primed with an
oligo(dT) primer
5'-GGCGTAGAGCGCTATGGCTTTTTTTTTTTTTTT-3';
double-stranded cDNA was ligated to a DraIII adaptor
5'-GCCACUUGG-3', digested and directionally cloned into
distinct DraIII sites of the pME18S-FL3. Library was size
selected for >1.0 kb, with a average insert size of ~1.2
kb and is not amplified. Library constructed by Yutaka
Suzuki (University of Tokyo Institute of Medical Science).
Custom primers recommended for sequencing: 5' end primer
5'-GGATTTGCTTACTTCTA-3' and 3' end primer
5'-CCACGTGAGCTCGACACA-3'. Reference for library
construction: Methods Mol Bio 221:73-91. Note: this is a
(http://zgc.nci.nih.gov/) Zebrafish Gene Collection
library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 729;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 571 AAGGCCACACGACACCCAA 552

RESULT 71
DT060396/c
LOCUS DT060396 735 bp mRNA linear EST 11-AUG-2005
DEFINITION AGENCOURT 55719638 NICHD_XGC Fab Xenopus laevis cDNA clone
IMAGE:8072872 5', mRNA sequence.
ACCESSION DT060396
VERSION DT060396.1 GI:72359645
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1..(bases 1 to 735)
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Daniela S. Gerhard, Ph.D.
COMMENT Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgsbbs-r@mail.nih.gov
Tissue Procurement: Tom Sargent
cDNA Library Preparation: Express Genomics
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM17351 row: c column: 14
High quality sequence stop: 719.
FEATURES
source
1..735
location/Qualifiers
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:8072872"
/lab_host="DH10B Tona"
/clone_lib="NICHD_XGC Fab"
/note="Organ: fat body; Vector: pExpress-1; Site 1: EcoRV;
Site 2: NotI; cDNA was primed using oligo-dT primer:
5'-pGACTAGTCTTAGATCGGCGCGGCC(T)25-3' and cloned into

```

```

the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb
resulted in an average insert size of 1.8kb. This is a
primary library (normalized library is NICHD_XGC Fabw) and
was constructed by Express Genomics (Frederick, MD). Note:
this is a (http://xgc.nci.nih.gov/) Xenopus Gene
Collection library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 8; Length 735;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 159 AAGGAAACACGACACCCAA 140

RESULT 72
AG429016
LOCUS AG429016 737 bp DNA linear GSS 21-DEC-2004
DEFINITION Mus musculus molossinus DNA, clone:MSMg01-303G16.T7, genomic survey
sequence.
ACCESSION AG429016
VERSION AG429016.1 GI:48072079
KEYWORDS GSS.
SOURCE Mus musculus molossinus (Japanese wild mouse)
ORGANISM Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1
REFERENCE Abe, K., Noguchi, H., Tagawa, K., Yuzuriha, M., Toyoda, A., Kojima, T.,
AUTHORS Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriawaki, K. and
Shiroishi, T.
TITLE Contribution of Asian mouse subspecies Mus musculus molossinus to
genomic constitution of strain C57BL/6J, as defined by BAC-end
sequence-SNP analysis
JOURNAL Genome Res. 14 (12), 2439-2447 (2004)
PUBMED 15574823
REFERENCE 2 (bases 1 to 737)
AUTHORS Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC); Japan
1-7-22 Suenhiro-chou, Tsurumi-Ku, Yokohama, Kanagawa, 230-0045; Japan
(E-mail:hattori@gsc.riken.jp, URL:http://bgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the mouse BAC library MSMg01. For BAC
library availability, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute, Bio Resource Center,
The Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
PRIMERS
Sequencing : T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
FEATURES
source
1..737
location/Qualifiers
/organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/sub_species="molossinus"
/db_xref="taxon:57486"
/clone="MSMg01-303G16.T7"
/sex="male"
/tissue_type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 737;

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Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 535 AAGGAAACACGACACCCAA 554

RESULT 73
CNS0FY62/c
LOCUS Tetraodon nigroviridis full-length cDNA.
DEFINITION CR693646
VERSION CR693646.2 GI:56286064
KEYWORDS HTc; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, P., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anhouard, V., Jubin, C., Castelli, V., Katinka, M.,
Vacherie, B., Biemont, C., Skalli, Z., Cattolico, L., Poulain, J., De
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C.,
McSwain, P., Boeak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.,
and Roest Crolius, H.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)
15496914
REFERENCE 2 (bases 1 to 742)
Direct Submission
Genoscope.
TITL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
JOURNAL : 2 rue Gaston Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
AUTHORS (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51191553.
COMMENT The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
Location/Qualifiers
source 1..742
/organism="Tetraodon nigroviridis"
/mol_type="cDNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"

ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 742;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 407 AAGGAAACACGACACCCAA 388

RESULT 74
AQ740823/c
LOCUS HS_5508_A2_F10_SP6_RPCI-11 Human Male BAC Library Homo sapiens
DEFINITION genomic clone F10-SP6-RPCI-11 Human Male BAC Library Homo sapiens
AUTHORS genomic clone F10-SP6-RPCI-11 Human Male BAC Library Homo sapiens
TITLE genomic clone F10-SP6-RPCI-11 Human Male BAC Library Homo sapiens
ACCESSION AQ740823
VERSION AQ740823.1 GI:5518345

Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 309 AAGGAAACACGACACCCCTA 290

RESULT 75
DT060112/c
LOCUS DT060112
DEFINITION DT060112
AGENCOURT_55787745 NICHED_XGC_Faen Xenopus laevis cDNA clone
IMAGE:8074943 5', mRNA sequence.
ACCESSION DT060112
VERSION DT060112
KEYWORDS DT060112.1 GI:72359361
SOURCE EST.
ORGANISM Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 763)
NTH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.

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GSS.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 756)
REFERENCE
AUTHORS Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
Hood, L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1084 row: K column: 20
Seq primer: SP6
Class: BAC ends
High quality sequence stop: 756.
Location/Qualifiers
source 1..756
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=1084 Col=20 Row=K"
/sex="male"
/clone_lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN
Query Match 84.0%; Score 16.8; DB 9; Length 756;
Best Local Similarity 90.0%; Pred. No. 3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 309 AAGGAAACACGACACCCCTA 290

RESULT 75
DT060112/c
LOCUS DT060112
DEFINITION DT060112
AGENCOURT_55787745 NICHED_XGC_Faen Xenopus laevis cDNA clone
IMAGE:8074943 5', mRNA sequence.
ACCESSION DT060112
VERSION DT060112
KEYWORDS DT060112.1 GI:72359361
SOURCE EST.
ORGANISM Xenopus laevis (African clawed frog)
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 763)
NTH-MGC http://mgc.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.

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Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Tom Sargent  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM17356 row: i column: 21  
High quality sequence start: 52  
High quality sequence stop: 656.

FEATURES  
source  
1. .763  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:8074943"  
/lab\_host="DH10B TONR"  
/clone\_lib="NICHD\_XGC\_FaBN"  
/note="Organ: fat body; Vector: pExpress-1; Site\_1: EcoRV; Site 2: NotI; cDNA was primed using oligo-dT primer: 5'-pGACTAGTCTAGATCGAGCGGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb resulted in an average insert size of 1.5kb, and Cot value of 7. This is a normalized library (primary library is NICHD\_XGC\_FaB) and was constructed by Express Genomics (Frederick, MD). Note: this is a (  
http://xgc.nci.nih.gov/) Xenopus Gene Collection library."

ORIGIN  
Query Match 84.0%; Score 16.8; DB 8; Length 763;  
Best Local Similarity 90.0%; Pred. NO. 3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCCAA 20  
|||||  
Db 210 AAGGAACACGACGCCCAA 191

RESULT 76  
CB247499/c  
LOCUS  
DEFINITION UI-M-F10-cdz-j-16-0-UI-r1 NIH BMAP\_F10 Mus musculus CDNA clone  
IMAGE:6836561 5', mRNA sequence.  
CB247499  
ACCESSION CB247499.1 GI:28369143  
VERSION  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.  
1 (bases 1 to 780)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Robert Strausberg, Ph.D.  
Tissue Procurement: Dr. Jim Lin, University of Iowa  
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
Seq primer: pYX-5.  
Location/Qualifiers  
1. .780

FEATURES  
source  
1. .780  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:8075729"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 6; Length 780;  
Best Local Similarity 90.0%; Pred. NO. 3e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCCAA 20  
|||||  
Db 750 AAGGAACACGACGCCCAA 731

RESULT 77  
DT057062/c  
LOCUS  
DEFINITION DT057062 794 bp mRNA linear EST 11-AUG-2005  
AGENCOURT 55788803 NICHD\_XGC\_FaBN Xenopus laevis cDNA clone  
IMAGE:18075729 3', mRNA sequence.  
DT057062  
ACCESSION DT057062.1 GI:72356311  
VERSION  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae; Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 794)  
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Tom Sargent  
CDNA Library Preparation: Express Genomics  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLAM17358 row: j column: 15  
High quality sequence start: 42  
High quality sequence stop: 671.

FEATURES  
source  
1. .794  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="IMAGE:8075729"

/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6836561"  
/tissue\_type="whole brain"  
/dev\_stage="embryo 12.5dpc"  
/lab\_host="DH10B (TI phage resistant)"  
/clone\_lib="NIH\_BMAP\_F10"  
/note="Organ: Brain; Vector: pYX- Asc; Site\_1: EcoR I; Site\_2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CAGCCAGCAGC. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

/lab\_host="DH10B Tona"  
 /clone\_lib="NICHG\_XGC\_FaBn"  
 /note="Organ: fat body; Vector: pExpress-1; Site 1: EcoRV;  
 Site 2: NotI; cDNA was primed using oligo-dT primer:  
 5'-pGACTAGTTCTAGATCGGCGCGCC(T)25-3' and cloned into  
 the EcoRV/NotI sites of pExpress-1. Size-selection 1.2kb  
 resulted in an average insert size of 1.5kb, and Cot value  
 of 7. This is a normalized library (primary library is  
 NICHG\_XGC\_FaB) and was constructed by Express Genomics  
 (Frederick, MD). Note: this is a (  
 http://xgc.nci.nih.gov/) Xenopus Gene Collection library."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 794;  
 Best Local Similarity 90.0%; Pred. No. 3e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCCA 20  
 |||||  
 Db 140 AAGGAACACGACGCCCA 121

## RESULT 78

CV944482/c  
 LOCUS  
 DEFINITION P014G10 mycelium, subtracted infection mimic Phytophthora  
 infestans cDNA, mRNA sequence.  
 ACCESSION CV944482  
 VERSION  
 KEYWORDS EST  
 SOURCE Phytophthora infestans (potato late blight agent)  
 ORGANISM Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae;  
 Phytophthora.

REFERENCE 1 (bases 1 to 822)

AUTHORS Randall T., Dwyer, R.A., Huitena, E., Beyer, K., Cvitanich, C.,

Keikar, H., Fong, A.M., Gates, K., Roberts, S., Yatzkan, E., Gaffney, T.,  
 Law, M., Testa, A., Torto-Alalibo, A., Zhang, M., Zheng, L., Mueller, E.,  
 Windas, J., Binder, A., Birch, F.R.J., Gisi, U., Govers, F., Gow, N.A.,  
 Mauch, P., van West, P., Waugh, M.E., Yu, J., Boller, T., Kamoun, S.,  
 Lam, S.T. and Judelson, H.S.  
 Large-scale gene discovery in the oomycete Phytophthora infestans  
 reveals likely components of phytopathogenicity shared with true  
 fungi  
 Mol. Plant-Microbe Interact. 18 (3), 229-243 (2005)  
 15782637  
 Contact: Judelson HS  
 Department of Plant Pathology  
 University of California  
 Webber Hall, Riverside, CA 92521, USA  
 Tel: 909 787 4199  
 Fax: 909 787 4294  
 Email: howard.judelson@ucr.edu.  
 Location/Qualifiers

## TITLE

1. .822

## JOURNAL

## PUBMED

## COMMENT

/organism="Phytophthora infestans"  
 /mol\_type="mRNA"  
 /strain="88069"  
 /db\_xref="taxon:4787"  
 /sex="M"  
 /clone\_lib="mycelium, subtracted infection mimic"  
 /note="Vector: pSPORT1"

## FEATURES

## source

1. .822  
 /organism="Phytophthora infestans"  
 /mol\_type="mRNA"  
 /strain="88069"  
 /db\_xref="taxon:4787"  
 /sex="M"  
 /clone\_lib="mycelium, subtracted infection mimic"  
 /note="Vector: pSPORT1"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 8; Length 822;  
 Best Local Similarity 90.0%; Pred. No. 3e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGCCCA 20  
 |||||  
 Db 57 ACGGAACACGACGCCCA 38

## RESULT 79

## LOCUS

## DEFINITION

BF254545 829 bp mRNA linear EST 22-OCT-2001  
 HVSMEF0004F07f Hordeum vulgare seedling root EST library HVCDA0007  
 clone HVSMEF0004F07f, mRNA sequence.  
 ACCESSION BF254545  
 VERSION  
 KEYWORDS EST  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare

## REFERENCE

## AUTHORS

1 (bases 1 to 829)  
 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D.,  
 Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W.,  
 Fenton, R.D., Oates, R. and Main, D.  
 Development of a genetically and physically anchored EST resource  
 for barley genomics: Morex unstressed seedling root cDNA library  
 Unpublished (2001)  
 On Nov 16, 2000 this sequence version replaced gi:11183650.  
 Contact: Wing RA  
 Clemson University Genomics Institute  
 Clemson University  
 100 Jordan Hall, Clemson, SC 29634, USA  
 Tel: 864 656 7288  
 Fax: 864 656 4293  
 Email: rwing@clemson.edu  
 Total hg bases = 465  
 Seq primer: AATTACCCCTCACTAAAGGG  
 High quality sequence stop: 659.

## TITLE

## JOURNAL

## COMMENT

1. .829  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSMEF0004F07f"  
 /tissue\_type="Seedling root"  
 /lab\_host="TJCL21"  
 /clone\_lib="Hordeum vulgare seedling root EST library  
 HVCDA0007 (Etolated and unstressed)"  
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Seeds were surface sterilized then germinated under axenic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered  
 crystallization dishes. Five-day old seedling roots were  
 then harvested, total RNA was prepared, poly(A) RNA was  
 purified, one primary unamplified cDNA library was made,  
 and 1 million pfu were in vivo excised to give pBluescript  
 SK(-) cDNA phagemids. These steps were performed in the TJ  
 Close laboratory at the University of California,  
 Riverside (Choi, Close, Fenton). Phagemids were plated and  
 picked at the Clemson University Genomics Institute (CUGI)  
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA  
 preparations, DNA sequencing and sequence analysis were  
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,  
 Oates, Rambo, Main). The sequence has been trimmed to  
 remove vector sequence and contains a minimum of 100 bases  
 of phred value 20 or above. For more details on library  
 preparation and sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders Also  
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

## FEATURES

## source

1. .829  
 /organism="Hordeum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Morex"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="HVSMEF0004F07f"  
 /tissue\_type="Seedling root"  
 /lab\_host="TJCL21"  
 /clone\_lib="Hordeum vulgare seedling root EST library  
 HVCDA0007 (Etolated and unstressed)"  
 /note="Vector: lambdaZAP; Site 1: EcoRI; Site 2: XhoI;  
 Seeds were surface sterilized then germinated under axenic  
 conditions in the dark at room temperature on filter paper  
 with water, nystatin and cefotaxime in covered  
 crystallization dishes. Five-day old seedling roots were  
 then harvested, total RNA was prepared, poly(A) RNA was  
 purified, one primary unamplified cDNA library was made,  
 and 1 million pfu were in vivo excised to give pBluescript  
 SK(-) cDNA phagemids. These steps were performed in the TJ  
 Close laboratory at the University of California,  
 Riverside (Choi, Close, Fenton). Phagemids were plated and  
 picked at the Clemson University Genomics Institute (CUGI)  
 (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA  
 preparations, DNA sequencing and sequence analysis were  
 performed at CUGI (Wing, Yu, Frisch, Henry, Simmons,  
 Oates, Rambo, Main). The sequence has been trimmed to  
 remove vector sequence and contains a minimum of 100 bases  
 of phred value 20 or above. For more details on library  
 preparation and sequence analysis see  
 http://www.genome.clemson.edu/projects/barley. To order  
 this clone see http://www.genome.clemson.edu/orders Also  
 see Close TJ, Wing R, Kleinhofs A, Wise R (2001)  
 Genetically and physically anchored EST resources for  
 barley genomics. Barley Genetics Newsletter 31:29-30.  
 (http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 829;  
 Best Local Similarity 90.0%; Pred. No. 3e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 762 AAGGAACACGACACCCAA 781

RESULT 80  
 CD303542/c  
 LOCUS  
 DEFINITION AGNCOURT\_14236123 NICHD\_XGC\_Brn1 Xenopus laevis cDNA clone  
 IMAGE:6956191 5', mRNA sequence.

ACCESSION CD303542  
 VERSION CD303542.1 GI:31083408  
 KEYWORDS EST.

SOURCE  
 ORGANISM  
 Xenopus laevis (African clawed frog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.

REFERENCE 1 (bases 1 to 872)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

JOURNAL  
 COMMENT  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: cgabs-remail.nih.gov

Tissue Procurement:  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: L14M14582 row: 0 column: 06  
 High quality sequence start: 38  
 High quality sequence stop: 558.  
 Location/Qualifiers

FEATURES  
 source  
 1..872  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:6956191"  
 /dev\_stage="adult"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NICHD XGC Brn1"  
 /note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;  
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.5 kb. Constructed by Life  
 Technologies. Note: This is a Xenopus Gene Collection  
 (XGC) library."

ORIGIN  
 Query Match 84.0%; Score 16.8; DB 6; Length 872;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 194 AAGGAACACGACACCCAA 175

RESULT 81  
 BQ674913  
 LOCUS  
 DEFINITION AGNCOURT\_8062638 NIH\_MGC\_102 Homo sapiens cDNA clone IMAGE:6211356  
 5', mRNA sequence.

ACCESSION BQ674913  
 VERSION BQ674913.1 GI:21785747  
 KEYWORDS EST.

SOURCE  
 Homo sapiens (human)  
 899 bp mRNA linear EST 15-JUL-2002

ORGANISM

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT

1 (bases 1 to 899)  
 NIH-MGC http://mgs.nci.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)

Contact: Robert Strausberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov

Plate: L1CM2373 row: 1 column: 13  
 High quality sequence stop: 644.  
 Location/Qualifiers

FEATURES  
 source  
 1..899  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6211356"  
 /tissue\_type="epidermoid carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_102"  
 /note="Organ: salivary gland; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Library constructed  
 by Ling Hong in the laboratory of Gerald M. Rubin  
 (University of California, Berkeley) using ZAP-cDNA  
 synthesis kit (Stratagene) and Superscript II RT (Life  
 Technologies). Note: this is a NIH\_MGC Library."

ORIGIN  
 Query Match 84.0%; Score 16.8; DB 5; Length 899;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20  
 |||||  
 Db 846 AAGGAACACGACACCCAA 865

RESULT 82  
 CZ511376/c  
 LOCUS  
 DEFINITION GW2-49L8a.g1 GW2 Glycine max genomic, genomic survey sequence.  
 ACCESSION CZ511376  
 VERSION CZ511376.1 GI:63235674  
 KEYWORDS GSS.

SOURCE  
 ORGANISM  
 Glycine max (soybean)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.

REFERENCE 1 (bases 1 to 908)  
 Nunberg, A., Bedell, J.A., Citek, R.W., Robbins, D., McMenamy, J.,  
 Peterson, S., Jones, J., Fries, J., Budiman, M.A., Nguyen, H.,  
 Clifton, S.W. and Stacey, G.  
 BAC end sequences from Glycine max Williams 82 cultivar genome  
 Unpublished (2005)

TITLE  
 JOURNAL  
 COMMENT  
 Contact: Richard K Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@wustl.edu  
 Class: BAC ends.  
 Location/Qualifiers

FEATURES  
 source  
 1..908



```

/organism="Glycine max"
/mol_type="genomic DNA"
/db_xref="taxon:3847"
/clone_lib="GMW2"
/note="Glycine max BAC library"

ORIGIN

Query Match      84.0%; Score 16.8; DB 10; Length 908;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACACCCAA 20
    |||||
Db 112 AAGGAACACGACACCCAA 93

RESULT 83
CZ517024/c
LOCUS      CZ517024      916 bp      DNA      linear      GSS 11-MAY-2005
DEFINITION GMW2-49L8a.g2 GMW2 Glycine max genomic, genomic survey sequence.
ACCESSION  CZ517024
VERSION     CZ517024.1 GI:63242451
KEYWORDS   GSS.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE  1 (bases 1 to 916)
AUTHORS   Nunberg,A., Bedell,J.A., Citek,R.W., Robbins,D., McMenamy,J.,
            Peterson,S., Jones,J., Fries,J., Budiman,M.A., Nguyen,H.,
            Clifton,S.W. and Stacey,G.
TITLE     BAC end sequences from Glycine max Williams 82 cultivar genome
JOURNAL   Unpublished (2005)
COMMENT   Contact: Richard K Wilson
            Genome Sequencing Center
            Washington University School of Medicine
            Email: submissions@watson.wustl.edu
            Class: BAC ends.

FEATURES             Location/Qualifiers
     source           1..916
                     /organism="Glycine max"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:3847"
                     /clone_lib="GMW2"
                     /note="Glycine max BAC library"

ORIGIN

Query Match      84.0%; Score 16.8; DB 10; Length 916;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACACCCAA 20
    |||||
Db 125 AAGGAACACGACACCCAA 106

RESULT 84
CA789059/c
LOCUS      CA789059      918 bp      mRNA      linear      EST 04-DEC-2002
DEFINITION AGNCOURT_10304322 NICHG XGC_001 Xenopus laevis cDNA clone
            IMAGE:5084447 5', mRNA sequence.
ACCESSION  CA789059
VERSION     CA789059.1 GI:26033729
KEYWORDS   EST.
SOURCE     Xenopus laevis (African clawed frog)
ORGANISM   Xenopus laevis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
            Xenopodinae; Xenopus; Xenopus.
REFERENCE  1 (bases 1 to 918)
AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapsb@mail.nih.gov
Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLNL1226 row: a column: 24
High quality sequence start: 19
High quality sequence stop: 732.
Location/Qualifiers
     source           1..918
                     /organism="Xenopus laevis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8355"
                     /clone="IMAGE:5084447"
                     /tissue_type="oocytes"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NICHG XGC_001"
                     /note="vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;
                     Cloned unidirectionally. Primer: Oligo dt. Average insert
                     size 2.2 kb. Constructed by Life Technologies."

ORIGIN

Query Match      84.0%; Score 16.8; DB 6; Length 918;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACGACACCCAA 20
    |||||
Db 284 AAGGAACACGACGACCCAA 265

RESULT 85
BF029135
LOCUS      BF029135      919 bp      mRNA      linear      EST 10-OCT-2000
DEFINITION 601764643F1 NIH_MGC_53 Homo sapiens cDNA clone IMAGE:3996683 5',
            mRNA sequence.
ACCESSION  BF029135
VERSION     BF029135.1 GI:10736847
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Hominidae; Homo.
REFERENCE  1 (bases 1 to 919)
AUTHORS   NIH-MGC http://mgi.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.
            Email: cgapsb@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM849 row: f column: 12
            High quality sequence stop: 487.
Location/Qualifiers
     source           1..919
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3996683"
                     /tissue_type="carcinoma, cell line"
                     /lab_host="DH10B (T1 phage-resistant)"

```

/clone lib="NIH\_MGC\_53"  
 /note="Organ: b1adder; Vector: pDNR-LIB (Clontech);  
 Site\_1: Sfil (ggcgctcgcc); Site\_2: Sfil  
 (ggcattagggc); Double-stranded cDNA was prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and  
 3' adaptor sequence:  
 5'-ATTCTAGAGCGGAGCGCGGCACATG-dT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.55  
 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA)."

## ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 919;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 767 AAGGAACACGAGGTACCCAA 786

## RESULT 86

CC694001/c  
 LOCUS CC694001 930 bp DNA linear GSS 19-JUN-2003  
 DEFINITION OGVAR91TV\_ZM\_0.7\_1.5\_KB\_Zea\_mays\_genomic\_clone\_ZMWBMA0491014,  
 genomic survey sequence.

ACCESSION CC694001

VERSION CC694001.1 GI:32098777

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

REFERENCE 1 (bases 1 to 930)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

## AUTHORS

Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,  
 Reenick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.

## TITLE

Consortium for Maize Genomics

Unpublished (2002)

Other\_GSSs: OGVAR91TH

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TF

Class: methylation filtered.

Location/Qualifiers

1..930

/organism="Zea mays"

/mol\_type="genomic DNA"

/strain="B73"

/db\_xref="taxon:4577"

/clone="ZMWBMA0491014"

/clone lib="ZM\_0.7\_1.5\_KB"

/note="Vector: pBC5K; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Query Match 84.0%; Score 16.8; DB 9; Length 930;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 397 AAGGAACACGACACCCAA 378

## RESULT 87

BE881640/c

LOCUS BE881640 935 bp mRNA linear EST 20-OCT-2000

DEFINITION 601490060F1 NIH\_MGC\_69 Homo sapiens cDNA clone IMAGE:3892287 5',

mRNA sequence.

ACCESSION BE881640

VERSION BE881640.1 GI:10330416

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 935)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: DCTD/DTP/Gazdar

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LAM9678 row: h column: 16

High quality sequence stop: 679.

Location/Qualifiers

1..935

/organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:3892287"

/tissue type="large cell carcinoma, undifferentiated"

/lab host="DH10B (phage-resistant)"

/clone lib="NIH\_MGC\_69"

/note="Organ: lung; Vector: pCMV-SPORT6; Site\_1: NotI;

Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dt.

Average insert size 1.1 kb. Library constructed by Life

Technologies."

ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 935;

Best Local Similarity 90.0%; Pred. No. 3.1e+03;

Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAACACGACACCCAA 20

Db 762 AAGGAATCCGACACCCAA 743

## RESULT 88

BU915367/c

LOCUS BU915367 950 bp mRNA linear EST 17-OCT-2002

DEFINITION AGENCOURT\_10493183 NICHD\_XGC\_001 Xenopus laevis cDNA clone

IMAGE:6642041 5', mRNA sequence.

ACCESSION BU915367

VERSION BU915367.1 GI:24097281

KEYWORDS EST.

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 950)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L14M14226 row: m column: 17  
 High quality sequence stop: 700.

Location/Qualifiers  
 1. .950

#### FEATURES

source  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:6642041"  
 /tissue\_type="oocytes"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NICHD XGC OOI"  
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;  
 Cloned unidirectionally. Primer: Oligo dT. Average insert  
 size 2.2 kb. Constructed by Life Technologies."

#### ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 950;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
 |||||  
 Db 706 AAGGAAACACGACACCCAA 687

#### RESULT 89

##### BU911794

##### LOCUS

DEFINITION AGENCOURT 10463379 NICHD XGC OOI Xenopus laevis cDNA clone  
 IMAGE:6637855 5', mRNA sequence.

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

Xenopus laevis (African clawed frog)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;  
 Xenopodinae; Xenopus; Xenopus.

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Martha Rebert, Steven L. Klein, Ph.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L14M14215 row: o column: 07  
 High quality sequence stop: 597.

#### FEATURES

source  
 /organism="Xenopus laevis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8355"  
 /clone="IMAGE:6637855"  
 /tissue\_type="oocytes"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NICHD XGC OOI"  
 /note="Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI;  
 Cloned unidirectionally. Primer: Oligo dT. Average insert  
 size 2.2 kb. Constructed by Life Technologies."

#### ORIGIN

Query Match 84.0%; Score 16.8; DB 5; Length 953;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
 |||||  
 Db 900 AAGGAAACACGAAACCCAA 919

#### RESULT 90

##### BG335613

##### LOCUS

DEFINITION BG335613 602404233F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4541840 5',  
 mRNA sequence.

##### ACCESSION

##### VERSION

##### KEYWORDS

##### SOURCE

##### ORGANISM

Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.

##### REFERENCE

##### AUTHORS

##### TITLE

##### JOURNAL

##### COMMENT

NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: L14M1221 row: a column: 09

High quality sequence stop: 373.

#### FEATURES

##### source

1. .959  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4541840"  
 /tissue\_type="choriocarcinoma"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH\_MGC\_21"  
 /note="Organ: Placenta; Vector: pOTB7; Site 1: XhoI;  
 Site 2: EcoRI; cDNA made by oligo-dT priming.  
 Directionally cloned into EcoRI/XhoI sites using the  
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp  
 for average insert size 1.8kb. Library constructed by  
 Ling Hong in the laboratory of Gerald M. Rubin (University  
 of California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies)."

#### ORIGIN

Query Match 84.0%; Score 16.8; DB 2; Length 959;  
 Best Local Similarity 90.0%; Pred. No. 3.1e+03;  
 Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAGGAAACACGACACCCAA 20  
 |||||  
 Db 926 AAGGAAACACGACACCCAA 945

#### RESULT 91

##### BF532081

##### LOCUS

DEFINITION 602073196F1 NCI\_CGAP\_Li9 Mus musculus cDNA clone IMAGE:4210415 5',  
 mRNA sequence.

##### ACCESSION

##### VERSION

BF532081 1031 bp mRNA linear EST 11-DEC-2000  
 BF532081 GI:11619547

## FEATURES

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CL049473
LOCUS          CL049473          1097 bp    DNA          linear    GSS 31-DEC-2003
DEFINITION    CH216-69P17_Sp6.1 CH216 Xenopus tropicalis genomic clone
ACCESSION     CH216-69P17, genomic survey sequence.
VERSION       CL049473
KEYWORDS      GSS.
SOURCE        CL049473.1 GI:40505386
ORGANISM      Xenopus tropicalis (western clawed frog)
               Xenopus tropicalis
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
               Xenopodinae; Xenopus; Silurana.
REFERENCE     1 (bases 1 to 1097)
AUTHORS       Krenitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
               Mardis,E. and Wilson,R.
TITLE         A physical map of the xenopus tropicalis genome
JOURNAL       Unpublished (2003)
COMMENT       Contact: Richard K Wilson
               Genome Sequencing Center
               Washington University School of Medicine
               Email: submissions@watson.wustl.edu
               Insert Length: 175000 Std Error: 0.00
               Seq primer: Sp6 ATTTAGGTGACACTAG
               Class: BAC ends
               High quality sequence start: 223
               High quality sequence stop: 392.
               Location/Qualifiers
                 1..1097
                   /organism="Xenopus tropicalis"
                   /mol_type="genomic DNA"
                   /strain="Nigerian frog"
                   /db_xref="taxon:8364"
                   /clone="CH216-69P17"
                   /sex="male"
                   /cell_line="Stock 248 F7A2, inbred N7"
                   /clone_lib="CH216"
                   /note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
                   BAC library"

ORIGIN
Query Match      84.0%; Score 16.8; DB 10; Length 1097;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
    |||||
Db 114 AAGCAACACGGACACCA 133

RESULT 95
CC276125
LOCUS          CC276125          1123 bp    DNA          linear    GSS 13-MAY-2003
DEFINITION    CH261-128F17_Sp6.1 CH261 Gallus gallus genomic clone CH261-128F17,
               genomic survey sequence.
ACCESSION     CC276125
VERSION       CC276125.1 GI:30634975
KEYWORDS      GSS.
SOURCE        Gallus gallus (chicken)
ORGANISM      Gallus gallus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
               Phasianinae; Gallus.
REFERENCE     1 (bases 1 to 1123)
AUTHORS       Krenitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,
               Warren,W., Graves,T., Mardis,E. and Wilson,R.
TITLE         Gallus gallus BAC End Reads
JOURNAL       Unpublished (2003)
COMMENT       Contact: Richard K. Wilson
               Genome Sequencing Center
               Washington University School of Medicine
               Email: submissions@watson.wustl.edu
               Insert Length: 182000 Std Error: 0.00.
               Seq primer: Sp6 ATTTAGGTGACACTAG

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Class: BAC ends
High quality sequence start: 91
High quality sequence stop: 469.
Location/Qualifiers
  1..1123
    /organism="Gallus gallus"
    /mol_type="genomic DNA"
    /strain="Red Jungle Fowl"
    /db_xref="taxon:9031"
    /clone="CH261-128F17"
    /sex="female"
    /cell_line="UCD001, inbred 256"
    /clone_lib="CH261"
    /note="Vector: pTARBAC2.1; Site 1: EcoRI; Site 2: EcoRI;
    CH261 Female Chicken library - for library and clone
    ordering information: http://www.chori.org/bacpac"

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 1123;
Best Local Similarity 90.0%; Pred. No. 3.1e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
    |||||
Db 921 AAGGAACACATACCCAA 940

RESULT 96
BZ576789/c
LOCUS          BZ576789          1251 bp    DNA          linear    GSS 17-DEC-2002
DEFINITION    msh2_5104.x1 msh Pseudomonas aeruginosa genomic clone msh2_5104,
               genomic survey sequence.
ACCESSION     BZ576789
VERSION       BZ576789.1 GI:27211850
KEYWORDS      GSS.
SOURCE        Pseudomonas aeruginosa
ORGANISM      Pseudomonas aeruginosa
               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
               Pseudomonadaceae; Pseudomonas.
REFERENCE     1 (bases 1 to 1251)
AUTHORS       Spencer,D.H., Raymond,C.K., Smith,E.E., Sims,E.E., Hastings,M.,
               Burns,J.L., Kaul,R. and Olsen,M.V.
TITLE         Whole-Genome-Sequence variation among multiple isolates of
               Pseudomonas aeruginosa library
JOURNAL       J. Bacteriol. (2002) In press
COMMENT       Contact: Chris K. Raymond
               Genome Center
               University of Washington
               Box 352145, Seattle, WA 98105-2145, USA
               Tel: 2062216954
               Fax: 2066857244
               Email: craymond@u.washington.edu
               Class: shotgun.
               Location/Qualifiers
                 1..1251
                   /organism="Pseudomonas aeruginosa"
                   /mol_type="genomic DNA"
                   /strain="MSH"
                   /db_xref="taxon:287"
                   /clone="msh2_5104"
                   /clone_lib="msh"
                   /note="Environmental isolate. Whole genomic shotgun
                   library."

ORIGIN
Query Match      84.0%; Score 16.8; DB 9; Length 1251;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 1 AAGGAACACGGACACCCAA 20
    |||||
Db 1112 AAGGAACACGGACACCA 1093

```

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RESULT 97
CNSOG3AI/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CNSOG3AI
Tetraodon nigroviridis full-length cDNA.
CR700286
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Cattolico, L., Poulain, J., De
Vacherie, B., Biemont, C., Skalli, Z., Bottier, P., Coutanceau, J.P.,
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., McKernan, K.J.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)
15496914
PUBMED
REFERENCE
2 (bases 1 to 1338)
Genoscope.
Direct Submission
Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51198195.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1..1338
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"
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Query Match 84.0%; Score 16.8; DB 4; Length 1338;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 1017 AAGGAAACACGACACCCAA 998

RESULT 98
CNSOFHXN/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CNSOFHXN
Tetraodon nigroviridis full-length cDNA.
CR672581
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Cattolico, L., Poulain, J., De
Vacherie, B., Biemont, C., Skalli, Z., Bottier, P., Coutanceau, J.P.,
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., McKernan, K.J.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)
15496914
PUBMED
REFERENCE
2 (bases 1 to 1338)
Genoscope.
Direct Submission
Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51198195.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1..1338
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Eyes"
ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 1338;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 1017 AAGGAAACACGACACCCAA 998

RESULT 99
CNSOEYFW/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CNSOEYFW
Tetraodon nigroviridis full-length cDNA.
CR647318
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Cattolico, L., Poulain, J., De
Vacherie, B., Biemont, C., Skalli, Z., Bottier, P., Coutanceau, J.P.,
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., McKernan, K.J.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)
15496914
PUBMED
REFERENCE
2 (bases 1 to 1490)
Genoscope.
Direct Submission
Submitted (25-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51169026.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
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1..1490
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Muscle"
ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 1490;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 1158 AAGGAAACACGACACCCAA 1139

RESULT 99
CNSOEYFW/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

CNSOEYFW
Tetraodon nigroviridis full-length cDNA.
CR647318
HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Jailon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,
Segurens, B., Dasilva, C., Salanoubat, M., Levy, M., Boudet, N.,
Castellano, S., Anthouard, V., Jubin, C., Cattolico, L., Poulain, J., De
Vacherie, B., Biemont, C., Skalli, Z., Bottier, P., Coutanceau, J.P.,
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., McKernan, K.J.,
Gouzy, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J., Zody, M.C.,
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.
Genome duplication in the teleost fish Tetraodon nigroviridis
reveals the early vertebrate proto-karyotype
Nature 431 (7011), 946-957 (2004)
15496914
PUBMED
REFERENCE
2 (bases 1 to 1490)
Genoscope.
Direct Submission
Submitted (25-NOV-2004) Genoscope - Centre National de Sequencage -
: 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
On Dec 3, 2004 this sequence version replaced gi:51169026.
The sequences are based on single pass reads.
More information available at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source
1..1490
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="mRNA"
/db_xref="taxon:99883"
/tissue_type="Muscle"
ORIGIN
Query Match 84.0%; Score 16.8; DB 4; Length 1490;
Best Local Similarity 90.0%; Pred. No. 3.2e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 AAGGAAACACGACACCCAA 20
|||||
Db 1158 AAGGAAACACGACACCCAA 1139

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JOURNAL Nature 431 (7011), 946-957 (2004)  
PUBMED 15496914  
REFERENCE 2 (bases 1 to 1541)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT On Dec 3, 2004 this sequence version replaced gi:51143763.  
The sequences are based on single pass reads.  
More information available at  
http://www.genoscope.cns.fr/tetraodon.  
FEATURES  
source  
1. .1541  
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/mol\_type="mRNA"  
/db\_xref="taxon:99883"  
/tissue\_type="Liver"

ORIGIN  
Query Match 84.0%; Score 16.8; DB 4; Length 1541;  
Best Local Similarity 90.0%; Pred. No. 3.2e+03;  
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 AAGGAACACGGACACCCAA 20  
|||||  
Db 1222 AAGGAACACGGACACCCAA 1203

RESULT 100  
CNS0GLAC 1559 bp mRNA linear HTC 05-JUL-2005  
LOCUS Tetraodon nigroviridis full-length cDNA.  
DEFINITION CR697688  
ACCESSION CR697688.2 GI:56350687  
VERSION  
KEYWORDS HTC; cDNA; full-length; full-length cDNA; Tetraodon nigroviridis.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontidae; Tetraodontidae; Tetraodon.  
REFERENCE 1  
AUTHORS Jaillon, O., Aury, J.M., Brunet, F., Petit, J.L., Stange-Thomann, N.,  
Mauceli, E., Bouneau, L., Fischer, C., Ozouf-Costaz, C., Bernot, A.,  
Nicaud, S., Jaffe, D., Fisher, S., Lutfalla, G., Dossat, C.,  
Segurens, B., Dasilva, C., Salancoubat, M., Levy, M., Boudet, N.,  
Castellano, S., Anthouard, V., Jubin, C., Castelli, V., Katinka, M.,  
Vacherie, B., Bieumont, C., Skalli, Z., Cattolico, L., Poulain, J., De  
Berardinis, V., Cruaud, C., Duprat, S., Brottier, P., Coutanceau, J.P.,  
Goury, J., Parra, G., Lardier, G., Chapple, C., McKernan, K.J.,  
McEwan, P., Bosak, S., Kellis, M., Volff, J.N., Guigo, R., Zody, M.C.,  
Mesirov, J., Lindblad-Toh, K., Birren, B., Nusbaum, C., Kahn, D.,  
Robinson-Rechavi, M., Laudet, V., Schachter, V., Quetier, F.,  
Saurin, W., Scarpelli, C., Wincker, P., Lander, E.S., Weissbach, J.  
and Roest Crollius, H.  
TITLE Genome duplication in the teleost fish Tetraodon nigroviridis  
reveals the early vertebrate proto-karyotype  
JOURNAL Nature 431 (7011), 946-957 (2004)  
PUBMED 15496914  
REFERENCE 2 (bases 1 to 1559)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (24-NOV-2004) Genoscope - Centre National de Sequencage -  
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE  
(E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)  
COMMENT On Dec 3, 2004 this sequence version replaced gi:51195597.  
The sequences are based on single pass reads.  
More information available at  
http://www.genoscope.cns.fr/tetraodon.  
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Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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|||||  
Db 1241 AAGGAACACGGACACCCAA 1222

Search completed: March 9, 2006, 02:45:43  
Job time : 1603.68 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model  
Run on: March 9, 2006, 00:09:45 ; Search time 1055.34 Seconds  
(without alignments)  
1346.567 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 500 summaries

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- 2: gb.in.\*
- 3: gb.env.\*
- 4: gb.om.\*
- 5: gb.ov.\*
- 6: gb.pat.\*
- 7: gb.ph.\*
- 8: gb.pr.\*
- 9: gb.ro.\*
- 10: gb.sts.\*
- 11: gb.sy.\*
- 12: gb.un.\*
- 13: gb.vi.\*
- 14: gb.hcg.\*
- 15: gb.pl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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C 5	25	100.0	109	13	DQ229093 Human ech
C 6	25	100.0	109	13	EU008071 Enterovirus
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C 8	25	100.0	112	13	AY189929 Human ent
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C 290	AY899106	Human ech	359	13	AY899106	Human ech	359	13	AY899106	Human ech
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C 361	AY899179	Human ech	359	13	AY899179	Human ech	359	13		

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C 385	25	100.0	391	13	AF532049	AF532049 Human ech	AF167996 Enterovir
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C 391	25	100.0	409	13	S76769	X87606 Enterovirus	X87388 Coxsackievi
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C 393	25	100.0	467	13	HEC295173	AJ295173 Human ech	M74567 Coxsackievi
C 394	25	100.0	497	13	HEC295183	AJ295183 Human ech	-
C 395	25	100.0	502	6	AX711934	AX711934 Sequence	AB162756 Human cox
C 396	25	100.0	513	13	HCO420884	AJ420884 Human cox	AB162606 Human cox
C 397	25	100.0	548	6	AX711931	AX711931 Sequence	AB081342 Human ent
C 398	25	100.0	551	6	AX711936	AX711936 Sequence	AB081343 Human ent
C 399	25	100.0	552	6	AX711935	AX711935 Sequence	AB081347 Human ent
C 400	25	100.0	589	13	HEC295177	AJ295177 Human ech	AB081348 Human ent
C 401	25	100.0	594	13	AF447480	AF447480 Human ech	AB081349 Human ent
C 402	25	100.0	595	13	AF447481	AF447481 Human ech	AB081357 Human ent
C 403	25	100.0	596	13	AF447482	AF447482 Human ech	AB081358 Human ent
C 404	25	100.0	597	13	AF447472	AF447472 Human ech	AB081359 Human ent
C 405	25	100.0	597	13	AF447475	AF447475 Human ech	AB081360 Human ent
C 406	25	100.0	617	13	AB059820	AB059820 Enterovir	AB081361 Human ent
C 407	25	100.0	617	13	AB059821	AB059821 Enterovir	AB081362 Human ent
C 408	25	100.0	617	13	AB059822	AB059822 Enterovir	AB081363 Human ent
C 409	25	100.0	617	13	AB059823	AB059823 Enterovir	AB081365 Human ent
C 410	25	100.0	617	13	AB059824	AB059824 Enterovir	AB081366 Human ent
C 411	25	100.0	617	13	AB059826	AB059826 Enterovir	AB081370 Human ent
C 412	25	100.0	644	13	AY055125	AY055125 Human ent	AB081372 Human ent
C 413	25	100.0	644	13	AY055126	AY055126 Human ent	AB081373 Human ent
C 414	25	100.0	644	13	AY055127	AY055127 Human ent	AB081375 Human ent
C 415	25	100.0	644	13	AY055128	AY055128 Human ent	AB081376 Human ent
C 416	25	100.0	644	13	AY055129	AY055129 Human ent	AB081377 Human ent
C 417	25	100.0	644	13	AY055130	AY055130 Human ent	AB081383 Human ent
C 418	25	100.0	644	13	AY055131	AY055131 Human ent	AB081387 Human ent
C 419	25	100.0	644	13	AY055132	AY055132 Human ent	AB081387 Human ent
C 420	25	100.0	644	13	AY055133	AY055133 Human ent	AB081345 Human ent
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C 433	25	100.0	645	13	AY055147	AY055147 Human ent	
C 434	25	100.0	645	13	AY055146	AY055146 Human ent	
C 435	25	100.0	647	13	AF117632	AF117632 Enterovir	
C 436	25	100.0	648	13	AF117623	AF117623 Enterovir	
C 437	25	100.0	648	13	AF117635	AF117635 Enterovir	
C 438	25	100.0	649	13	AF117619	AF117619 Enterovir	
C 439	25	100.0	649	13	AF117620	AF117620 Enterovir	
C 440	25	100.0	649	13	AF117621	AF117621 Enterovir	
C 441	25	100.0	649	13	AF117625	AF117625 Enterovir	
C 442	25	100.0	649	13	AF117627	AF117627 Enterovir	
C 443	25	100.0	649	13	AF117628	AF117628 Enterovir	
C 444	25	100.0	649	13	AY055173	AY055173 Human ent	
C 445	25	100.0	650	13	AF117622	AF117622 Enterovir	
C 446	25	100.0	650	13	AF117624	AF117624 Enterovir	
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C 449	25	100.0	650	13	AF117633	AF117633 Enterovir	
C 450	25	100.0	650	13	AF117634	AF117634 Enterovir	
C 451	25	100.0	657	13	CA12RNAPA	X87593 Coxsackievi	
C 452	25	100.0	660	13	CB3VCO1	AF169665 Coxsackie	
C 453	25	100.0	703	13	AF225473	AF225473 Coxsackie	
C 454	25	100.0	703	13	AF225474	AF225474 Coxsackie	
C 455	25	100.0	703	13	ECH5UTRA	L76396 Echovirus t	
C 456	25	100.0	707	13	AB071699	AB071699 Human cox	

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C 458	25	100.0	732	13	AF167996	AF167996 Enterovir
C 459	25	100.0	776	13	EV8VP2GEN	X89539 Echovirus 8
C 460	25	100.0	799	13	E69RNAPA	X87605 Enterovirus
C 461	25	100.0	810	6	Q0840452	Q0840452 Sequence
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C 463	25	100.0	867	13	CA5RNAPA	AB162749 Human cox
C 464	25	100.0	868	13	CA7RNAPA	X87589 Coxsackievi
C 465	25	100.0	894	13	CX4MYOJ	M74567 Coxsackievi
C 466	25	100.0	939	13	AB162756	AB162756 Human cox
C 467	25	100.0	1029	13	AB162606	AB162606 Human cox
C 468	25	100.0	1037	13	AB081342	AB081342 Human ent
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C 471	25	100.0	1037	13	AB081348	AB081348 Human ent
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C 474	25	100.0	1037	13	AB081358	AB081358 Human ent
C 475	25	100.0	1037	13	AB081359	AB081359 Human ent
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C 477	25	100.0	1037	13	AB081361	AB081361 Human ent
C 478	25	100.0	1037	13	AB081362	AB081362 Human ent
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C 483	25	100.0	1037	13	AB081372	AB081372 Human ent
C 484	25	100.0	1037	13	AB081373	AB081373 Human ent
C 485	25	100.0	1037	13	AB081375	AB081375 Human ent
C 486	25	100.0	1037	13	AB081376	AB081376 Human ent
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C 489	25	100.0	1037	13	AB081387	AB081387 Human ent
C 490	25	100.0	1038	13	AB081345	AB081345 Human ent
C 491	25	100.0	1038	13	AB081346	AB081346 Human ent
C 492	25	100.0	1038	13	AB081350	AB081350 Human ent
C 493	25	100.0	1038	13	AB081351	AB081351 Human ent
C 494	25	100.0	1038	13	AB081352	AB081352 Human ent
C 495	25	100.0	1038	13	AB081353	AB081353 Human ent
C 496	25	100.0	1038	13	AB081354	AB081354 Human ent
C 497	25	100.0	1038	13	AB081355	AB081355 Human ent
C 498	25	100.0	1038	13	AB081356	AB081356 Human ent
C 499	25	100.0	1038	13	AB081368	AB081368 Human ent
C 500	25	100.0	1038	13	AB081369	AB081369 Human ent

ALIGNMENTS

RESULT 1

AY189930/c

LOCUS

AY189930

73 bp

RNA

linear

VRL 08-MAY-2003

DEFINITION

Human enterovirus B isolate NSW/51/97 5' untranslated region, partial sequence.

ACCESSION

AY189930

VERSION

AY189930.1

GI:28395429

KEYWORDS

Human enterovirus B

SOURCE

Human enterovirus B

ORGANISM

Human enterovirus B

REFERENCE

1 (bases 1 to 73)

AUTHORS

Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

TITLE

Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1

JOURNAL

Diabetes Associated with Enterovirus RNA

PUBMED

J. Infect. Dis. 187 (10), 1562-1570 (2003)

AUTHORS

2 (bases 1 to 73)

TITLE

Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

JOURNAL

Submitted (03-DEC-2002) Virology Division, University of New South

PUBMED

Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia

```
FEATURES
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        /mol_type="genomic RNA"
        /isolate="NSW/51/97"
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 31 TCCGCTGCAGAGTTGCCCGTTACGA 7

RESULT 2
AY189933/c
LOCUS
DEFINITION
  Human enterovirus 71 isolate NSW/167/97 5' untranslated region,
  partial sequence.
ACCESSION
  AY189933
VERSION
  AY189933.1 GI:28395432
KEYWORDS
  SOURCE
  Human enterovirus 71
  Organism
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 73)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
  Diabetes Associated with Enterovirus RNA
  J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
  PUBMED
  12721936
REFERENCE
  2 (bases 1 to 73)
  Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
  Direct Submission
  Submitted (03-DEC-2002) Virology Division, University of New South
  Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,
  Australia
FEATURES
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        /db_xref="taxon:39054"
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  Best Local Similarity 100.0%; Pred. No. 0.32;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 31 TCCGCTGCAGAGTTGCCCGTTACGA 7

RESULT 3
ESU55870/c
LOCUS
DEFINITION
  Enterovirus sp. 5' NTR sequence from patient B6.
ACCESSION
  U55870
VERSION
  U55870.1 GI:1330335
KEYWORDS
  SOURCE
  Enterovirus sp.
  Organism
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 83)
  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
JOURNAL
  PUBMED
  8757988
REFERENCE
  2 (bases 1 to 100)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
  Road, London SE1 7EH, UK
FEATURES
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  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 58 TCCGCTGCAGAGTTGCCCGTTACGA 34

RESULT 4
ESU55868/c
LOCUS
DEFINITION
  Enterovirus sp. 5' NTR sequence from patient A23.
ACCESSION
  U55868
VERSION
  U55868.1 GI:1330333
KEYWORDS
  SOURCE
  Enterovirus sp.
  Organism
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 100)
  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Khan,M., Archard,L.C., Cairns,N.J., Anderson,V.E.R., Leigh,P.N.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
JOURNAL
  PUBMED
  8757988
REFERENCE
  2 (bases 1 to 100)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
  Road, London SE1 7EH, UK
FEATURES
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ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 0.32;
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 41 TCCGCTGCAGAGTTGCCCGTTACGA 17

RESULT 5
DQ029093/c
LOCUS
DEFINITION
  Human echovirus 11 strain Gregory prototype 5' UTR.
ACCESSION
  DQ029093
VERSION
  DQ029093.1 GI:1330335
KEYWORDS
  SOURCE
  Human echovirus 11
  Organism
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 83)
  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
JOURNAL
  PUBMED
  8757988
REFERENCE
  2 (bases 1 to 100)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
  Road, London SE1 7EH, UK
FEATURES
  source
    Location/Qualifiers
      1..100
        /organism="Enterovirus sp."
        /mol_type="genomic RNA"
        /db_xref="taxon:47681"
        /note="from patient B6"
ORIGIN
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  Best Local Similarity 100.0%; Pred. No. 0.32;
  Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 58 TCCGCTGCAGAGTTGCCCGTTACGA 34

RESULT 6
DQ029093/c
LOCUS
DEFINITION
  Human echovirus 11 strain Gregory prototype 5' UTR.
ACCESSION
  DQ029093
VERSION
  DQ029093.1 GI:1330335
KEYWORDS
  SOURCE
  Human echovirus 11
  Organism
  Viruses; ssRNA positive-strand viruses, no DNA stage;
  Picornaviridae; Enterovirus.
REFERENCE
  1 (bases 1 to 83)
  Muir,P., Nicholson,F., Spencer,G.T., Ajetumobi,J.F., Starkey,W.G.,
  Howard,R.S. and Banatvala,J.E.
  Enterovirus infection of the central nervous system of humans: lack
  of association with chronic neurological disease
  J. Gen. Virol. 77 (Pt 7), 1469-1476 (1996)
JOURNAL
  PUBMED
  8757988
REFERENCE
  2 (bases 1 to 100)
  Muir,P.
  Direct Submission
  Submitted (22-APR-1996) Peter Muir, Virology, UMDS, Lambeth Palace
  Road, London SE1 7EH, UK
FEATURES
  source
    Location/Qualifiers
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        /db_xref="taxon:47681"
        /note="from patient B6"
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 58 TCCGCTGCAGAGTTGCCCGTTACGA 34
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ACCESSION DQ029093
VERSION DQ029093.1 GI:66473301
KEYWORDS
SOURCE Human echovirus 11
ORGANISM Human echovirus 11
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 109)
N'Saibia,S. and Aouni,M.
Nucleotide sequences of the IRES domains IV and V of natural
isolates ECHO virus type 11 with different replicative capacities
phenotypes
JOURNAL Unpublished (2005)
PUBMED
REFERENCE 2 (bases 1 to 109)
AUTHORS Garbi,J., Elharr,R., Ben M'Hadheb,M., Jaidane,H., Bouslama,L.,
N'Saibia,S. and Aouni,M.
Direct Submission
TITLE Submitted (06-MAY-2005) Virology, Faculty of Pharmacy & Higher
JOURNAL Institute of Biotechnology, Avicenne Street, Monastir 5000, Tunisia
FEATURES
source
1..109
/organism="Human echovirus 11"
/mol_type="genomic RNA"
/strain="Gregory prototype"
/db_xref="taxon:12078"
<1..>109
/note="domain V of IRES (internal ribosome entry site)"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 88 TCCGCTGCAGAGTTGCCCGTTACGA 64
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RESULT 6
E7U00871/c
LOCUS Enterovirus 71 prototype BrCr 5' untranslated region.
DEFINITION
ACCESSION U00871
VERSION U00871.1 GI:405114
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 109)
Zheng,Z.M., He,P.J., Caueffield,D., Neumann,M., Specter,S.,
Baker,C.C. and Bankowski,M.J.
Enterovirus 71 isolated from China is serologically similar to the
prototype E71 BrCr strain but differs in the 5'-noncoding region
JOURNAL J. Med. Virol. 47 (2), 161-167 (1995)
PUBMED 8830120
REFERENCE 2 (bases 1 to 109)
AUTHORS Bankowski,M.J.
Direct Submission
TITLE Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
JOURNAL Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
FEATURES
source
1..109
/organism="Human enterovirus 71"
/mol_type="unassigned DNA"
/strain="E 71 H"
/isolate="H"
/db_xref="taxon:39054"
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 67 TCCGCTGCAGAGTTGCCCGTTACGA 43
|||||
RESULT 7
E7U00872/c
LOCUS Enterovirus E71 H 5' untranslated region.
DEFINITION
ACCESSION U00872
VERSION U00872.1 GI:405115
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 109)
Zheng,Z.M., He,P.J., Caueffield,D., Neumann,M., Specter,S.,
Baker,C.C. and Bankowski,M.J.
Enterovirus 71 isolated from China is serologically similar to the
prototype E71 BrCr strain but differs in the 5'-noncoding region
JOURNAL J. Med. Virol. 47 (2), 161-167 (1995)
PUBMED 8830120
REFERENCE 2 (bases 1 to 109)
AUTHORS Bankowski,M.J.
Direct Submission
TITLE Submitted (17-AUG-1993) Bankowski M.J., Diagnostic Services, Inc.,
JOURNAL Clinical Virology & Molecular Medicine, 340 Goodlette Road South,
Naples, FL 33940, USA
FEATURES
source
1..109
/organism="Human enterovirus 71"
/mol_type="unassigned DNA"
/strain="E 71 H"
/isolate="H"
/db_xref="taxon:39054"
ORIGIN
Query Match 100.0%; Score 25; DB 13; Length 109;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 67 TCCGCTGCAGAGTTGCCCGTTACGA 43
|||||
RESULT 8
AY189929/c
LOCUS Human enterovirus B isolate NSW/47/97 5' untranslated region,
DEFINITION partial sequence.
ACCESSION AY189929
VERSION AY189929.1 GI:28395428
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;
AUTHORS Picornaviridae; Enterovirus.
TITLE 1 (bases 1 to 112)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 112)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
TITLE Submitted (03-DEC-2002) Virology Division, University of New South
JOURNAL Wales, Prince of Wales Hospital, High Street, Randwick, NSW 2031,

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FEATURES             Location/Qualifiers
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                   /mol_type="genomic RNA"
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                   /db_xref="taxon:138949"
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ORIGIN
Query Match        100.0%; Score 25; DB 13; Length 112;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 9
AY189179/c
LOCUS             AY189179             115 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/100/98 5' UTR, partial sequence.
ACCESSION        AY189179
VERSION          AY189179.1 GI:28274402
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE        1 (bases 1 to 115)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
                  Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL          12721936
PUBMED
REFERENCE        2 (bases 1 to 115)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Direct Submission
JOURNAL          Submitted (29-NOV-2002) Virology Division, South Eastern Area
                  Laboratory Services, University of New South Wales/Prince of Wales
                  Hospital, High Street, Randwick, NSW 2031, Australia
                  Location/Qualifiers
FEATURES             Location/Qualifiers
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                   /isolate="NSW/100/98"
                   /db_xref="taxon:138949"
                   <1..>115
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ORIGIN
Query Match        100.0%; Score 25; DB 13; Length 115;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 10
AY189158/c
LOCUS             AY189158             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/01/97 5' UTR, partial sequence.
ACCESSION        AY189158
VERSION          AY189158.1 GI:28274381
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE        1 (bases 1 to 116)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
                  Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL          12721936
PUBMED
REFERENCE        2 (bases 1 to 116)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Direct Submission
JOURNAL          Submitted (29-NOV-2002) Virology Division, South Eastern Area
                  Laboratory Services, University of New South Wales/Prince of Wales
                  Hospital, High Street, Randwick, NSW 2031, Australia
                  Location/Qualifiers
FEATURES             Location/Qualifiers
source              1..116
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                   /mol_type="genomic RNA"
                   /isolate="NSW/01/97"
                   /db_xref="taxon:138949"
                   <1..>116
5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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TITLE              Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
                  Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL            12721936
PUBMED
REFERENCE          2 (bases 1 to 116)
AUTHORS            Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE              Direct Submission
JOURNAL            Submitted (29-NOV-2002) Virology Division, South Eastern Area
                  Laboratory Services, University of New South Wales/Prince of Wales
                  Hospital, High Street, Randwick, NSW 2031, Australia
                  Location/Qualifiers
FEATURES             Location/Qualifiers
source              1..116
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                   /mol_type="genomic RNA"
                   /isolate="NSW/01/97"
                   /db_xref="taxon:138949"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 11
AY189159/c
LOCUS             AY189159             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/02/97 5' UTR, partial sequence.
ACCESSION        AY189159
VERSION          AY189159.1 GI:28274382
KEYWORDS
SOURCE           Human enterovirus B
ORGANISM         Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE        1 (bases 1 to 116)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
                  Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL          12721936
PUBMED
REFERENCE        2 (bases 1 to 116)
AUTHORS          Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE            Direct Submission
JOURNAL          Submitted (29-NOV-2002) Virology Division, South Eastern Area
                  Laboratory Services, University of New South Wales/Prince of Wales
                  Hospital, High Street, Randwick, NSW 2031, Australia
                  Location/Qualifiers
FEATURES             Location/Qualifiers
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                   <1..>116
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 12
AY189160/c
LOCUS             AY189160             116 bp             RNA             linear             VRL 08-MAY-2003
DEFINITION       Human enterovirus B isolate NSW/07/97 5' UTR, partial sequence.

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ACCESSION      AY189160
VERSION        AY189160.1  GI:28274383
KEYWORDS
SOURCE         Human enterovirus B
ORGANISM       Human enterovirus B
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
               Diabetes Associated with Enterovirus RNA
JOURNAL        J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED        12721936
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Direct Submission
JOURNAL        Submitted (29-NOV-2002) Virology Division, South Eastern Area
               Laboratory Services, University of New South Wales/Prince of Wales
               Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES       source
               1..116
               /organism="Human enterovirus B"
               /mol_type="genomic RNA"
               /isolate="NSW/07/97"
               /db_xref="taxon:138949"
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5'UTR
ORIGIN
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  TCCGCTGCAGAGTTGCCGTTACGA 25
Db  74 TCCGCTGCAGAGTTGCCGTTACGA 50

RESULT 13
AY189161/c
LOCUS          Human enterovirus 71 isolate NSW/08/97 5' UTR, partial sequence.
DEFINITION
ACCESSION      AY189161
VERSION        AY189161.1  GI:28274384
KEYWORDS
SOURCE         Human enterovirus 71
ORGANISM       Human enterovirus 71
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
               Diabetes Associated with Enterovirus RNA
JOURNAL        J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED        12721936
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Direct Submission
JOURNAL        Submitted (29-NOV-2002) Virology Division, South Eastern Area
               Laboratory Services, University of New South Wales/Prince of Wales
               Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES       source
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               /mol_type="genomic RNA"
               /isolate="NSW/08/97"
               /db_xref="taxon:39054"
               /note="Human enterovirus 71"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy  1  TCCGCTGCAGAGTTGCCGTTACGA 25
Db  74 TCCGCTGCAGAGTTGCCGTTACGA 50

RESULT 14
AY189162/c
LOCUS          Human enterovirus B isolate NSW/14/97 5' UTR, partial sequence.
DEFINITION
ACCESSION      AY189162
VERSION        AY189162.1  GI:28274385
KEYWORDS
SOURCE         Human enterovirus B
ORGANISM       Human enterovirus B
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
               Diabetes Associated with Enterovirus RNA
JOURNAL        J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED        12721936
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Direct Submission
JOURNAL        Submitted (29-NOV-2002) Virology Division, South Eastern Area
               Laboratory Services, University of New South Wales/Prince of Wales
               Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES       source
               1..116
               /organism="Human enterovirus B"
               /mol_type="genomic RNA"
               /isolate="NSW/14/97"
               /db_xref="taxon:138949"
               <1..>116
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ORIGIN
Query Match    100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  TCCGCTGCAGAGTTGCCGTTACGA 25
Db  74 TCCGCTGCAGAGTTGCCGTTACGA 50

RESULT 15
AY189163/c
LOCUS          Human enterovirus B isolate NSW/16/97 5' UTR, partial sequence.
DEFINITION
ACCESSION      AY189163
VERSION        AY189163.1  GI:28274386
KEYWORDS
SOURCE         Human enterovirus B
ORGANISM       Human enterovirus B
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
               Diabetes Associated with Enterovirus RNA
JOURNAL        J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED        12721936
REFERENCE
AUTHORS        Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE          Direct Submission
JOURNAL        Submitted (29-NOV-2002) Virology Division, South Eastern Area
               Laboratory Services, University of New South Wales/Prince of Wales
               Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES       source
               1..116
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/mol type="genomic RNA"
/isolate="NSW/16/97"
/db_xref="taxon:138949"
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Query Match      100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 16
AY189164/c
LOCUS      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/17/97 5' UTR, partial sequence.
ACCESSION  AY189164
VERSION     AY189164.1 GI:28274387
KEYWORDS   Human enterovirus B
SOURCE     Human enterovirus B
ORGANISM   Human enterovirus B
VIRUSES; sRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 116)
AUTHORS   Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE     Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL   J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED    12721936
REFERENCE  2 (bases 1 to 116)
AUTHORS   Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
            1..116
            /organism="Human enterovirus B"
            /mol type="genomic RNA"
            /isolate="NSW/17/97"
            /db_xref="taxon:138949"
            <1..>116

5'UTR
ORIGIN
Query Match      100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 17
AY189166/c
LOCUS      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus NSW/23/97 5' UTR, partial sequence.
ACCESSION  AY189166
VERSION     AY189166.1 GI:28274389
KEYWORDS   Human enterovirus NSW/23/97
SOURCE     Human enterovirus NSW/23/97
ORGANISM   Human enterovirus NSW/23/97
VIRUSES; sRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 116)
AUTHORS   Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE     Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL   J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED    12721936

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2 (bases 1 to 116)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
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            /organism="Human enterovirus NSW/23/97"
            /mol type="genomic RNA"
            /isolate="NSW/23/97"
            /db_xref="taxon:220228"
            <1..>116

5'UTR
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 18
AY189167/c
LOCUS      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/25/97 5' UTR, partial sequence.
ACCESSION  AY189167
VERSION     AY189167.1 GI:28274390
KEYWORDS   Human enterovirus B
SOURCE     Human enterovirus B
ORGANISM   Human enterovirus B
VIRUSES; sRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE  1 (bases 1 to 116)
AUTHORS   Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE     Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
          Diabetes Associated with Enterovirus RNA
JOURNAL   J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED    12721936
REFERENCE  2 (bases 1 to 116)
AUTHORS   Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE     Direct Submission
JOURNAL   Submitted (29-NOV-2002) Virology Division, South Eastern Area
          Laboratory Services, University of New South Wales/Prince of Wales
          Hospital, High Street, Randwick, NSW 2031, Australia
FEATURES   Location/Qualifiers
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            /db_xref="taxon:138949"
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RESULT 19
AY189169/c
LOCUS      116 bp      RNA      linear      VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/45/97 5' UTR, partial sequence.
ACCESSION  AY189169
VERSION     AY189169.1 GI:28274392
KEYWORDS   Human enterovirus B
SOURCE     Human enterovirus B

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ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 20
AY189170/c
LOCUS Human enterovirus B isolate NSW/48/97 5' UTR, partial sequence.
ACCESSION AY189170
VERSION AY189170.1 GI:28274393
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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RESULT 21
AY189171/c
LOCUS Human enterovirus B isolate NSW/60/97 5' UTR, partial sequence.
ACCESSION AY189171
VERSION AY189171.1 GI:28274394
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 22
AY189173/c
LOCUS Human enterovirus B isolate NSW/73/97 5' UTR, partial sequence.
ACCESSION AY189173
VERSION AY189173.1 GI:28274396
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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            /db_xref="taxon:138949"
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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Query Match      100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 23
AY189174/c
LOCUS AY189174 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/76/97 5' UTR, partial sequence.
ACCESSION AY189174
VERSION AY189174.1 GI:28274397
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 24
AY189175/c
LOCUS AY189175 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/82/97 5' UTR, partial sequence.
ACCESSION AY189175
VERSION AY189175.1 GI:28274398
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Hospital, High Street, Randwick, NSW 2031, Australia
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 25
AY189176/c
LOCUS AY189176 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/83/97 5' UTR, partial sequence.
ACCESSION AY189176
VERSION AY189176.1 GI:28274399
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
JOURNAL J. Infect. Dis. 187 (10), 1562-1570 (2003)
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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ORIGIN

Query Match      100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 26
AY189180/c
LOCUS AY189180 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/111/98 5' UTR, partial sequence.
ACCESSION AY189180
VERSION AY189180.1 GI:28274403
KEYWORDS
SOURCE
ORGANISM Human enterovirus B
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.

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TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
12721936  
PUBMED  
2 (bases 1 to 116)  
REFERENCE Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
AUTHORS Direct Submission  
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area  
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
LOCATION/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50  
RESULT 27  
AY189183/c  
LOCUS Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.  
DEFINITION Human enterovirus B isolate NSW/141/98 5' UTR, partial sequence.  
ACCESSION AY189183  
VERSION AY189183.1 GI:28274406  
KEYWORDS  
SOURCE Human enterovirus B  
ORGANISM Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
JOURNAL 12721936  
PUBMED  
2 (bases 1 to 116)  
REFERENCE Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
AUTHORS Direct Submission  
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area  
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
LOCATION/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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|||||  
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50  
RESULT 28  
AY189184/c  
LOCUS Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.  
DEFINITION Human enterovirus B isolate NSW/143/98 5' UTR, partial sequence.

AY189184  
AY189184.1 GI:28274407  
Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
JOURNAL 12721936  
PUBMED  
2 (bases 1 to 116)  
REFERENCE Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
AUTHORS Direct Submission  
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area  
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
LOCATION/Qualifiers  
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/isolate="NSW/143/98"  
/db\_xref="taxon:138949"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50  
RESULT 29  
AY189186/c  
LOCUS Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.  
DEFINITION Human enterovirus B isolate NSW/147/98 5' UTR, partial sequence.  
ACCESSION AY189186  
VERSION AY189186.1 GI:28274409  
KEYWORDS  
SOURCE Human enterovirus B  
ORGANISM Human enterovirus B  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 116)  
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
TITLE Reduced Frequency of HLA DRB1\*03-DQB1\*02 in Children with Type 1 Diabetes Associated with Enterovirus RNA  
J. Infect. Dis. 187 (10), 1562-1570 (2003)  
JOURNAL 12721936  
PUBMED  
2 (bases 1 to 116)  
REFERENCE Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.  
AUTHORS Direct Submission  
TITLE Submitted (29-NOV-2002) Virology Division, South Eastern Area  
JOURNAL Laboratory Services, University of New South Wales/Prince of Wales Hospital, High Street, Randwick, NSW 2031, Australia  
LOCATION/Qualifiers  
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/isolate="NSW/147/98"  
/db\_xref="taxon:138949"  
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Query Match 100.0%; Score 25; DB 13; Length 116;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 30
AY189187/c
LOCUS Human enterovirus B 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/149/98 5' UTR, partial sequence.
ACCESSION AY189187
VERSION AY189187.1 GI:28274410
KEYWORDS Human enterovirus B
SOURCE Human enterovirus B
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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/isolate="NSW/149/98"
/db_xref="taxon:138949"
<1. .>116

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Query Match 100.0%; Score 25; DB 13; Length 116;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 31
AY189191/c
LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/156/98 5' UTR, partial sequence.
ACCESSION AY189191
VERSION AY189191.1 GI:28274414
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 32
AY189192/c
LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION AY189192
VERSION AY189192.1 GI:28274415
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/166/98 5' UTR, partial sequence.
ACCESSION AY189195
VERSION AY189195.1 GI:28274418
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 32
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LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/157/98 5' UTR, partial sequence.
ACCESSION AY189192
VERSION AY189192.1 GI:28274415
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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DEFINITION Human enterovirus 71 isolate NSW/166/98 5' UTR, partial sequence.
ACCESSION AY189195
VERSION AY189195.1 GI:28274418
KEYWORDS Human enterovirus 71
SOURCE Human enterovirus 71
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL 12721936
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig, M.E., Howard, N.J., Silink, M. and Rawlinson, W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50
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PUBMED
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 34
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DEFINITION Human enterovirus 71 isolate NSW/169/98 5' UTR, partial sequence.
ACCESSION AY189196
VERSION AY189196.1 GI:28274419
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 35
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DEFINITION Human enterovirus 71 isolate NSW/180/98 5' UTR, partial sequence.
ACCESSION AY189198
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VERSION AY189198.1 GI:28274421
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ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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LOCUS AY189199 Human enterovirus 71 isolate NSW/182/98 5' UTR linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/182/98 5' UTR, partial sequence.
ACCESSION AY189199
VERSION AY189199.1 GI:28274422
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
PUBMED 12721936
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/194/99 5' UTR, partial sequence.
ACCESSION AY189201
VERSION AY189201.1 GI:28274424
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 38
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LOCUS Human enterovirus 71 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus 71 isolate NSW/196/99 5' UTR, partial sequence.
ACCESSION AY189202
VERSION AY189202.1 GI:28274425
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 39
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LOCUS Human enterovirus B 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/208/99 5' UTR, partial sequence.
ACCESSION AY189206
VERSION AY189206.1 GI:28274429
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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RESULT 40
AY189215/c
LOCUS Human enterovirus B 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
ACCESSION AY189215
VERSION AY189215.1 GI:28274438
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 41
AY189215/c
LOCUS Human enterovirus B 116 bp RNA linear VRL 08-MAY-2003
DEFINITION Human enterovirus B isolate NSW/338/99 5' UTR, partial sequence.
ACCESSION AY189215
VERSION AY189215.1 GI:28274438
KEYWORDS
SOURCE Human enterovirus B
ORGANISM Human enterovirus B
REFERENCE 1 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
JOURNAL Diabetes Associated with Enterovirus RNA
PUBMED J. Infect. Dis. 187 (10), 1562-1570 (2003)
REFERENCE 2 (bases 1 to 116)
AUTHORS Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
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J. Infect. Dis. 187 (10), 1562-1570 (2003)
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PUBMED
AUTHORS
TITLE
JOURNAL
SUBMITTED (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

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DEFINITION
Human enterovirus 71 genomic RNA, 5' UTR, partial sequence,
isolate: 2279/EV71/Hyogo/2003.
ACCESSION
AB183003
VERSION
AB183003.1 GI:49614920
KEYWORDS
Human enterovirus 71
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 Fujimoto,T., Yoshida,S., Munemura,T., Yoshida,H., Chikahira,M. and
Nishio,O.
Enterovirus 71 sequence detected from cerebrospinal fluid
Unpublished
JOURNAL
REFERENCE
2 (bases 1 to 117)
Fujimoto,T., Munemura,T. and Chikahira,M.
Direct Submission
Submitted (30-JUN-2004) Taiguto Fujimoto, Hyogo Prefectural
Institute of Public Health and Environmental Sciences, Infectious
Disease Research Division; 2-1-29, Arata-Cho, Hyogo-Ku, Kobe, Hyogo
652-0032, Japan (E-mail:Taiguto-Fujimoto@pref.hyogo.jp,
URL:http://www.iphes.pref.hyogo.jp/, Tel:81-78-511-6640(ex.236),
Fax:81-78-531-7080)
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RESULT 42
AY189205/c
LOCUS
DEFINITION
Human enterovirus B isolate NSW/204/99 5' UTR, partial sequence.
ACCESSION
AY189205
VERSION
AY189205.1 GI:28274428
KEYWORDS
Human enterovirus B
SOURCE
Human enterovirus B
ORGANISM
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 117)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Reduced Frequency of HLA DRB1*03-DQB1*02 in Children with Type 1
Diabetes Associated with Enterovirus RNA
J. Infect. Dis. 187 (10), 1562-1570 (2003)
JOURNAL
PUBMED
1271936
REFERENCE
2 (bases 1 to 117)
Craig,M.E., Howard,N.J., Silink,M. and Rawlinson,W.D.
Direct Submission
Submitted (29-NOV-2002) Virology Division, South Eastern Area
Laboratory Services, University of New South Wales/Prince of Wales
Hospital, High Street, Randwick, NSW 2031, Australia
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Db 74 TCCGCTGCAGAGTTGCCCGTTACGA 50

RESULT 43
AF314005/c
LOCUS
DEFINITION
Enterovirus 5656/SIN/002209 5' UTR, partial sequence.
ACCESSION
AF314005
VERSION
AF314005.2 GI:13111668
KEYWORDS
Enterovirus 5656/SIN/002209
SOURCE
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 154)
Singh,S., Chow,V.T.K., Phoon,M.C., Chan,K.P. and Poh,C.L.
Direct Detection of Enterovirus 71 (EV71) in Clinical Specimens
from a Hand Foot, and Mouth Disease Outbreak in Singapore by
Reverse Transcription-PCR with Universal Enterovirus and
EV71-Specific Primers
J. Clin. Microbiol. 40 (8), 2823-2827 (2002)
JOURNAL
PUBMED
12149336
REFERENCE
2 (bases 1 to 154)
Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (18-OCT-2000) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
3 (bases 1 to 154)
Singh,S., Chow,V.T.K. and Poh,C.L.
Direct Submission
Submitted (23-FEB-2001) Microbiology, National University of
Singapore, 5 Science Drive 2, Singapore 117597, Singapore
Sequence update by submitter
On Feb 23, 2001 this sequence version replaced gi:12667228.
REMARK
COMMENT
Location/Qualifiers
FEATURES

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DEFINITION Human coxsackievirus B3 isolate subject 6 5' UTR.
ACCESSION AY626235
VERSION AV626235.1 GI:48526363
KEYWORDS
SOURCE Human coxsackievirus B3
ORGANISM Human coxsackievirus B3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE Coxsackievirus B in myocardium tissue
JOURNAL Unpublished
AUTHORS Lednicky, J.A. and Ohr, J.S.
REFERENCE 2 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
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LOCUS AV626236 162 bp RNA linear VRL 15-JUN-2004
DEFINITION Human coxsackievirus B3 isolate subject 9 5' UTR.
ACCESSION AY626236
VERSION AV626236.1 GI:48526364
KEYWORDS
SOURCE Human coxsackievirus B3
ORGANISM Human coxsackievirus B3
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE 5' untranslated region (5' UTR) of Human coxsackievirus B in
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myocardium tissue of subject 9
Unpublished
2 (bases 1 to 162)
AUTHORS Lednicky, J.A. and Ohr, J.S.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-2004) Pathology, Loyola University Medical
Center, 2160 South First Avenue, Maywood, IL 60153, USA
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Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51
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DEFINITION Human enterovirus 71 partial 5'UTR, strain /di/Roma98.
ACCESSION AJ312088
VERSION AJ312088.1 GI:16555706
KEYWORDS
SOURCE Human enterovirus 71
ORGANISM Human enterovirus 71
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1
AUTHORS Manzara, S., Muscillo, M., La Rosa, G., Marianelli, C., Cattani, P. and
Fadda, G.
TITLE Molecular identification and typing of enteroviruses isolated from
clinical specimens
JOURNAL J. Clin. Microbiol. 40 (12), 4554-4560 (2002)
PUBMED 12454151
REFERENCE 2 (bases 1 to 172)
AUTHORS Muscillo, M.
TITLE Direct Submission
JOURNAL Submitted (08-MAY-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
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    SOURCE Echovirus sp.
    ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
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REFERENCE 1
AUTHORS Muscillo,M., La Rosa,G., Marianelli,C., Capobianchi,M.R.,
Zaniratti,S., Cattani,P., Manzara,S., Fadda,G., Comparcola,D. and
Ticca,F.
TITLE A phylogenetic analysis of the two echovirus 30 isolated in Rome
(Italy) in 1997 from an outbreak of aseptic meningitis associated
with swimming pools
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 177)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (03-NOV-2000) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita', Viale Regina Elena 299, Rome, RM
00161, Italy
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LOCUS AF521433 Human echovirus 30 isolate BE00-14 5' UTR, partial sequence.
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ACCESSION AF521433
VERSION AF521433.1 GI:31790775
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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DEFINITION
ACCESSION AF521436
VERSION AF521436.1 GI:31790778
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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DEFINITION
ACCESSION AF521436
VERSION AF521436.1 GI:31790778
KEYWORDS Human echovirus 30
SOURCE Human echovirus 30
ORGANISM Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE 2 (bases 1 to 185)
AUTHORS Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
Lindberg,M.A. and Van Ranst,M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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LOCUS AF521447 185 bp RNA linear VRL 17-JUN-2003  
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ACCESSION AF521447  
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KEYWORDS  
SOURCE  
ORGANISM Human echovirus 30  
Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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ACCESSION AF521449  
VERSION AF521449.1 GI:31790791  
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SOURCE Human echovirus 30  
Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
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ACCESSION AF521450  
VERSION AF521450.1 GI:31790792  
KEYWORDS  
SOURCE Human echovirus 30  
Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M. and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, M.A. and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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LOCUS AF521451/c  
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VERSION AF521451.1 GI:31790793  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
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LOCUS AF521451/c  
DEFINITION Human echovirus 30 isolate BE00-34 5' UTR, partial sequence.  
ACCESSION AF521451  
VERSION AF521451.1 GI:31790793  
KEYWORDS

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SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 56
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LOCUS      AF521474
DEFINITION Human echovirus 30 isolate BE00-43 5' UTR, partial sequence.
ACCESSION AF521474
VERSION    AF521474.1 GI:31790800
KEYWORDS   .
SOURCE     Human echovirus 30
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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ACCESSION AF521461
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SOURCE     Human echovirus 30
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            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED    12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
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            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 56
AF521474/c
LOCUS      AF521474
DEFINITION Human echovirus 30 isolate BE00-16 5' UTR, partial sequence.
ACCESSION AF521474
VERSION    AF521474.1 GI:31790816
KEYWORDS   .
SOURCE     Human echovirus 30
ORGANISM   Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)

```

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers  
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/viral  
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
98 TCCGCTGCAGAGTTGCCCGTTACGA 74

Db

RESULT 57  
AF521475/c

LOCUS Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.

DEFINITION AF521475

ACCESSION AF521475.1 GI:31790817

VERSION

KEYWORDS

SOURCE Human echovirus 30

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers  
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/organism="Human echovirus 30"  
/viral  
/mol\_type="genomic RNA"  
/isolate="BE00-17"  
/isolation\_source="patient 17 - zipcode Belgium 3550"  
/db\_xref="taxon:41846"  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
98 TCCGCTGCAGAGTTGCCCGTTACGA 74

Db

RESULT 57  
AF521475/c

LOCUS Human echovirus 30 isolate BE00-17 5' UTR, partial sequence.

DEFINITION AF521475

ACCESSION AF521475.1 GI:31790817

VERSION

KEYWORDS

SOURCE Human echovirus 30

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers  
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/viral  
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/isolate="BE00-17"  
/isolation\_source="patient 17 - zipcode Belgium 3550"  
/db\_xref="taxon:41846"  
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5'UTR  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
98 TCCGCTGCAGAGTTGCCCGTTACGA 74

Db

RESULT 59  
AF521477/c

LOCUS Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.

DEFINITION AF521477

ACCESSION AF521477.1 GI:31790819

VERSION

KEYWORDS

SOURCE Human echovirus 30

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

Query Match 100.0%; Score 25; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
98 TCCGCTGCAGAGTTGCCCGTTACGA 74

Db

RESULT 58  
AF521476/c

LOCUS Human echovirus 30 isolate BE00-18 5' UTR, partial sequence.

DEFINITION AF521476

ACCESSION AF521476.1 GI:31790818

VERSION

KEYWORDS

SOURCE Human echovirus 30

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)

PUBMED 12767006

REFERENCE 2 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

TITLE Direct Submission

JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source Location/Qualifiers  
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/organism="Human echovirus 30"  
/viral  
/mol\_type="genomic RNA"  
/isolate="BE00-18"  
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/db\_xref="taxon:41846"  
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5'UTR  
ORIGIN

Query Match 100.0%; Score 25; DB 13; Length 185;  
Best Local Similarity 100.0%; Pred. No. 0.32;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
98 TCCGCTGCAGAGTTGCCCGTTACGA 74

Db

RESULT 59  
AF521477/c

LOCUS Human echovirus 30 isolate BE00-19 5' UTR, partial sequence.

DEFINITION AF521477

ACCESSION AF521477.1 GI:31790819

VERSION

KEYWORDS

SOURCE Human echovirus 30

ORGANISM Human echovirus 30

REFERENCE 1 (bases 1 to 185)

AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

TITLE Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

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J. Med. Virol. 70 (3), 420-429 (2003)
12767006
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Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
FEATURES
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        /viroion
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        /db_xref="taxon:41846"
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|||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
|||||

RESULT 60
AF521478/c
LOCUS AF521478 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-20 5' UTR, partial sequence.
ACCESSION AF521478
VERSION AF521478.1 GI:31790820
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
FEATURES
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        1. .185
        /organism="Human echovirus 30"
        /viroion
        /mol_type="genomic RNA"
        /isolate="BE00-20"
        /isolation_source="patient 20 - zipcode Belgium 3294"
        /db_xref="taxon:41846"
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Query Match 100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
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RESULT 61
AF521483/c
LOCUS AF521483 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-74 5' UTR, partial sequence.
ACCESSION AF521483
VERSION AF521483.1 GI:31790825
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
Location/Qualifiers
FEATURES
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        1. .185
        /organism="Human echovirus 30"
        /viroion
        /mol_type="genomic RNA"
        /isolate="BE00-74"
        /isolation_source="patient 74 - zipcode Belgium 8930"
        /db_xref="taxon:41846"
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ORIGIN
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
|||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74
|||||

RESULT 62
AF521485/c
LOCUS AF521485 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-76 5' UTR, partial sequence.
ACCESSION AF521485
VERSION AF521485.1 GI:31790827
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE 1 (bases 1 to 185)
AUTHORS Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
2 (bases 1 to 185)
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.

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TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source  
1..185  
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/viroion  
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/db\_xref="taxon:41846"  
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ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 63  
AF521486/c  
LOCUS AF521486 Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.  
DEFINITION AF521486  
ACCESSION AF521486.1 GI:31790828  
VERSION AF521486.1  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

TITLE  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE  
2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
Direct Submission  
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
source  
1..185  
/organism="Human echovirus 30"  
/viroion  
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/isolation\_source="patient 77 - zipcode Belgium 8560"  
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ORIGIN

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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 64  
AF521486/c  
LOCUS AF521486 Human echovirus 30 isolate BE00-77 5' UTR, partial sequence.  
DEFINITION AF521486  
ACCESSION AF521486.1 GI:31790828  
VERSION AF521486.1  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

TITLE  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE  
2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
Direct Submission  
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

AF521492/c  
LOCUS AF521492 Human echovirus 30 isolate BE00-83 5' UTR, partial sequence.  
DEFINITION AF521492  
ACCESSION AF521492.1 GI:31790834  
VERSION AF521492.1  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

TITLE  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE  
2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
Direct Submission  
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

FEATURES  
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 65  
AF521495/c  
LOCUS AF521495 Human echovirus 30 isolate BE00-58 5' UTR, partial sequence.  
DEFINITION AF521495  
ACCESSION AF521495.1 GI:31790837  
VERSION AF521495.1  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.

REFERENCE  
1 (bases 1 to 185)  
Thoelen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.  
Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

TITLE  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE  
2 (bases 1 to 185)  
Thoelen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.  
Direct Submission  
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium





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/isolate="BE00-67"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 69
AF521505/c
LOCUS      AF521505      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-68 5' UTR, partial sequence.
ACCESSION  AF521505
VERSION     AF521505.1 GI:31790847
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
JOURNAL    J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES   source
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            /viroion
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Query Match      100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 70
AF521515/c
LOCUS      AF521515      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-90 5' UTR, partial sequence.
ACCESSION  AF521515
VERSION     AF521515.1 GI:31790857
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.

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1 (bases 1 to 185)
Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
Lindberg,A.M. and Van Ranst,M.
Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
FEATURES   source
            1..185
            /organism="Human echovirus 30"
            /viroion
            /mol_type="genomic RNA"
            /isolate="BE00-90"
            /isolation_source="patient 90 - zipcode Belgium 8560"
            /db_xref="taxon:41846"
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ORIGIN

Query Match      100.0%; Score 25; DB 13; Length 185;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 71
AF521517/c
LOCUS      AF521517      185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-92 5' UTR, partial sequence.
ACCESSION  AF521517
VERSION     AF521517.1 GI:31790859
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
            Viruses; ssRNA positive-strand viruses, no DNA stage;
            Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
            Lindberg,A.M. and Van Ranst,M.
TITLE      Molecular typing and epidemiology of enteroviruses identified from
            an outbreak of aseptic meningitis in Belgium during the summer of
            2000
J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED     12767006
REFERENCE   2 (bases 1 to 185)
AUTHORS    Thoelen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
            Lindberg,M.A. and Van Ranst,M.
TITLE      Direct Submission
JOURNAL    Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
            Virology, Department of Microbiology and Immunology, Rega Institute
            for Medical Research, University of Leuven, Minderbroedersstraat
            10, Leuven BE-3000, Belgium
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ORIGIN

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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 72
AF521519/c
LOCUS          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-95 5' UTR, partial sequence.
ACCESSION     AF521519
VERSION       AF521519.1 GI:31790861
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,A.M. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of
               2000
JOURNAL       J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED        12767006
AUTHORS       Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 73
AF521525/c
LOCUS          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-54 5' UTR, partial sequence.
ACCESSION     AF521525
VERSION       AF521525.1 GI:31790867
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,A.M. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of

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2000
J. Med. Virol. 70 (3), 420-429 (2003)
12767006
REFERENCE     2 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 74
AF521538/c
LOCUS          185 bp      RNA      linear      VRL 17-JUN-2003
DEFINITION    Human echovirus 30 isolate BE00-111 5' UTR, partial sequence.
ACCESSION     AF521538
VERSION       AF521538.1 GI:31790890
KEYWORDS
SOURCE        Human echovirus 30
ORGANISM      Human echovirus 30
               Viruses; ssRNA positive-strand viruses, no DNA stage;
               Picornaviridae; Enterovirus.
REFERENCE     1 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemey,P., Van Der Donck,I., Beuselinck,K.,
               Lindberg,A.M. and Van Ranst,M.
TITLE         Molecular typing and epidemiology of enteroviruses identified from
               an outbreak of aseptic meningitis in Belgium during the summer of
               2000
JOURNAL       J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED        12767006
REFERENCE     2 (bases 1 to 185)
AUTHORS       Thoenen,I., Lemey,P., van der Donck,I., Beuselinck,K.,
               Lindberg,M.A. and Van Ranst,M.
TITLE         Direct Submission
JOURNAL       Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
               Virology, Department of Microbiology and Immunology, Rega Institute
               for Medical Research, University of Leuven, Minderbroedersstraat
               10, Leuven BE-3000, Belgium
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 75
AF521539/c
LOCUS AF521539 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 7 isolate BE00-113 5' UTR, partial sequence.
ACCESSION AF521539
VERSION AF521539.1 GI:31790881
KEYWORDS
SOURCE Human echovirus 7
ORGANISM Human echovirus 7
REFERENCE
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
AUTHORS 2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 76
AF521542/c
LOCUS AF521542 185 bp RNA linear VRL 17-JUN-2003
DEFINITION Human echovirus 30 isolate BE00-116 5' UTR, partial sequence.
ACCESSION AF521542
VERSION AF521542.1 GI:31790884
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
REFERENCE
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
AUTHORS 2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,

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Lindberg, M.A. and Van Ranst, M.
Direct Submission
Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

RESULT 77
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DEFINITION Human coxsackievirus B4 isolate BE00-117 5' UTR, partial sequence.
ACCESSION AF521543
VERSION AF521543.1 GI:31790885
KEYWORDS
SOURCE Human coxsackievirus B4
ORGANISM Human coxsackievirus B4
REFERENCE
AUTHORS Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
1 (bases 1 to 185)
Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,
Lindberg, A.M. and Van Ranst, M.
TITLE Molecular typing and epidemiology of enteroviruses identified from
an outbreak of aseptic meningitis in Belgium during the summer of
2000
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)
PUBMED 12767006
REFERENCE
AUTHORS 2 (bases 1 to 185)
Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,
Lindberg, M.A. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological
Virology, Department of Microbiology and Immunology, Rega Institute
for Medical Research, University of Leuven, Minderbroedersstraat
10, Leuven BE-3000, Belgium
LOCATION/Qualifiers
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74

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RESULT 78  
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LOCUS AF521546 185 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-120 5' UTR, partial sequence.  
ACCESSION AF521546  
VERSION AF521546.1 GI:31790888  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen,I., Lemeey,P., Van Der Donck,I., Beuselinck,K.,  
Lindberg,A.M. and Van Ranst,M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
J. Med. Virol. 70 (3), 420-429 (2003)  
JOURNAL  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen,I., Lemeey,P., van der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
RESULT 79  
AF521547/c  
LOCUS AF521547 185 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-121 5' UTR, partial sequence.  
ACCESSION AF521547  
VERSION AF521547.1 GI:31790889  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen,I., Lemeey,P., Van Der Donck,I., Beuselinck,K.,  
Lindberg,A.M. and Van Ranst,M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
J. Med. Virol. 70 (3), 420-429 (2003)  
JOURNAL  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen,I., Lemeey,P., van der Donck,I., Beuselinck,K.,  
Lindberg,M.A. and Van Ranst,M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat

10, Leuven BE-3000, Belgium  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
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LOCUS AY342855 185 bp RNA linear VRL 04-MAR-2004  
DEFINITION Human echovirus 30 patient BE00-CC2313 5' UTR, partial sequence.  
ACCESSION AY342855  
VERSION AY342855.1 GI:37623508  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 185)  
AUTHORS Thoelen,I., Moes,E., Lemeey,P., Mostmans,S., Wollants,E.,  
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.  
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'  
noncoding region in an epidemiological survey of the human  
enterovirus B species  
J. Clin. Microbiol. 42 (3), 963-971 (2004)  
JOURNAL  
REFERENCE 2 (bases 1 to 185)  
AUTHORS Thoelen,I., Moes,E., Lemeey,P., Mostmans,S., Wollants,E.,  
Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,  
Laboratory of Clinical and Epidemiological Virology, Rega Institute  
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
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LOCUS AF521454 186 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-37 5' UTR, partial sequence.  
ACCESSION AF521454  
VERSION AF521454.1 GI:31790796  
KEYWORDS

SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 186)  
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M., and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 186)  
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M., and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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Db 98 TCCGCTGCAGAGTTGCCCGTTACGA 74  
RESULT 82  
AF521479/c  
LOCUS AF521479 186 bp RNA linear VRL 17-JUN-2003  
DEFINITION Human echovirus 30 isolate BE00-23 5' UTR, partial sequence.  
ACCESSION AF521479  
VERSION AF521479.1 GI:31790821  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 186)  
AUTHORS Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K.,  
Lindberg, A.M., and Van Ranst, M.  
TITLE Molecular typing and epidemiology of enteroviruses identified from  
an outbreak of aseptic meningitis in Belgium during the summer of  
2000  
JOURNAL J. Med. Virol. 70 (3), 420-429 (2003)  
PUBMED 12767006  
REFERENCE 2 (bases 1 to 186)  
AUTHORS Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K.,  
Lindberg, A.M., and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological  
Virology, Department of Microbiology and Immunology, Rega Institute  
for Medical Research, University of Leuven, Minderbroedersstraat  
10, Leuven BE-3000, Belgium  
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RESULT 83  
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ACCESSION AY343038  
VERSION AY343038.1 GI:37623691  
KEYWORDS  
SOURCE Human echovirus 5  
ORGANISM Human echovirus 5  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 186)  
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.  
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'  
noncoding region in an epidemiological survey of the human  
enterovirus B species  
JOURNAL J. Clin. Microbiol. 42 (3), 963-971 (2004)  
REFERENCE 2 (bases 1 to 186)  
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,  
Laboratory of Clinical and Epidemiological Virology, Rega Institute  
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium  
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DEFINITION Human echovirus 30 patient BE02-7181 5' UTR, partial sequence.  
ACCESSION AY343032  
VERSION AY343032.1 GI:37623685  
KEYWORDS  
SOURCE Human echovirus 30  
ORGANISM Human echovirus 30  
Viruses; ssRNA positive-strand viruses, no DNA stage;  
Picornaviridae; Enterovirus.  
REFERENCE 1 (bases 1 to 187)  
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

**TITLE** Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

**JOURNAL** J. Clin. Microbiol. 42 (3), 963-971 (2004)

**REFERENCE** 2 (bases 1 to 187)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

**FEATURES** Location/Qualifiers

**source** 1..187

**5'UTR** /organism="Human echovirus 30"

**ORIGIN** /mol\_type="genomic RNA"

**Query Match** 100.0%; Score 25; DB 13; Length 187;

**Best Local Similarity** 100.0%; Pred. No. 0.32;

**Matches** 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 TCCGCTGCAGAGTTGCCGTTACGA 25

**Db** 101 TCCGCTGCAGAGTTGCCGTTACGA 77

**RESULT 85**

**AF521468/c**

**LOCUS** AF521468 Human echovirus 30 isolate BE00-26 5' UTR, partial sequence. VRL 17-JUN-2003

**DEFINITION** Human echovirus 30 isolate BE00-26 5' UTR, partial sequence.

**ACCESSION** AF521468

**VERSION** AF521468.1 GI:31790810

**KEYWORDS** 1 (bases 1 to 188)

**SOURCE** Human echovirus 30

**ORGANISM** Human echovirus 30

**REFERENCE** 1 (bases 1 to 188)

**AUTHORS** Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 188)

**AUTHORS** Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

**FEATURES** Location/Qualifiers

**source** 1..188

**5'UTR** /organism="Human echovirus 30"

**ORIGIN** /mol\_type="genomic RNA"

**Query Match** 100.0%; Score 25; DB 13; Length 188;

**Best Local Similarity** 100.0%; Pred. No. 0.32;

**Matches** 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 TCCGCTGCAGAGTTGCCGTTACGA 25

**Db** 101 TCCGCTGCAGAGTTGCCGTTACGA 77

**RESULT 86**

**AF342837/c**

**LOCUS** AF342837 Human echovirus 11 patient BE99-135 5' UTR, partial sequence. VRL 04-MAR-2004

**DEFINITION** Human echovirus 11 patient BE99-135 5' UTR, partial sequence.

**ACCESSION** AF342837

**VERSION** AF342837.1 GI:37623490

**KEYWORDS** 1 (bases 1 to 188)

**SOURCE** Human echovirus 11

**ORGANISM** Human echovirus 11

**REFERENCE** 1 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

**JOURNAL** J. Clin. Microbiol. 42 (3), 963-971 (2004)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

**FEATURES** Location/Qualifiers

**source** 1..188

**5'UTR** /organism="Human echovirus 11"

**ORIGIN** /mol\_type="genomic RNA"

**Query Match** 100.0%; Score 25; DB 13; Length 188;

**Best Local Similarity** 100.0%; Pred. No. 0.32;

**Matches** 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 TCCGCTGCAGAGTTGCCGTTACGA 25

**Db** 101 TCCGCTGCAGAGTTGCCGTTACGA 77

**RESULT 87**

**AF342838/c**

**LOCUS** AF342838 Human echovirus 11 patient BE99-1509 5' UTR, partial sequence. VRL 04-MAR-2004

**DEFINITION** Human echovirus 11 patient BE99-1509 5' UTR, partial sequence.

**ACCESSION** AF342838

**VERSION** AF342838.1 GI:37623491

**KEYWORDS** 1 (bases 1 to 188)

**SOURCE** Human echovirus 11

**ORGANISM** Human echovirus 11

**REFERENCE** 1 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

**JOURNAL** J. Clin. Microbiol. 42 (3), 963-971 (2004)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2003) Department of Microbiology and Immunology,

**TITLE** Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

**JOURNAL** J. Clin. Microbiol. 42 (3), 963-971 (2004)

**REFERENCE** 2 (bases 1 to 187)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2003) Department of Microbiology and Immunology, Laboratory of Clinical and Epidemiological Virology, Rega Institute for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

**FEATURES** Location/Qualifiers

**source** 1..187

**5'UTR** /organism="Human echovirus 30"

**ORIGIN** /mol\_type="genomic RNA"

**Query Match** 100.0%; Score 25; DB 13; Length 187;

**Best Local Similarity** 100.0%; Pred. No. 0.32;

**Matches** 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 TCCGCTGCAGAGTTGCCGTTACGA 25

**Db** 101 TCCGCTGCAGAGTTGCCGTTACGA 77

**RESULT 85**

**AF521468/c**

**LOCUS** AF521468 Human echovirus 30 isolate BE00-26 5' UTR, partial sequence. VRL 17-JUN-2003

**DEFINITION** Human echovirus 30 isolate BE00-26 5' UTR, partial sequence.

**ACCESSION** AF521468

**VERSION** AF521468.1 GI:31790810

**KEYWORDS** 1 (bases 1 to 188)

**SOURCE** Human echovirus 30

**ORGANISM** Human echovirus 30

**REFERENCE** 1 (bases 1 to 188)

**AUTHORS** Thoenen, I., Lemey, P., Van Der Donck, I., Beuselinck, K., Lindberg, A.M. and Van Ranst, M.

**TITLE** Molecular typing and epidemiology of enteroviruses identified from an outbreak of aseptic meningitis in Belgium during the summer of 2000

**JOURNAL** J. Med. Virol. 70 (3), 420-429 (2003)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 188)

**AUTHORS** Thoenen, I., Lemey, P., van der Donck, I., Beuselinck, K., Lindberg, M.A. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (12-JUN-2002) Laboratory of Clinical & Epidemiological Virology, Department of Microbiology and Immunology, Rega Institute for Medical Research, University of Leuven, Minderbroedersstraat 10, Leuven BE-3000, Belgium

**FEATURES** Location/Qualifiers

**source** 1..188

**5'UTR** /organism="Human echovirus 30"

**ORIGIN** /mol\_type="genomic RNA"

**Query Match** 100.0%; Score 25; DB 13; Length 188;

**Best Local Similarity** 100.0%; Pred. No. 0.32;

**Matches** 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Qy** 1 TCCGCTGCAGAGTTGCCGTTACGA 25

**Db** 101 TCCGCTGCAGAGTTGCCGTTACGA 77

**RESULT 86**

**AF342837/c**

**LOCUS** AF342837 Human echovirus 11 patient BE99-135 5' UTR, partial sequence. VRL 04-MAR-2004

**DEFINITION** Human echovirus 11 patient BE99-135 5' UTR, partial sequence.

**ACCESSION** AF342837

**VERSION** AF342837.1 GI:37623490

**KEYWORDS** 1 (bases 1 to 188)

**SOURCE** Human echovirus 11

**ORGANISM** Human echovirus 11

**REFERENCE** 1 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Analysis of the serotype and genotype correlation of VP1 and the 5' noncoding region in an epidemiological survey of the human enterovirus B species

**JOURNAL** J. Clin. Microbiol. 42 (3), 963-971 (2004)

**PUBMED** 12767006

**REFERENCE** 2 (bases 1 to 188)

**AUTHORS** Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E., Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.

**TITLE** Direct Submission

**JOURNAL** Submitted (16-JUL-2003) Department of Microbiology and Immunology,

FEATURES source  
 Laboratory of Clinical and Epidemiological Virology, Rega Institute  
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium  
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 /isolate="patient BE99-1509"  
 /db\_xref="taxon:12078"  
 /country="Belgium"  
 /note="isolated in February 1999"  
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
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 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 88  
 AY342840/c  
 LOCUS AY342840 188 bp RNA linear VRL 04-MAR-2004  
 DEFINITION Human coxsackievirus B4 patient BE99-3672 5' UTR, partial sequence.  
 ACCESSION AY342840  
 VERSION AY342840.1 GI:37623493  
 KEYWORDS  
 SOURCE Human coxsackievirus B4  
 ORGANISM Human coxsackievirus B4

REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.  
 AUTHORS Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'  
 noncoding region in an epidemiological survey of the human  
 enterovirus B species  
 J. Clin. Microbiol. 42 (3), 963-971 (2004)  
 2. (bases 1 to 188)

REFERENCE Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,  
 Laboratory of Clinical and Epidemiological Virology, Rega Institute  
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium  
 Location/Qualifiers

FEATURES source  
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 /mol\_type="genomic RNA"  
 /isolate="patient BE99-3672"  
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 /note="isolated in March 1999"  
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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 89  
 AY342841/c  
 LOCUS AY342841 188 bp RNA linear VRL 04-MAR-2004  
 DEFINITION Human echovirus 11 patient BE99-4376 5' UTR, partial sequence.  
 ACCESSION AY342841  
 VERSION AY342841.1 GI:37623494

KEYWORDS  
 SOURCE Human echovirus 11

REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

AUTHORS Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'  
 noncoding region in an epidemiological survey of the human  
 enterovirus B species  
 J. Clin. Microbiol. 42 (3), 963-971 (2004)

JOURNAL  
 REFERENCE 2. (bases 1 to 188)

AUTHORS Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,  
 Laboratory of Clinical and Epidemiological Virology, Rega Institute  
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium  
 Location/Qualifiers

FEATURES source  
 1. .188  
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 /country="Belgium"  
 /note="isolated in April 1999"  
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ORIGIN

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 |||||  
 Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 90  
 AY342843/c

LOCUS AY342843 188 bp RNA linear VRL 04-MAR-2004  
 DEFINITION Human coxsackievirus A9 patient BE99-5750 5' UTR, partial sequence.

ACCESSION AY342843  
 VERSION AY342843.1 GI:37623496

KEYWORDS  
 SOURCE Human coxsackievirus A9

ORGANISM Human coxsackievirus A9

REFERENCE 1 Viruses; ssRNA positive-strand viruses, no DNA stage;  
 Picornaviridae; Enterovirus.

AUTHORS Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'  
 noncoding region in an epidemiological survey of the human  
 enterovirus B species  
 J. Clin. Microbiol. 42 (3), 963-971 (2004)

JOURNAL  
 REFERENCE 2. (bases 1 to 188)

AUTHORS Thoelen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,  
 Lindberg, A.M., Vandamme, A.-M., and Van Ranst, M.

TITLE Direct Submission  
 JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,  
 Laboratory of Clinical and Epidemiological Virology, Rega Institute  
 for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium  
 Location/Qualifiers

FEATURES source  
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 /country="Belgium"  
 /note="isolated in May 1999"  
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5'UTR

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    |||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 91
AY342844/c
LOCUS      AY342844      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human coxsackievirus B4 patient BE99-6504 5' UTR, partial sequence.
ACCESSION  AY342844
VERSION     AY342844.1 GI:37623497
KEYWORDS
SOURCE      Human coxsackievirus B4
ORGANISM    Human coxsackievirus B4
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

FEATURES
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Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 92
AY342846/c
LOCUS      AY342846      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 11 patient BE99-7222 5' UTR, partial sequence.
ACCESSION  AY342846
VERSION     AY342846.1 GI:37623499
KEYWORDS
SOURCE      Human echovirus 11
ORGANISM    Human echovirus 11
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species

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J. Clin. Microbiol. 42 (3), 963-971 (2004)
2 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

FEATURES
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5'UTR
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Query Match      100.0%; Score 25; DB 13; Length 188;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

RESULT 93
AY342854/c
LOCUS      AY342854      188 bp      RNA      linear      VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-518 5' UTR, partial sequence.
ACCESSION  AY342854
VERSION     AY342854.1 GI:37623507
KEYWORDS
SOURCE      Human echovirus 30
ORGANISM    Human echovirus 30
Viruses; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE   1 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Analysis of the serotype and genotype correlation of VP1 and the 5'
            noncoding region in an epidemiological survey of the human
            enterovirus B species
JOURNAL     J. Clin. Microbiol. 42 (3), 963-971 (2004)
REFERENCE   2 (bases 1 to 188)
AUTHORS     Thoenen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
            Lindberg,A.M., Vandamme,A.-M. and Van Ranst,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-JUL-2003) Department of Microbiology and Immunology,
            Laboratory of Clinical and Epidemiological Virology, Rega Institute
            for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

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            /country="Belgium"
            /note="isolated in February 2000"
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5'UTR
ORIGIN

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Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||
Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77

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RESULT 94
AY342856/c
LOCUS AY342856 188 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC3574 5' UTR, partial sequence.
ACCESSION AY342856
VERSION AY342856.1 GI:37623509
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 188)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
JOURNAL
REFERENCE 2 (bases 1 to 188)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
FEATURES
source
Location/Qualifiers
1..188
/organism="Human echovirus 30"
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Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
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Db 101 TCCGCTGCAGAGTTGCCCGTTACGA 77
RESULT 95
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LOCUS AY342857 188 bp RNA linear VRL 04-MAR-2004
DEFINITION Human echovirus 30 patient BE00-CC2641 5' UTR, partial sequence.
ACCESSION AY342857
VERSION AY342857.1 GI:37623510
KEYWORDS
SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
REFERENCE
1 (bases 1 to 188)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
JOURNAL
REFERENCE 2 (bases 1 to 188)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
FEATURES
source
Location/Qualifiers
1..188
/organism="Human echovirus 30"
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/mol_type="genomic RNA"
/isolate="patient BE00-CC2641"
/db_xref="taxon:41846"
/country="Belgium"
/note="isolated in March 2000"
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SOURCE Human echovirus 30
ORGANISM Human echovirus 30
VIRUSES; ssRNA positive-strand viruses, no DNA stage;
Picornaviridae; Enterovirus.
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AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Analysis of the serotype and genotype correlation of VP1 and the 5'
noncoding region in an epidemiological survey of the human
enterovirus B species
J. Clin. Microbiol. 42 (3), 963-971 (2004)
JOURNAL
REFERENCE 2 (bases 1 to 188)
AUTHORS Thoenen, I., Moes, E., Lemey, P., Mostmans, S., Wollants, E.,
Lindberg, A.M., Vandamme, A.-M. and Van Ranst, M.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2003) Department of Microbiology and Immunology,
Laboratory of Clinical and Epidemiological Virology, Rega Institute
for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
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ACCESSION AY342859
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ORGANISM Human echovirus 30
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              Thoelen,I., Moes,E., Lemey,P., Mostmans,S., Wollants,E.,
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TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
              noncoding region in an epidemiological survey of the human
              enterovirus B species
JOURNAL      J. Clin. Microbiol. 42 (3), 963-971 (2004)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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JOURNAL      J. Clin. Microbiol. 42 (3), 963-971 (2004)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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              for Medical Research, Minderbroederstraat 10, Leuven 3000, Belgium
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TITLE        Analysis of the serotype and genotype correlation of VP1 and the 5'
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JOURNAL      J. Clin. Microbiol. 42 (3), 963-971 (2004)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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TITLE        Direct Submission
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JOURNAL      J. Clin. Microbiol. 42 (3), 963-971 (2004)
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TITLE        Direct Submission
JOURNAL      Submitted (16-JUL-2003) Department of Microbiology and Immunology,
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Laboratory of Clinical and Epidemiological Virology, Rega Institute  
for Medical Research, Minderbroedersstraat 10, Leuven 3000, Belgium

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Copyright (c) 1993 - 2006 Bioceleration Ltd.

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C 98	15.4	61.6	601	3	US-09-949-016-47418	Sequence 47418, A	171	15.2	60.8	601	3	US-09-949-016-98284	Sequence 98284, A
C 99	15.4	61.6	601	3	US-09-949-016-47430	Sequence 47430, A	172	15.2	60.8	601	3	US-09-949-016-98549	Sequence 98549, A
C 100	15.4	61.6	601	3	US-09-949-002-1736	Sequence 1736, Ap	173	15.2	60.8	601	3	US-09-949-016-98550	Sequence 98550, A
C 101	15.4	61.6	601	3	US-09-949-002-6426	Sequence 6426, Ap	174	15.2	60.8	601	3	US-09-949-016-98815	Sequence 98815, A
C 102	15.4	61.6	618	2	US-08-646-981-9	Sequence 9, Appli	175	15.2	60.8	601	3	US-09-949-016-98816	Sequence 98816, A
C 103	15.4	61.6	620	3	US-09-602-787A-427	Sequence 427, App	176	15.2	60.8	601	3	US-09-949-016-99081	Sequence 99081, A
C 104	15.4	61.6	684	3	US-09-489-039A-3021	Sequence 3021, Ap	177	15.2	60.8	601	3	US-09-949-016-99082	Sequence 99082, A
C 105	15.4	61.6	1029	2	US-08-096-182A-3	Sequence 3, Appli	178	15.2	60.8	601	3	US-09-949-016-99347	Sequence 99347, A
C 106	15.4	61.6	1029	2	US-08-877-109-3	Sequence 3, Appli	179	15.2	60.8	601	3	US-09-949-016-99348	Sequence 99348, A
C 107	15.4	61.6	1029	2	US-08-798-760-3	Sequence 3, Appli	180	15.2	60.8	601	3	US-09-949-016-99613	Sequence 99613, A
C 108	15.4	61.6	1029	6	PCT-US94-08327-3	Sequence 3, Appli	181	15.2	60.8	601	3	US-09-949-016-99614	Sequence 99614, A
C 109	15.4	61.6	1092	2	US-08-096-182A-5	Sequence 5, Appli	182	15.2	60.8	601	3	US-09-949-016-99879	Sequence 99879, A
C 110	15.4	61.6	1092	2	US-08-877-109-5	Sequence 5, Appli	183	15.2	60.8	601	3	US-09-949-016-99880	Sequence 99880, A
C 111	15.4	61.6	1092	3	US-08-798-760-5	Sequence 5, Appli	184	15.2	60.8	601	3	US-09-949-016-100145	Sequence 100145, A
C 112	15.4	61.6	1092	6	PCT-US94-08327-5	Sequence 5, Appli	185	15.2	60.8	601	3	US-09-949-016-100146	Sequence 100146, A
C 113	15.4	61.6	1143	3	US-09-700-820C-27	Sequence 27, Appli	186	15.2	60.8	601	3	US-09-949-016-100411	Sequence 100411, A
C 114	15.4	61.6	1205	3	US-09-949-002-177	Sequence 177, App	187	15.2	60.8	601	3	US-09-949-016-100412	Sequence 100412, A
C 115	15.4	61.6	1298	3	US-08-911-894-73	Sequence 73, Appli	188	15.2	60.8	601	3	US-09-949-016-100677	Sequence 100677, A
C 116	15.4	61.6	1540	2	US-07-932-915-1	Sequence 1, Appli	189	15.2	60.8	601	3	US-09-949-016-100678	Sequence 100678, A
C 117	15.4	61.6	1540	6	PCT-US91-05826-1	Sequence 1, Appli	190	15.2	60.8	601	3	US-09-949-016-100981	Sequence 100981, A
C 118	15.4	61.6	1710	3	US-09-902-540-2848	Sequence 2848, Ap	191	15.2	60.8	601	3	US-09-949-016-100982	Sequence 100982, A
C 119	15.4	61.6	1782	3	US-09-949-002-372	Sequence 372, Appli	192	15.2	60.8	601	3	US-09-949-016-101247	Sequence 101247, A
C 120	15.4	61.6	1800	3	US-10-104-047-1254	Sequence 1254, Ap	193	15.2	60.8	601	3	US-09-949-016-101248	Sequence 101248, A
C 121	15.4	61.6	1806	2	US-09-980-060-1	Sequence 1, Appli	194	15.2	60.8	601	3	US-09-949-016-101513	Sequence 101513, A
C 122	15.4	61.6	1806	3	US-09-307-185-1	Sequence 1, Appli	195	15.2	60.8	601	3	US-09-949-016-101514	Sequence 101514, A
C 123	15.4	61.6	1806	3	US-09-773-753-1	Sequence 1, Appli	196	15.2	60.8	601	3	US-09-949-016-101779	Sequence 101779, A
C 124	15.4	61.6	1920	3	US-09-700-820C-39	Sequence 39, Appli	197	15.2	60.8	601	3	US-09-949-016-101780	Sequence 101780, A
C 125	15.4	61.6	1983	3	US-09-066-281B-18	Sequence 18, Appli	C 198	15.2	60.8	789	3	US-09-023-855-1300	Sequence 1300, Ap
C 126	15.4	61.6	1983	3	US-09-468-433C-18	Sequence 18, Appli	C 199	15.2	60.8	845	3	US-09-949-016-14992	Sequence 4992, Ap
C 127	15.4	61.6	2313	3	US-08-738-168B-14	Sequence 14, Appli	C 200	15.2	60.8	849	3	US-09-270-767-11094	Sequence 11094, A
C 128	15.4	61.6	2553	3	US-09-620-312D-340	Sequence 340, App	C 201	15.2	60.8	858	3	US-09-248-796A-6414	Sequence 6414, Ap
C 129	15.4	61.6	2940	3	US-09-066-281B-20	Sequence 20, Appli	C 202	15.2	60.8	1288	3	US-09-602-787A-417	Sequence 417, App
C 130	15.4	61.6	2940	3	US-09-468-433C-20	Sequence 20, Appli	C 203	15.2	60.8	1354	3	US-08-902-540-167	Sequence 167, App
C 131	15.4	61.6	3459	2	US-09-980-060-3	Sequence 3, Appli	C 204	15.2	60.8	1380	3	US-09-513-783A-169	Sequence 169, App
C 132	15.4	61.6	3459	3	US-09-307-185-3	Sequence 3, Appli	C 205	15.2	60.8	1380	3	US-10-100-957A-169	Sequence 169, App
C 133	15.4	61.6	3459	3	US-09-773-753-3	Sequence 3, Appli	C 206	15.2	60.8	1599	3	US-09-252-991A-13921	Sequence 13921, A
C 134	15.4	61.6	3722	3	US-10-164-595-9	Sequence 9, Appli	C 207	15.2	60.8	2077	3	US-09-321-017B-821	Sequence 821, App
C 135	15.4	61.6	3862	3	US-10-164-595-5	Sequence 5, Appli	C 208	15.2	60.8	2280	3	US-09-252-991A-13535	Sequence 13535, A
C 136	15.4	61.6	3937	3	US-10-164-595-7	Sequence 7, Appli	C 209	15.2	60.8	2992	3	US-09-362-123A-3	Sequence 3, Appli
C 137	15.4	61.6	3972	3	US-09-489-039A-6774	Sequence 6774, Ap	C 210	15.2	60.8	3805	3	US-09-220-132-9	Sequence 9, Appli
C 138	15.4	61.6	3985	3	US-10-164-595-3	Sequence 3, Appli	C 211	15.2	60.8	5688	3	US-09-949-016-16734	Sequence 16734, A
C 139	15.4	61.6	4977	2	US-08-030-096-7	Sequence 7, Appli	C 212	15.2	60.8	17590	3	US-09-762-311-1	Sequence 1, Appli
C 140	15.4	61.6	15132	3	US-09-902-540-1137	Sequence 1137, Ap	C 213	15.2	60.8	17710	3	US-08-976-254-70	Sequence 70, Appli
C 141	15.4	61.6	19917	3	US-09-949-016-13129	Sequence 13129, A	C 214	15.2	60.8	17710	3	US-09-956-009-10	Sequence 10, Appli
C 142	15.4	61.6	18917	3	US-09-949-016-13130	Sequence 13130, A	C 215	15.2	60.8	19988	3	US-09-596-002-10	Sequence 10, Appli
C 143	15.4	61.6	18917	3	US-09-949-016-13131	Sequence 13131, A	C 216	15.2	60.8	26492	3	US-09-902-540-1234	Sequence 1234, Ap
C 144	15.4	61.6	36907	3	US-09-949-002-749	Sequence 749, Ap	C 217	15.2	60.8	44971	3	US-09-949-016-17049	Sequence 17049, A
C 145	15.4	61.6	65902	3	US-09-949-002-509	Sequence 609, App	C 218	15.2	60.8	87870	3	US-09-949-016-14461	Sequence 14461, A
C 146	15.4	61.6	65902	3	US-09-949-016-96422	Sequence 17, Appli	C 219	15.2	60.8	107085	3	US-09-949-016-13157	Sequence 13157, A
C 147	15.4	61.6	247299	3	US-09-949-016-96422	Sequence 17590, A	C 220	15.2	60.8	120727	3	US-09-949-016-15787	Sequence 15787, A
C 148	15.2	60.8	404	3	US-09-621-976-1578	Sequence 13708, A	C 221	15.2	60.8	120727	3	US-09-949-016-15788	Sequence 15788, A
C 149	15.2	60.8	468	3	US-09-252-991A-13708	Sequence 419, App	C 222	15.2	60.8	818128	3	US-09-949-016-14546	Sequence 14546, A
C 150	15.2	60.8	487	3	US-09-489-039A-5535	Sequence 5535, App	C 223	15.2	60.8	818128	3	US-09-949-016-14547	Sequence 14547, A
C 151	15.2	60.8	531	3	US-09-949-016-97219	Sequence 97219, A	C 224	15.2	60.8	818128	3	US-09-949-016-14548	Sequence 14548, A
C 152	15.2	60.8	601	3	US-09-949-016-97219	Sequence 27835, A	C 225	15.2	60.8	818128	3	US-09-949-016-14549	Sequence 14549, A
C 153	15.2	60.8	601	3	US-09-949-016-97219	Sequence 27836, A	C 226	15.2	60.8	818128	3	US-09-949-016-14550	Sequence 14550, A
C 154	15.2	60.8	601	3	US-09-949-016-94157	Sequence 94157, A	C 227	15.2	60.8	818128	3	US-09-949-016-14551	Sequence 14551, A
C 155	15.2	60.8	601	3	US-09-949-016-94158	Sequence 94158, A	C 228	15.2	60.8	818128	3	US-09-949-016-14552	Sequence 14552, A
C 156	15.2	60.8	601	3	US-09-949-016-96421	Sequence 96421, A	C 229	15.2	60.8	818128	3	US-09-949-016-14553	Sequence 14553, A
C 157	15.2	60.8	601	3	US-09-949-016-96422	Sequence 96422, A	C 230	15.2	60.8	818128	3	US-09-949-016-14554	Sequence 14554, A
C 158	15.2	60.8	601	3	US-09-949-016-96687	Sequence 96687, A	C 231	15.2	60.8	818128	3	US-09-949-016-14555	Sequence 14555, A
C 159	15.2	60.8	601	3	US-09-949-016-96688	Sequence 96688, A	C 232	15.2	60.8	818128	3	US-09-949-016-14556	Sequence 14556, A
C 160	15.2	60.8	601	3	US-09-949-016-96953	Sequence 96953, A	C 233	15.2	60.8	818128	3	US-09-949-016-14557	Sequence 14557, A
C 161	15.2	60.8	601	3	US-09-949-016-96954	Sequence 96954, A	C 234	15.2	60.8	818128	3	US-09-949-016-14558	Sequence 14558, A
C 162	15.2	60.8	601	3	US-09-949-016-97219	Sequence 97219, A	C 235	15.2	60.8	818128	3	US-09-949-016-14559	Sequence 14559, A
C 163	15.2	60.8	601	3	US-09-949-016-97220	Sequence 97220, A	C 236	15.2	60.8	818128	3	US-09-949-016-14560	Sequence 14560, A
C 164	15.2	60.8	601	3	US-09-949-016-97485	Sequence 97485, A	C 237	15.2	60.8	818128	3	US-09-949-016-14561	Sequence 14561, A
C 165	15.2	60.8	601	3	US-09-949-016-97486	Sequence 97486, A	C 238	15.2	60.8	818128	3	US-09-949-016-14562	Sequence 14562, A
C 166	15.2	60.8	601	3	US-09-949-016-97751	Sequence 97751, A	C 239	15.2	60.8	818128	3	US-09-949-016-14564	Sequence 14564, A
C 167	15.2	60.8	601	3	US-09-949-016-97752	Sequence 97752, A	C 240	15.2	60.8	818128	3	US-09-949-016-14565	Sequence 14565, A
C 168	15.2	60.8	601	3	US-09-949-016-98017	Sequence 98017, A	C 241	15.2	60.8	818128	3	US-09-949-016-14566	Sequence 14566, A
C 169	15.2	60.8	601	3	US-09-949-016-98018	Sequence 98018, A	C 242	15.2	60.8	818128	3	US-09-949-016-14567	Sequence 14567, A
C 170	15.2	60.8	601	3	US-09-949-016-98283	Sequence 98283, A	C 243	15	60.0	30	3	US-09-085-686-9	Sequence 9, Appli

244	15	60.0	30	3	US-09-085-686-10	Sequence 10, Appl	C 317	14.8	59.2	612	3	US-08-998-416-752	Sequence 752, App
C 245	15	60.0	135	3	US-09-533-559-3714	Sequence 3714, Ap	C 318	14.8	59.2	705	3	US-09-270-767-13560	Sequence 13560, A
C 246	15	60.0	234	3	US-09-252-991A-3316	Sequence 3316, Ap	C 319	14.8	59.2	860	3	US-09-636-499-18	Sequence 18, Appl
C 247	15	60.0	266	3	US-09-313-294A-659	Sequence 659, App	C 320	14.8	59.2	1026	3	US-09-614-221A-512	Sequence 512, App
248	15	60.0	267	3	US-09-023-655-499	Sequence 499, App	321	14.8	59.2	1296	3	US-10-037-927B-9	Sequence 9, Appl
249	15	60.0	321	3	US-09-513-999C-2705	Sequence 2705, Ap	322	14.8	59.2	1464	3	US-09-636-499-3	Sequence 3, Appl
C 250	15	60.0	399	3	US-09-902-540-6974	Sequence 6974, Ap	323	14.8	59.2	1584	3	US-09-636-499-2	Sequence 2, Appl
251	15	60.0	409	3	US-09-513-999C-15817	Sequence 15817, A	324	14.8	59.2	1695	3	US-09-227-853A-1	Sequence 1, Appl
252	15	60.0	463	3	US-09-621-976-3068	Sequence 3068, Ap	325	14.8	59.2	1695	6	PCT-US95-06385-1	Sequence 27, Appl
253	15	60.0	480	3	US-09-270-767-2307	Sequence 2307, Ap	326	14.8	59.2	1721	2	US-08-820-170A-27	Sequence 1, Appl
254	15	60.0	480	3	US-09-270-767-17589	Sequence 17589, A	327	14.8	59.2	1721	3	US-09-055-699-27	Sequence 27, Appl
255	15	60.0	601	3	US-09-949-016-47146	Sequence 47146, A	328	14.8	59.2	1721	3	US-09-273-565-27	Sequence 27, Appl
256	15	60.0	601	3	US-09-949-016-58170	Sequence 58170, A	329	14.8	59.2	1721	3	US-09-565-538-27	Sequence 27, Appl
C 257	15	60.0	601	3	US-09-949-016-70149	Sequence 70149, A	330	14.8	59.2	1721	3	US-09-661-468-27	Sequence 27, Appl
C 258	15	60.0	601	3	US-09-949-016-155131	Sequence 155131, A	331	14.8	59.2	1721	3	US-09-976-165-27	Sequence 27, Appl
259	15	60.0	601	3	US-09-252-991A-3988	Sequence 3988, Ap	332	14.8	59.2	1920	3	US-10-104-047-1847	Sequence 1847, Ap
C 260	15	60.0	765	3	US-09-252-991A-3980	Sequence 3980, Ap	333	14.8	59.2	1922	3	US-09-636-499-1	Sequence 1, Appl
C 261	15	60.0	895	3	US-09-270-767-10093	Sequence 10093, A	334	14.8	59.2	2612	3	US-10-104-047-1320	Sequence 1320, Ap
262	15	60.0	896	3	US-09-533-559-1448	Sequence 1448, Ap	335	14.8	59.2	2992	2	US-08-426-236-3	Sequence 3, Appl
263	15	60.0	1218	3	US-09-489-039A-170	Sequence 170, App	336	14.8	59.2	4898	3	US-09-636-499-17	Sequence 17, Appl
264	15	60.0	1301	2	US-08-641-314C-1	Sequence 1, Appl	337	14.8	59.2	4898	3	US-09-949-016-13433	Sequence 13433, A
265	15	60.0	1302	3	US-09-252-991A-7155	Sequence 7155, Ap	338	14.8	59.2	24593	3	US-09-949-016-11984	Sequence 11984, A
266	15	60.0	1335	3	US-09-252-991A-3925	Sequence 3925, Ap	339	14.8	59.2	26763	3	US-09-949-016-15566	Sequence 15566, A
C 267	15	60.0	1344	3	US-09-489-039A-534	Sequence 534, App	340	14.8	59.2	26764	3	US-09-817-1398C-3	Sequence 3, Appl
C 268	15	60.0	1347	3	US-09-252-991A-7339	Sequence 7339, Ap	341	14.8	59.2	28770	3	US-09-949-016-16874	Sequence 16874, A
269	15	60.0	1500	3	US-09-252-991A-7277	Sequence 7277, Ap	342	14.8	59.2	31867	3	US-09-949-016-15728	Sequence 15728, A
C 270	15	60.0	1504	3	US-09-949-016-2633	Sequence 2633, Ap	343	14.8	59.2	31875	3	US-09-949-016-17191	Sequence 17191, A
C 271	15	60.0	1896	2	US-08-605-541B-11	Sequence 11, Appl	344	14.8	59.2	52661	3	US-09-949-016-15369	Sequence 15369, A
C 272	15	60.0	2223	3	US-09-252-991A-4015	Sequence 4015, Ap	345	14.8	59.2	73757	3	US-08-952-793-368	Sequence 368, App
C 273	15	60.0	2574	3	US-08-887-534A-46	Sequence 46, Appl	346	14.6	58.4	66	3	US-09-849-928-368	Sequence 368, App
C 274	15	60.0	2574	3	US-09-527-431-46	Sequence 46, Appl	347	14.6	58.4	66	6	PCT-US96-09455A-368	Sequence 368, App
C 275	15	60.0	2574	3	US-09-446-861-46	Sequence 46, Appl	348	14.6	58.4	66	6	US-09-513-999C-30170	Sequence 30170, A
C 276	15	60.0	2574	3	US-09-960-428-20	Sequence 20, Appl	349	14.6	58.4	440	3	US-08-266-311-5	Sequence 5, Appl
C 277	15	60.0	2657	3	US-10-104-047-879	Sequence 879, App	350	14.6	58.4	441	2	US-08-467-527A-5	Sequence 5, Appl
278	15	60.0	2858	3	US-10-104-047-1226	Sequence 1226, Ap	351	14.6	58.4	441	2	US-08-467-527A-5	Sequence 5, Appl
C 279	15	60.0	3380	3	US-09-902-540-606	Sequence 606, App	352	14.6	58.4	441	3	US-09-222-575-61	Sequence 61, Appl
C 280	15	60.0	4417	3	US-07-741-453A-57	Sequence 57, Appl	353	14.6	58.4	447	3	US-09-389-681-61	Sequence 61, Appl
C 281	15	60.0	5749	3	US-09-262-537-48	Sequence 48, Appl	354	14.6	58.4	447	3	US-09-620-405B-61	Sequence 61, Appl
282	15	60.0	8514	3	US-09-949-016-11938	Sequence 11938, A	355	14.6	58.4	447	3	US-09-339-338-61	Sequence 61, Appl
C 283	15	60.0	9442	3	US-09-949-016-12571	Sequence 12571, A	356	14.6	58.4	447	3	US-09-433-826B-61	Sequence 61, Appl
C 284	15	60.0	9443	3	US-09-949-016-15877	Sequence 15877, A	357	14.6	58.4	447	3	US-09-604-287A-61	Sequence 61, Appl
285	15	60.0	9792	3	US-09-635-872A-14	Sequence 14, Appl	358	14.6	58.4	447	3	US-09-285-480-61	Sequence 61, Appl
286	15	60.0	9792	3	US-09-636-077A-14	Sequence 14, Appl	359	14.6	58.4	447	3	US-09-834-759-61	Sequence 61, Appl
287	15	60.0	9792	3	US-09-636-060C-14	Sequence 14, Appl	360	14.6	58.4	447	3	US-09-590-751A-61	Sequence 61, Appl
288	15	60.0	9792	3	US-09-986-552-14	Sequence 14, Appl	361	14.6	58.4	447	3	US-09-551-621-61	Sequence 61, Appl
289	15	60.0	9792	3	US-09-636-596C-14	Sequence 14, Appl	362	14.6	58.4	447	3	US-09-551-621A-61	Sequence 61, Appl
290	15	60.0	9792	3	US-10-023-894-21	Sequence 21, Appl	363	14.6	58.4	447	3	US-10-076-622-61	Sequence 61, Appl
291	15	60.0	9792	3	US-10-306-686-14	Sequence 14, Appl	364	14.6	58.4	447	3	US-09-270-767-10269	Sequence 10269, A
292	15	60.0	9792	3	US-09-895-072-14	Sequence 14, Appl	365	14.6	58.4	514	3	US-09-489-039A-335	Sequence 335, App
293	15	60.0	9792	3	US-10-023-888-21	Sequence 21, Appl	366	14.6	58.4	525	3	US-09-702-705-812	Sequence 812, App
C 294	15	60.0	10701	3	US-09-949-016-14375	Sequence 14375, A	367	14.6	58.4	594	3	US-09-736-457-812	Sequence 812, App
295	15	60.0	11820	3	US-09-949-016-11887	Sequence 11887, A	368	14.6	58.4	594	3	US-09-328-352-3456	Sequence 3456, App
296	15	60.0	11826	3	US-09-949-016-13767	Sequence 13767, A	369	14.6	58.4	594	3	US-09-614-124B-812	Sequence 812, App
C 297	15	60.0	15472	3	US-09-453-702B-71	Sequence 71, Appl	370	14.6	58.4	594	3	US-09-589-184-812	Sequence 812, App
C 298	15	60.0	15472	3	US-10-114-170-71	Sequence 71, Appl	371	14.6	58.4	594	3	US-09-589-184-812	Sequence 812, App
299	15	60.0	16780	3	US-09-949-002-796	Sequence 796, App	372	14.6	58.4	594	3	US-10-017-754-812	Sequence 812, App
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301	15	60.0	33885	3	US-09-949-016-16081	Sequence 16081, A	374	14.6	58.4	594	3	US-09-949-016-22151	Sequence 22151, A
C 302	15	60.0	41171	3	US-08-311-731A-122	Sequence 122, App	375	14.6	58.4	601	3	US-09-949-016-105276	Sequence 105276, A
303	15	60.0	64309	3	US-09-949-016-14581	Sequence 14581, A	376	14.6	58.4	601	3	US-09-949-016-115513	Sequence 115513, A
C 304	15	60.0	67479	3	US-09-949-016-11804	Sequence 11804, A	377	14.6	58.4	601	3	US-09-949-016-115606	Sequence 115606, A
305	15	60.0	76985	3	US-09-949-016-12416	Sequence 12416, A	378	14.6	58.4	601	3	US-09-949-016-115699	Sequence 115699, A
306	15	60.0	76986	3	US-09-949-016-13120	Sequence 13120, A	379	14.6	58.4	601	3	US-09-949-016-115792	Sequence 115792, A
C 307	15	60.0	110585	3	US-09-949-016-13427	Sequence 13427, A	380	14.6	58.4	601	3	US-09-949-016-115978	Sequence 115978, A
C 308	15	60.0	118067	3	US-09-497-855A-32	Sequence 32, Appl	381	14.6	58.4	601	3	US-09-949-016-116071	Sequence 116071, A
C 309	15	60.0	128470	3	US-09-949-016-13765	Sequence 13765, A	382	14.6	58.4	601	3	Sequence 64665, A	Sequence 64665, A
C 310	15	60.0	169971	3	US-09-949-016-13807	Sequence 13807, A	383	14.6	58.4	601	3	Sequence 105276, A	Sequence 105276, A
C 311	15	60.0	227750	3	US-09-949-016-17175	Sequence 17175, A	384	14.6	58.4	601	3	Sequence 115513, A	Sequence 115513, A
312	15	60.0	229354	3	US-09-705-400-64	Sequence 64, Appl	385	14.6	58.4	601	3	Sequence 115606, A	Sequence 115606, A
C 313	14.8	59.2	308	3	US-09-094-207A-2	Sequence 2, Appl	386	14.6	58.4	601	3	Sequence 115699, A	Sequence 115699, A
C 314	14.8	59.2	308	3	US-10-109-725A-2	Sequence 2, Appl	387	14.6	58.4	601	3	Sequence 115792, A	Sequence 115792, A
C 315	14.8	59.2	484	3	US-09-621-976-11034	Sequence 11034, A	388	14.6	58.4	601	3	Sequence 115978, A	Sequence 115978, A
316	14.8	59.2	601	3	US-09-949-016-58342	Sequence 58342, A	389	14.6	58.4	601	3	Sequence 116071, A	Sequence 116071, A

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 C 500 14.4 57.6 25 3 US-09-396-196G-4446

ALIGNMENTS

RESULT 1

US-09-724-678D-16/c  
 ; Sequence 16, Application US/09724678D  
 ; Patent No. 6818397  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lee, Kang-Hung  
 ; APPLICANT: Baier, Chi-Hong  
 ; APPLICANT: Tseng, Yang-Yuan  
 ; APPLICANT: Wang, Yih-Weng  
 ; APPLICANT: Wang, Shing-Hwan  
 ; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses and the Probes Thereof  
 ; TITLE OF INVENTION: and Probes Thereof  
 ; FILE REFERENCE: TAI 3L6  
 ; CURRENT APPLICATION NUMBER: US/09/724, 678D  
 ; CURRENT FILING DATE: 2000-11-28  
 ; NUMBER OF SEQ ID NOS: 16  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 16  
 ; LENGTH: 1560  
 ; TYPE: DNA  
 ; ORGANISM: Enterovirus 71  
 US-09-724-678D-16

Query Match 100.0%; Score 25; DB 3; Length 1560;  
 Best Local Similarity 100.0%; Pred. No. 0.03; Indels 0; Gaps 0;  
 Matches 25; Conservative 0; Mismatches 0;  
 Oy 1 TCCGCTCAGAGTTGCCGTTACGA 25  
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 Db 540 TCCGCTCAGAGTTGCCGTTACGA 516



```

US-09-724-678D-10/c
; Sequence 10, Application US/09724678D
; Patent No. 6818397
; GENERAL INFORMATION:
; APPLICANT: Lee, Kang-Hung
; APPLICANT: Lee, Chi-Horng
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Tseng, Yang-Yuan
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Wang, Shing-Hwan
; TITLE OF INVENTION: Methods for Detecting and differentiating Enteroviruses
; TITLE OF INVENTION: and Probes Therefor
; FILE REFERENCE: TAI 3L6
; CURRENT APPLICATION NUMBER: US/09/724,678D
; NUMBER FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial Sequence is Synthesized
; Patent No. 6818397
US-09-724-678D-10

Query Match          92.0%; Score 23; DB 3; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.17;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0

QY 1 TCCGCTGCACAGTTCGCCGTTACGA 25
DB 27 TCCGCTGCACAGTTCGCCGTTACGA 3

RESULT 5
US-09-489-039A-680/c
; Sequence 680, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBS
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 680
; LENGTH: 3366
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-680

Query Match          75.2%; Score 18.8; DB 3; Length 3366;
Best Local Similarity 90.9%; Pred. No. 0.28;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 2 CCCTCGAGAGTTCGCCGTTAC 23
DB 1112 CCCTCGAGAGTTCGCCGTTAC 1091

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RESULT 8  
US-09-349-016-15569  
; Sequence 15369, Application US/09949016  
; Patent NO. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307

```

RESULT 9
US-09-171-209-45
; Sequence 45, Application US/09171209
; Patent No. 6448000
; GENERAL INFORMATION:
; APPLICANT: VANDERBILT UNIVERSITY
;              305 Kirkland Hall
;              Nashville, TN 37240
; TITLE OF INVENTION: MAMMALIAN GENES INVOLVED IN VIRAL
;                     INFECTION
; NUMBER OF SEQUENCES: 83
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C. 1200
; STREET: 127 Peachtree Street, Suite 1200
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303-1811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/171,209
; FILING DATE: 08-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/06067
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Selby, Elizabeth
; REGISTRATION NUMBER: 38,298
; REFERENCE/DOCKET NUMBER: 22000.0061/P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404 688 0770
; TELEFAX: 404 688 9880
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 919 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 45:
US-09-171-209-45

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Best Local Similarity 94.7%; Pred. No. 1.1e+02; Mismatches 1; Indels 0; Gaps 0;

Matches 18; Conservative 0;

QY 5 CTGCAGAGTTGCCCGTTAC 23

Db 491 CTGCAGAGTTGCCCGTTAC 509

## RESULT 10

US-08-998-416-523/c  
; Sequence 523, Application US/08998416  
; Patent No. 6239264

## GENERAL INFORMATION:

APPLICANT: Philippsen, Peter

APPLICANT: Pohlmann, Rainer

APPLICANT: Steiner, Sabine

APPLICANT: Mohr, Christine

APPLICANT: Wendland, Jergen

APPLICANT: Knechtle, Philipp

APPLICANT: Rebischung, Corinne

TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPPII

TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1152

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 6239264artis Corporation

STREET: 3054 Cornwallis Road

CITY: Research Triangle Park

STATE: No. 6239264th Carolina

COUNTRY: USA

ZIP: 27709

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/998,416

FILING DATE: 24-DEC-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: CH 0016/97

FILING DATE: 31-DEC-1996

ATTORNEY/AGENT INFORMATION:

NAME: Meigs, J. Timothy

REGISTRATION NUMBER: 38,241

REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919-541-8587

TELEFAX: 919-541-8689

INFORMATION FOR SEQ ID NO: 523:

SEQUENCE CHARACTERISTICS:

LENGTH: 824 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: PAG1367RP

US-08-998-416-523

Query Match 68.8%; Score 17.2; DB 3; Length 824;

Best Local Similarity 86.4%; Pred. No. 1.3e+02;

Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCTGCTGCAGAGTTGCCCGTTA 22

Db 559 TCGCGGCAGAGTTGCCCGTTA 538

## RESULT 11

US-08-988-988-27

; Sequence 27, Application US/0868988B

; Patent No. 6096545

Query Match

68.0%; Score 17; DB 2; Length 628;

## GENERAL INFORMATION:

APPLICANT: Lefebvre, Daniel D.

APPLICANT: Malboobi, Mohammad A.

TITLE OF INVENTION: PHOSPHATE STARVATION-INDUCIBLE PROTEINS

FILE REFERENCE: PPL96-03

CURRENT APPLICATION NUMBER: US/08/688,988B

CURRENT FILING DATE: 1996-07-31

NUMBER OF SEQ ID NOS: 48

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 27

LENGTH: 319

TYPE: DNA

ORGANISM: Brassica Nigra

US-08-688-988-27

Query Match

Best Local Similarity 80.0%; Pred. No. 1.5e+02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 162 TGCCTTCAGATTGCCCGTTGAGA 186

## RESULT 12

US-08-387-845-5/c

; Sequence 5, Application US/08387845

; Patent No. 5665567

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a

bicistronic vector system in mammalian cells

NUMBER OF SEQUENCES: 16

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25 (EPA)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/387,845

FILING DATE:

CLASSIFICATION: 435

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 628 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

ORIGINAL SOURCE:

ORGANISM: Poliovirus Typ 1 (Mahoney strain)

IMMEDIATE SOURCE:

CLONE: pGEM 3-5' Polio (M) (4708 bp), (Sarnow, 1989)

FEATURE:

NAME/KEY: -

LOCATION: 1..628

OTHER INFORMATION: /note= "shown are the first

628 nt of the 5' non-translated region of

poliovirus Typ 1 (Mahoney)"

FEATURE:

NAME/KEY: -

LOCATION: 610

OTHER INFORMATION: /note= "non-authentic sequence

due to a base pair substitution from C to G

OTHER INFORMATION: at position 610"

PUBLICATION INFORMATION:

AUTHORS: Sarnow, P.

JOURNAL: J. Virol.

VOLUME: 63

PAGES: 467-470

DATE: 1989

US-08-387-845-5

Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
||||| ||||| ||||| ||||| |||||  
Db 535 TCCGCCACGGACTTGGCGTTACGA 511

## RESULT 13

US-08-778-275-5/c  
; Sequence 5, Application US/08778275  
; Patent No. 5935819  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Preparation of heterodimeric PDGF-AB using a  
; TITLE OF INVENTION: bicistronic vector system in mammalian cells  
; NUMBER OF SEQUENCES: 16  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/778,275  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,845  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 628 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)  
; IMMEDIATE SOURCE:  
; CLONE: pGEM 3-5'Polio (M) (4708 bp), (Sarnow, 1989)  
; FEATURE:

NAME/KEY: -  
LOCATION: 1..628 /note= "shown are the first  
OTHER INFORMATION: 628 nt of the 5' non-translated region of  
OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"

PUBLICATION INFORMATION:  
AUTHORS: Sarnow, P.  
JOURNAL: J. Virol.  
VOLUME: 63  
PAGES: 467-470  
DATE: 1989

US-08-778-275-5  
Query Match 68.0%; Score 17; DB 2; Length 628;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
||||| ||||| ||||| ||||| |||||  
Db 535 TCCGCCACGGACTTGGCGTTACGA 511

## RESULT 14

US-08-867-352-5/c  
; Sequence 5, Application US/08867352  
; Patent No. 606273  
; GENERAL INFORMATION:

; APPLICANT:  
; TITLE OF INVENTION: Multicistronic expression units and their use  
; NUMBER OF SEQUENCES: 25  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/867,352  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/387,847  
; FILING DATE:  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 628 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; ORGANISM: Poliovirus Typ 1 (Mahoney strain)  
; IMMEDIATE SOURCE:  
; CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)  
; FEATURE:

NAME/KEY: -  
LOCATION: 1..628 /note= "non-authentic sequence  
OTHER INFORMATION: due to a base pair substitution from C to G  
OTHER INFORMATION: at position 610"

PUBLICATION INFORMATION:  
AUTHORS: Sarnow, P.  
JOURNAL: J. Virol.  
VOLUME: 63  
PAGES: 467-470  
DATE: 1989

US-08-867-352-5  
Query Match 68.0%; Score 17; DB 2; Length 628;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
||||| ||||| ||||| ||||| |||||  
Db 535 TCCGCCACGGACTTGGCGTTACGA 511

APPLICANT:  
TITLE OF INVENTION: Multicistronic expression units and their use  
NUMBER OF SEQUENCES: 25  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPA)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/867,352  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/387,847  
FILING DATE:  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 628 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
ORGANISM: Poliovirus Typ 1 (Mahoney strain)  
IMMEDIATE SOURCE:  
CLONE: pGEM3-5'Polio (M) (4708 bp), (Sarnow, 1989)  
FEATURE:

NAME/KEY: -  
LOCATION: 1..628 /note= "shown are the first  
OTHER INFORMATION: 628 nt of the 5' non-translated region of  
OTHER INFORMATION: poliovirus Typ 1 (Mahoney)"

PUBLICATION INFORMATION:  
AUTHORS: Sarnow, P.  
JOURNAL: J. Virol.  
VOLUME: 63  
PAGES: 467-470  
DATE: 1989

US-08-867-352-5  
Query Match 68.0%; Score 17; DB 3; Length 628;  
Best Local Similarity 80.0%; Pred. No. 1.6e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
||||| ||||| ||||| ||||| |||||  
Db 535 TCCGCCACGGACTTGGCGTTACGA 511

## RESULT 15

US-09-221-017B-435/c  
; Sequence 435, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:

; APPLICANT: Ross, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows

Query Match 68.0%; Score 17; DB 3; Length 1823;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

RESULT 16  
US-09-949-016-5300/c  
; Sequence 5300, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: Fast-SEQ for Windows Version 4.0  
; SEQ ID NO 5300  
; LENGTH: 1865  
; TYPE: DNA  
; ORGANISM: Human

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Query Match      68.0%; Score 17; DB 3; Length 1865;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels

QY      . 1 TCGGCTGCAGAGTTGCCCGTTACGA 25
Db      971 TCGGTGGCAGAGTTGCCCTTTAAGA 947

```

```

US-09-949-016-5301/c
; Sequence 5301, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5301
; LENGTH: 1865
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5301

```

Query Match 68.0%; Score 17; DB 3; Length 1865;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels

**Qy** 1 TCGCTGCAGAGTTGCCGTTACGA 25  
||| ||| ||| ||| ||| ||| ||| |||  
**Dd** 971 TCGTGGCAGAGTTGCCCTTAAGA 947

US-08-403-388-1/c  
Sequence 1, Application US/08403388  
Patent No. 5587289  
GENERAL INFORMATION:  
APPLICANT: Lurquin, Christophe; Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felife & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/403,388  
FILING DATE: 14-MARCH-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5587289man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5408

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1866 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-403-388-1

Query Match 68.0%; Score 17; DB 2; Length 1866;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 973 TCGGTGCAGAGTTGCCCTTTAAGA 949

## RESULT 19

US-08-658-578-1/c  
Sequence 1, Application US/08658578  
Patent No. 5759783

GENERAL INFORMATION:  
APPLICANT: Lurquin, Christophe; Brasseur, Francis;  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/658,578  
FILING DATE: 5-MAY-1996  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,388  
FILING DATE: 14-MARCH-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 5759783man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5444

TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1866 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-658-578-1

Query Match 68.0%; Score 17; DB 2; Length 1866;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 973 TCGGTGCAGAGTTGCCCTTTAAGA 949

## RESULT 20

US-08-846-111D-1/c  
Sequence 1, Application US/08846111D  
Patent No. 6017705  
GENERAL INFORMATION:  
APPLICANT: Lurquin, Christophe; Brasseur, Francis;  
APPLICANT: Boon-Falleur, Thierry  
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Felfe & Lynch  
STREET: 805 Third Avenue  
CITY: New York City  
STATE: New York  
ZIP: 10022-7513

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage  
COMPUTER: IBM  
OPERATING SYSTEM: PC-DOS  
SOFTWARE: Wordperfect For DOS 6.0b

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/846,111D  
FILING DATE: 25-APRIL-1997  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/658,578  
FILING DATE: 5-MAY-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/403,388  
FILING DATE: 14-MARCH-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Hanson, No. 6017705man D.  
REGISTRATION NUMBER: 30,946  
REFERENCE/DOCKET NUMBER: LUD 5444.1

TELEPHONE: (212) 688-9200  
TELEFAX: (212) 838-3884  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1866 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

US-08-846-111D-1

Query Match 68.0%; Score 17; DB 3; Length 1866;  
Best Local Similarity 80.0%; Pred. No. 1.8e+02;  
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 973 TCGGTGCAGAGTTGCCCTTTAAGA 949

## RESULT 21

US-09-056-105-19/c  
Sequence 19, Application US/09056105  
Patent No. 6287569

GENERAL INFORMATION:  
APPLICANT: KIPPS, THOMAS J.  
APPLICANT: WU, YUNQI  
TITLE OF INVENTION: VACCINES WITH ENHANCED INTRACELLULAR  
TITLE OF INVENTION: PROCESSING  
FILE REFERENCE: 233/221

CURRENT APPLICATION NUMBER: US/09/056,105  
CURRENT FILING DATE: 1998-04-06  
EARLIER APPLICATION NUMBER: 60/043,467  
EARLIER FILING DATE: 1997-04-10

NUMBER OF SEQ ID NOS: 35  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 19  
LENGTH: 1866  
TYPE: DNA

```
; ORGANISM: Homo sapiens
US-09-056-105-19

Query Match      68.0%; Score 17; DB 3; Length 1866;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 973 TCGGTGGCAGAGTTGCCCTTTAAGA 949

RESULT 22
US-09-443-077-1/c
; Sequence 1, Application US/09443077
; Patent No. 6392016
; GENERAL INFORMATION:
; APPLICANT: Lurquin, Christophe; Brasseur, Francis;
; Boon-Falleur, Thierry.
; TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are
; Members Of The Mage-B Family and Uses Thereof
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; ZIP: 10022-7513
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect For DOS 6.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/443,077
; FILING DATE: 26-Jun-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,111
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/403,388
; FILING DATE: 14-MARCH-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6392016man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5444.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 698-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1866 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-443-077-1

Query Match      68.0%; Score 17; DB 3; Length 1866;
Best Local Similarity 80.0%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 973 TCGGTGGCAGAGTTGCCCTTTAAGA 949

RESULT 23
US-09-202-904A-10/c
; Sequence 10, Application US/09202904A
; Patent No. 6395471
; GENERAL INFORMATION:
; APPLICANT: Kang, Sung Key
```

```
; APPLICANT: Hahn, Bumsuk
; TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
; TITLE OF INVENTION: the Activity of Hepatitis C Virus Protease, a Recombinant
; FILE OF INVENTION: Gene and a Use Thereof
; FILE REFERENCE: A32210-PCT-USA 072944.0104
; CURRENT APPLICATION NUMBER: US/09/202,904A
; CURRENT FILING DATE: 2001-01-22
; PRIOR APPLICATION NUMBER: PCT/KR97/00120
; PRIOR FILING DATE: 1997-06-25
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 2320
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Genetically engineered virus derived from
; OTHER INFORMATION: poliovirus and hepatitis C virus
US-09-202-904A-10

Query Match      68.0%; Score 17; DB 3; Length 2320;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 535 TCCGCCAGGACTTGCGGTTACGA 511

RESULT 24
US-07-852-260-1/c
; Sequence 1, Application US/07852260
; Patent No. 5525715
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/852,260
; FILING DATE: 19920619
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
```

```
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-07-852-260-1

Query Match      68.0%; Score 17; DB 2; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGC CGTTACGA 514

RESULT 25
US-08-461-503-1/c
; Sequence 1, Application US/08461503
; Patent No. 5834302
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES
; TITLE OF INVENTION: FROM CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,503
; FILING DATE: 5-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-D-PCT-US
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-08-461-503-1

Query Match      68.0%; Score 17; DB 2; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGC CGTTACGA 514

RESULT 26
US-08-465-250-1/c
; Sequence 1, Application US/08465250
; Patent No. 6136570
; GENERAL INFORMATION:
; APPLICANT: Racaniello, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham LLP
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/465,250
; FILING DATE: 6-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-E-PCT-US
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
US-08-465-250-1

Query Match      68.0%; Score 17; DB 3; Length 7432;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    ||||| ||||| ||||| ||||| |||||
Db 538 TCCGCCACGAGCTTGC CGTTACGA 514

RESULT 27
US-09-284-349B-1/c
; Sequence 1, Application US/09284349B
; Patent No. 6696289
; GENERAL INFORMATION:
; APPLICANT: Yong Soo, Bae
; APPLICANT: Jung, Hye Rhan
; TITLE OF INVENTION: Replication-Competent Sabin Type 1 Strain
; FILE REFERENCE: Docket No. 6696289; 4220-109 US
; CURRENT APPLICATION NUMBER: US/09/284,349B
; CURRENT FILING DATE: 1999-06-04
; PRIOR APPLICATION NUMBER: PCT/KR98/00242
; PRIOR FILING DATE: 1998-07-08
; PRIOR APPLICATION NUMBER: KR 97/37812
; PRIOR FILING DATE: 1997-07-08
; NUMBER OF SEQ ID NOS: 30
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SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 7441

TYPE: DNA

ORGANISM: Human poliovirus 1

US-09-284-349B-1

Query Match 68.0%; Score 17; DB 3; Length 7441;

Best Local Similarity 80.0%; Pred. No. 2.1e+02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 535 TCCGCCACGACTTCCGGTTACGA 511

RESULT 28

US-09-949-016-17042/c

Sequence 17042, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0.

SEQ ID NO 17042

LENGTH: 12309

TYPE: DNA

ORGANISM: Human

US-09-949-016-17042

Query Match 68.0%; Score 17; DB 3; Length 12309;

Best Local Similarity 80.0%; Pred. No. 2.3e+02;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 9414 TCGTGGCAGAGTTGCCCTTTAAGA 9390

RESULT 29

US-09-949-016-17043/c

Sequence 17043, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 17043

LENGTH: 12309

TYPE: DNA

ORGANISM: Human

US-09-949-016-17043

Query Match

Best Local Similarity 68.0%; Score 17; DB 3; Length 12309;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 9414 TCGTGGCAGAGTTGCCCTTTAAGA 9390

RESULT 30

US-08-846-111D-15/c

Sequence 15, Application US/08846111D

Patent No. 6017705

GENERAL INFORMATION:

APPLICANT: Lurquin, Christophe; Brasseur, Francis;

APPLICANT: Boon-Falleur, Thierry

TITLE OF INVENTION: Isolated Nucleic Acid Molecules Which Are

Members Of The Mage-B Family and Uses Thereof

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

ZIP: 10022-7513

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage

COMPUTER: IBM

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect For DOS 6.0b

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/846,111D

FILING DATE: 25-APRIL-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/658,578

FILING DATE: 5-MAY-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/403,388

FILING DATE: 14-MARCH-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 6017705man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5444.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 40352 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-846-111D-15

Query Match

Best Local Similarity 68.0%; Score 17; DB 3; Length 40352;

Matches 20; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 38797 TCGTGGCAGAGTTGCCCTTTAAGA 38773

RESULT 31

US-09-443-077-15/c

Sequence 15, Application US/09443077

Patent No. 6392016

GENERAL INFORMATION:

APPLICANT: Lurquin, Christophe; Brasseur, Francis;

Boon-Falleur, Thierry



Db 356524 CCAATGCCAGTTGCCGATACG 356546

## RESULT 35

US-09-221-017B-301/c  
; Sequence 301, Application US/09221017B  
; Patent No. 6444799  
; GENERAL INFORMATION:  
; APPLICANT: ROSS, Bruce C.  
; TITLE OF INVENTION: P. GINGIVALIS NUCLEOTIDES AND USES THEREOF  
; NUMBER OF SEQUENCES: 1120  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 755 PAGE MILL ROAD  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304-1018  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: Windows  
; SOFTWARE: FastSeq for Windows Version 2.0b  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/221,017B  
; FILING DATE: 23-DEC-1998  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1182  
; FILING DATE: 31-DEC-1997  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP1546  
; FILING DATE: 30-JAN-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PP2911  
; FILING DATE: 09-APR-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: PCT/AU98/01023  
; FILING DATE: 10-DEC-1998  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Monroy, Gladys H  
; REGISTRATION NUMBER: 32,430  
; REFERENCE/DOCKET NUMBER: 27340-20021.00  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-813-5600  
; TELEFAX: 650-494-0792  
; TELEX: 706141  
; INFORMATION FOR SEQ ID NO: 301:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 508 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: UNKNOWN  
; ORIGINAL SOURCE:  
; ORGANISM: PORPHYROMONAS GINGIVALIS  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 1...508  
US-09-221-017B-301

Query Match 64.8%; Score 16.2; DB 3; Length 508;  
Best Local Similarity 85.7%; Pred. No. 3.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTTGCCCGTTACG 24

Db 201 GCTGCAGAGTAGCCCATTCG 181

## RESULT 36

US-09-949-016-5147  
; Sequence 5147, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5147  
; LENGTH: 3378  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-5147

Query Match 64.8%; Score 16.2; DB 3; Length 3378;  
Best Local Similarity 85.7%; Pred. No. 4.6e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTGCAGAGTTGCCCGTTACGA 25

Db 2711 CTGCATAGATGCCCGTTACTA 2731

## RESULT 37

US-09-949-016-16889  
; Sequence 16889, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16889  
; LENGTH: 17154  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16889

Query Match 64.8%; Score 16.2; DB 3; Length 17154;  
Best Local Similarity 85.7%; Pred. No. 5.7e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 CTGCAGAGTTGCCCGTTACGA 25

Db 14079 CTGCATAGATGCCCGTTACTA 14099

## RESULT 38

US-09-949-016-13873/c  
; Sequence 13873, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13873  
; LENGTH: 106450  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-13873

Query Match 64.8%; Score 16.2; DB 3; Length 106450;  
Best Local Similarity 85.7%; Pred. No. 6.9e+02;  
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTT 21  
Db 64365 TCTGCTGCAGAGTTGCTTTT 64345

RESULT 39  
US-09-891-735-5  
; Sequence 5, Application US/09891735  
; Patent No. 6511837  
; GENERAL INFORMATION:  
; APPLICANT: No. 6511837ozymes A/S  
; APPLICANT: Teutsumi, No. 6511837iko  
; TITLE OF INVENTION: Lipolytic Enzymes  
; FILE REFERENCE: 10057.200-US  
; CURRENT APPLICATION NUMBER: US/09/891,735  
; CURRENT FILING DATE: 2001-06-06  
; NUMBER OF SEQ ID NOS: 7  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 5  
; LENGTH: 32  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Primer  
US-09-891-735-5

Query Match 64.0%; Score 16; DB 3; Length 32;  
Best Local Similarity 79.2%; Pred. No. 3.3e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
Db 6 CTGGTGGAGAGTTCCGCGTTACGA 29

RESULT 40  
US-10-131-827-4079  
; Sequence 4079, Application US/10131827  
; Patent No. 6305827  
; GENERAL INFORMATION:  
; APPLICANT: Wohlgemuth, Jay  
; APPLICANT: Fry, Kirk  
; APPLICANT: Woodward, Robert  
; APPLICANT: Lv, Ngoc  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUNE  
; FILE REFERENCE: 506612000120  
; CURRENT APPLICATION NUMBER: US/10/131.827  
; CURRENT FILING DATE: 2002-09-06  
; PRIOR APPLICATION NUMBER: US 10/006,290

; PRIOR FILING DATE: 2001-10-22  
; PRIOR APPLICATION NUMBER: US 60/296,764  
; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 4079  
; LENGTH: 50  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-4079

Query Match 64.0%; Score 16; DB 3; Length 50;  
Best Local Similarity 79.2%; Pred. No. 3.5e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
Db 18 CCGCTCCAGCTTTCACGTTTCGA 41

RESULT 41  
US-09-252-991A-4772  
; Sequence 4772, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4772  
; LENGTH: 372  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4772

Query Match 64.0%; Score 16; DB 3; Length 372;  
Best Local Similarity 79.2%; Pred. No. 4.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24  
Db 66 TGGCTGCAGAACTGCCCGCAACG 89

RESULT 42  
US-09-252-991A-4736/C  
; Sequence 4736, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252,991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 4736  
; LENGTH: 447  
; TYPE: DNA  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-4736

```

; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 30653
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016--30653

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACG 24
      ||||| ||||| ||||| ||||| |||||
DB 436 TCCGCTTCAGAGCTGCCCTGGCG 459

RESULT 46
US-09-949-016-73156
; Sequence 73156, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73156
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016--73156

Query Match          64.0%; Score 16; DB 3; Length 601;
Best Local Similarity 79.2%; Pred.No. 4.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACG 24
      ||||| ||||| ||||| ||||| |||||
DB 436 TCCGCTTCAGAGCTGCCCTGGCG 459

RESULT 47
US-09-949-016-133356
; Sequence 133356, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03

```

;; PRIOR APPLICATION NUMBER: 60/231,498  
;; PRIOR FILING DATE: 2000-09-08  
;; NUMBER OF SEQ ID NOS: 207012  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 13356  
;; LENGTH: 601  
;; TYPE: DNA  
;; ORGANISM: Human  
US-09-949-016-13356

Query Match 64.0%; Score 16; DB 3; Length 601;  
Best Local Similarity 79.2%; Pred. No. 4.7e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTCGCCGTTACGA 25  
Db 453 CCTCTACAGAGTTCGCTTCTGA 476

RESULT 48  
US-08-998-416-961/c  
; Sequence 961, Application US/08998416  
; Patent No. 6239264  
; GENERAL INFORMATION:  
; APPLICANT: Philippsen, Peter  
; APPLICANT: Pohlmann, Rainer  
; APPLICANT: Steinert, Sabine  
; APPLICANT: Mohr, Christine  
; APPLICANT: Wendland, Jurgin  
; APPLICANT: Knechtle, Philipp  
; APPLICANT: Reibischung, Corinne  
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII  
; TITLE OF INVENTION: AND USES THEREOF  
; NUMBER OF SEQUENCES: 1152  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: No. 6239264artis Corporation  
; STREET: 3054 Cornwallis Road  
; CITY: Research Triangle Park  
; STATE: No. 6239264th Carolina  
; COUNTRY: USA  
; ZIP: 27709  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; APPLICATION NUMBER: US/08/998,416  
; FILING DATE: 24-DEC-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: CH 0016/97  
; FILING DATE: 31-DEC-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Meigs, J. Timothy  
; REGISTRATION NUMBER: 38,241  
; REFERENCE/DOCKET NUMBER: PP/5-30306/A/CCCL976  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 919-541-8587  
; TELEFAX: 919-541-8689  
; INFORMATION FOR SEQ ID NO: 961:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 718 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; ORIGINAL SOURCE:  
; ORGANISM: FAGL593RP  
US-08-998-416-961

Query Match 64.0%; Score 16; DB 3; Length 718;  
Best Local Similarity 79.2%; Pred. No. 4.8e+02;

Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
Qy 2 CCGCTGCAGAGTTCGCCGTTACGA 25  
Db 26 CCGTTCAGAGTTGCTCTATTTCGA 3

RESULT 49  
US-09-799-451-300/c  
; Sequence 300, Application US/09799451  
; Patent No. 6783969  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Zhou, Ping  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Ren, Feiyan  
; APPLICANT: Zhang, Jie  
; APPLICANT: Xue, Aidong J.  
; APPLICANT: Zhao, Qing A.  
; APPLICANT: Wang, Jian-Rui  
; APPLICANT: Ma, Yunging  
; APPLICANT: Yamazaki, Victoria  
; APPLICANT: Chen, Rui-hong  
; APPLICANT: Wang, Zhiwei  
; APPLICANT: Wang, Dunrui  
; APPLICANT: Yang, Yonghong  
; APPLICANT: Wehrman, Tom  
; APPLICANT: Ghosh, Reena  
; APPLICANT: Drmanac, Radoje T.  
; TITLE OF INVENTION: No. 6783969el Nucleic Acids and  
; TITLE OF INVENTION: Polypeptides  
; FILE REFERENCE: 803  
; CURRENT APPLICATION NUMBER: US/09/799,451  
; CURRENT FILING DATE: 2001-03-05  
; NUMBER OF SEQ ID NOS: 948  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 300  
; LENGTH: 942  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (52)..(807)  
US-09-799-451-300

Query Match 64.0%; Score 16; DB 3; Length 942;  
Best Local Similarity 79.2%; Pred. No. 4.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACG 24  
Db 190 TCCGCTGCAGAGTTCGCCGTTACG 167

RESULT 50  
US-09-640-211A-154/c  
; Sequence 154, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; TITLE OF INVENTION: Modification of Gene Transcription  
; FILE REFERENCE: 11000,1021CIU  
; CURRENT APPLICATION NUMBER: US/09/640,211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 154  
; LENGTH: 1144

```

; Patent No. 6432898
; GENERAL INFORMATION:
; APPLICANT: Rev, Michael W.
; APPLICANT: Golightly, Elizabeth J.
; TITLE OF INVENTION: Polypeptides Having Lipase Activity And
; FILE REFERENCE: 10052.000-US
; CURRENT APPLICATION NUMBER: US/09/703,416
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-09-703-416-1

Query Match 64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred.No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 2 CCGCTGCAGAGTTCGCCGTTACGA 25
DB 2132 CTGGTGAGAGATCCCGGTTACGA 2155

RESULT 54
US-09-703-414-1
; Sequence 1, Application US/09703414
; Patent No. 6558715
; GENERAL INFORMATION:
; APPLICANT: Rev, Michael W.
; APPLICANT: Golightly, Elizabeth J.
; APPLICANT: Spendler, Tina
; TITLE OF INVENTION: Methods For Using Lipases In Baking
; FILE REFERENCE: 10074.000-US
; CURRENT APPLICATION NUMBER: US/09/703,414
; CURRENT FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-09-703-414-1

Query Match 64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred.No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0

QY 2 CCGCTGCAGAGTTCGCCGTTACGA 25
DB 2132 CTGGTGAGAGATCCCGGTTACGA 2155

RESULT 55
US-10-171-229-1
; Sequence 1, Application US/10171229
; Patent No. 6686189
; GENERAL INFORMATION:
; APPLICANT: Rev, Michael W.
; APPLICANT: Golightly, Elizabeth J.
; TITLE OF INVENTION: Polypeptides Having Lipase Activity And
; FILE REFERENCE: 10052.000-US
; CURRENT APPLICATION NUMBER: US/10/171,229
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/703,416
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2940

```

```
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-171-229-1

Query Match      64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 2132 CTGCTGGAGAGTTCCGCGTTACGA 2155

RESULT 56
US-10-429-398-1
; Sequence 1, Application US/10429398
; Patent No. 6730346
; GENERAL INFORMATION:
; APPLICANT: Rev. Michael W.
; APPLICANT: Golightly, Elizabeth J.
; APPLICANT: Spendler, Tina
; TITLE OF INVENTION: Methods For Using Lipases In Baking
; FILE REFERENCE: 10074.000-US
; CURRENT APPLICATION NUMBER: US/10/429,398
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US/09/703,414
; PRIOR FILING DATE: 2000-10-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2940
; TYPE: DNA
; ORGANISM: Fusarium venenatum
US-10-429-398-1

Query Match      64.0%; Score 16; DB 3; Length 2940;
Best Local Similarity 79.2%; Pred. No. 5.7e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 2132 CTGCTGGAGAGTTCCGCGTTACGA 2155

RESULT 57
5175383-1
; Patent No. 5175383
; APPLICANT: LEDER, PHILIP; MULLER, WILLIAM J.
; TITLE OF INVENTION: ANIMAL MODEL FOR BENIGN PROSTATIC DISEASE
; NUMBER OF SEQUENCES: 9
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/312,641
; FILING DATE: 17-FEB-1989
; SEQ ID NO:1
; LENGTH: 7868
5175383-1

Query Match      64.0%; Score 16; DB 9; Length 7868;
Best Local Similarity 79.2%; Pred. No. 6.4e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
| | | | | | | | | | | | | | | | | | | | | |
Db 5893 CTGCTGCAGAGTAGCCGCCACGA 5916

RESULT 58
US-09-949-016-13876
; Sequence 13876, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
```

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13876
; LENGTH: 36171
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13876

Query Match      64.0%; Score 16; DB 3; Length 36171;
Best Local Similarity 79.2%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
| | | | | | | | | | | | | | | | | | | | | |
Db 26651 TCCGCTTCAGAGCTGCCCTGGCG 26674

RESULT 59
US-09-949-016-12389
; Sequence 12389, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12389
; LENGTH: 36274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12389

Query Match      64.0%; Score 16; DB 3; Length 36274;
Best Local Similarity 79.2%; Pred. No. 7.6e+02;
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
| | | | | | | | | | | | | | | | | | | | | |
Db 26762 TCCGCTTCAGAGCTGCCCTGGCG 26785

RESULT 60
US-09-949-016-17230/c
; Sequence 17230, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
```



; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17230  
; LENGTH: 90776  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-17230

Query Match 64.0%; Score 16; DB 3; Length 90776;  
Best Local Similarity 79.2%; Pred. No. 8.4e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
Db 85436 CCAGTGCAGAGTTGACCGTTTCCA 85413

RESULT 61  
US-09-949-016-15494  
; Sequence 15494, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15494  
; LENGTH: 183770  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(183770)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-15494

Query Match 64.0%; Score 16; DB 3; Length 183770;  
Best Local Similarity 79.2%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
Db 66481 CCTCTACAGAGTTGCCTGTCTGA 66504

RESULT 62  
US-09-949-016-13418  
; Sequence 13418, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13418  
; LENGTH: 236474  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(236474)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13418

Query Match 64.0%; Score 16; DB 3; Length 236474;  
Best Local Similarity 79.2%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24  
Db 34694 TCCGCTGCAGAGTTGCCCGTCCG 34717

RESULT 63  
US-09-214-808-1  
; Sequence 1, Application US/09214808A  
; Patent No. 6475793  
; GENERAL INFORMATION:  
; APPLICANT: Rosenthal, Andre  
; APPLICANT: Freiberg, Christoph  
; APPLICANT: Perret, Xavier Philippe  
; APPLICANT: Broughton, William John  
; TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic  
; Patent No. 6475793  
; TITLE OF INVENTION: Plasmid  
; FILE REFERENCE: CARP0068  
; CURRENT APPLICATION NUMBER: US/09/214,808A  
; CURRENT FILING DATE: 1999-06-22  
; PRIOR APPLICATION NUMBER: PCT/IB97/00950  
; PRIOR FILING DATE: 1997-07-10  
; NUMBER OF SEQ ID NOS: 1  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 536165  
; TYPE: DNA  
; ORGANISM: Rhizobium  
US-09-214-808-1

Query Match 64.0%; Score 16; DB 3; Length 536165;  
Best Local Similarity 79.2%; Pred. No. 9.1e+02;  
Matches 19; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24  
Db 510096 TCCGCTGCAGAGTTGCTGTGACG 510119

RESULT 64  
US-09-513-999C-30616  
; Sequence 30616, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2 REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26  
; SOFTWARE: Patent.pm  
; SEQ ID NO 30616  
; LENGTH: 290  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-513-999C-30616

Query Match 63.2%; Score 15.8; DB 3; Length 290;  
Best Local Similarity 89.5%; Pred. No. 5.3e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTGCCTGT 20  
Db 106 CCGCTGCAGAGTGCCTGT 124

## RESULT 65

US-09-953-318-100/c  
; Sequence 100, Application US/09953318  
; Patent No. 6710174  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR  
; FILE REFERENCE: RTS-0232  
; CURRENT APPLICATION NUMBER: US/09/953.318  
; CURRENT FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 154  
; SEQ ID NO 100  
; LENGTH: 3394  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (252)...(2318)  
US-09-953-318-100

Query Match 63.2%; Score 15.8; DB 3; Length 3394;  
Best Local Similarity 89.5%; Pred. No. 7.2e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGCCTGT 22  
Db 524 GCTGCAGAGTGCCTGT 506

## RESULT 66

US-09-953-318-10/c  
; Sequence 10, Application US/09953318  
; Patent No. 6710174  
; GENERAL INFORMATION:  
; APPLICANT: C. Frank Bennett  
; APPLICANT: Andrew T. Watt  
; TITLE OF INVENTION: ANTISENSE MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR  
; FILE REFERENCE: RTS-0232  
; CURRENT APPLICATION NUMBER: US/09/953.318  
; CURRENT FILING DATE: 2001-09-13  
; NUMBER OF SEQ ID NOS: 154  
; SEQ ID NO 10  
; LENGTH: 6055  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (27)...(4028)  
US-09-953-318-10

Query Match 63.2%; Score 15.8; DB 3; Length 6055;  
Best Local Similarity 89.5%; Pred. No. 7.7e+02;

Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 4 GCTGCAGAGTGCCTGT 22  
Db 299 GCTGCAGAGTGCCTGT 281

## RESULT 67

US-09-949-016-14973/c  
; Sequence 14973, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14973  
; LENGTH: 7620  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14973

Query Match 63.2%; Score 15.8; DB 3; Length 7620;  
Best Local Similarity 89.5%; Pred. No. 7.9e+02;  
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTGCCTG 19  
Db 7418 TCCGCTGCAGAGTGCCTG 7400

## RESULT 68

US-09-396-196G-74495  
; Sequence 74495, Application US/09396196G  
; Patent No. 6821724  
; GENERAL INFORMATION:  
; APPLICANT: Michael Mittmann  
; APPLICANT: David Mack  
; APPLICANT: David Lockhart  
; APPLICANT: Affymetrix, Inc.  
; TITLE OF INVENTION: Methods of Genetic Analysis  
; FILE REFERENCE: 3101.1  
; CURRENT APPLICATION NUMBER: US/09/396,196G  
; CURRENT FILING DATE: 1999-09-15  
; PRIOR APPLICATION NUMBER: 60/100,678  
; PRIOR FILING DATE: 1998-09-17  
; NUMBER OF SEQ ID NOS: 127806  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 74495  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: mus musculus  
US-09-396-196G-74495

Query Match 62.4%; Score 15.6; DB 3; Length 25;  
Best Local Similarity 81.8%; Pred. No. 4.9e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTGCCTG 22  
Db 4 TCCACTGCAGAGTGGACGTCA 25

## RESULT 69

US-09-976-594-305/c  
; Sequence 305, Application US/09976594  
; Patent No. 6673549  
; GENERAL INFORMATION:  
; APPLICANT: Furness, Michael  
; APPLICANT: Buchbinder, Jenny  
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS  
; FILE REFERENCE: PA-0041 US  
; CURRENT APPLICATION NUMBER: US/09/976,594  
; CURRENT FILING DATE: 2001-10-12  
; PRIOR APPLICATION NUMBER: 60/240,409  
; PRIOR FILING DATE: 2000-10-12  
; NUMBER OF SEQ ID NOS: 1143  
; SOFTWARE: PERL Program  
; SEQ ID NO 305  
; LENGTH: 452  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No. 6673549 1329120.10  
; NAME/KEY: unsure  
; LOCATION: 299  
; OTHER INFORMATION: a, t, c, g, or other  
US-09-976-594-305

Query Match 62.4%; Score 15.6; DB 3; Length 452;

Best Local Similarity 81.8%; Pred. No. 7e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTGGCCCGTTACG 24

Db 212 CGCTCCACAGATGCCAGTTACG 191

## RESULT 70

US-09-533-559-4705  
; Sequence 4705, Application US/09533559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjarke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; FILE REFERENCE: Expression  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4705  
; LENGTH: 685  
; TYPE: DNA  
; ORGANISM: Aspergillus oryzae  
US-09-533-559-4705

Query Match 62.4%; Score 15.6; DB 3; Length 685;

Best Local Similarity 81.8%; Pred. No. 7.3e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25

Db 186 GCTGCAGAGTGGCCCGCTAAGA 207

## RESULT 71

US-09-543-681A-1424

; Sequence 1424, Application US/09543681A  
; Patent No. 6605709  
; GENERAL INFORMATION:  
; APPLICANT: GARY BRETON  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
; FILE REFERENCE: 2709.1002-001  
; CURRENT APPLICATION NUMBER: US/09/543,681A  
; CURRENT FILING DATE: 2000-04-05  
; PRIOR APPLICATION NUMBER: US 60/128,706  
; PRIOR FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 8344  
; SEQ ID NO 1424  
; LENGTH: 1059  
; TYPE: DNA  
; ORGANISM: Proteus mirabilis  
US-09-543-681A-1424

Query Match 62.4%; Score 15.6; DB 3; Length 1059;

Best Local Similarity 81.8%; Pred. No. 7.7e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTGGCCCGTTA 22

Db 124 TCCGCTGCTGATTACCCGGTA 145

## RESULT 72

US-08-106-981-5  
; Sequence 5, Application US/08106981  
; Patent No. 5731419  
; GENERAL INFORMATION:  
; APPLICANT: SARHAN, Fathey  
; APPLICANT: HOUE, Mario  
; APPLICANT: LALIBERT, Jean-Fran ois  
; TITLE OF INVENTION: DNA MOLECULES ENCODING FREEZING  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/106,981  
; FILING DATE: 16-AUG-1993  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 163-23  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1136  
; TYPE: Nucleic acid  
; STRANDEDNESS: Double  
; TOPOLOGY: Linear  
; MOLECULE TYPE: cDNA to mRNA  
; ORIGINAL SOURCE: Triticum aestivum L.  
US-08-106-981-5

Query Match

62.4%; Score 15.6; DB 2; Length 1136;

Best Local Similarity 81.8%; Pred. No. 7.8e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTGGCCCGTTACG 24  
Db 674 CGCTGCTGCGGTGCCCGTCACG 695

RESULT 73

US-09-232-468A-13/c  
; Sequence 13, Application US/09232468A  
; Patent No. 6207165  
; GENERAL INFORMATION:  
; APPLICANT: AUDONNET et al.  
; TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA AGAINST PORCINE  
; TITLE OF INVENTION: REPRODUCTIVE AND RESPIRATORY PATHOLOGIES  
; FILE REFERENCE: 454313-2230  
; CURRENT APPLICATION NUMBER: US/09/232.468A  
; CURRENT FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Porcine Flu Virus (SIV, H1N1 "Sw" Strain)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1698)  
US-09-232-468A-13

Query Match 62.4%; Score 15.6; DB 3; Length 1701;  
Best Local Similarity 81.8%; Pred. No. 8.2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25  
Db 180 GCTGCAGAGTGGCCCGTTATGA 159

RESULT 74

US-09-784-984B-11/c  
; Sequence 11, Application US/09784984B  
; Patent No. 6576243  
; GENERAL INFORMATION:  
; APPLICANT: Meril Ltd.  
; APPLICANT: Audonnet, Jean-Christophe  
; APPLICANT: Bouchardon, Annabelle  
; APPLICANT: Baudu, Philippe  
; APPLICANT: Riviere, Michael  
; TITLE OF INVENTION: Polynucleotide Vaccine Formula Against Porcine Reproductive and  
; TITLE OF INVENTION: Respiratory Pathologies  
; FILE REFERENCE: 454313-2230.1  
; CURRENT APPLICATION NUMBER: US/09/784.984B  
; CURRENT FILING DATE: 2001-02-16  
; PRIOR APPLICATION NUMBER: FR 96/09338  
; PRIOR FILING DATE: 1996-07-19  
; PRIOR APPLICATION NUMBER: PCT/FR97/01313  
; PRIOR FILING DATE: 1997-07-15  
; PRIOR APPLICATION NUMBER: US 6,207,165  
; PRIOR FILING DATE: 2001-03-27  
; NUMBER OF SEQ ID NOS: 54  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 11  
; LENGTH: 1701  
; TYPE: DNA  
; ORGANISM: Porcine Flu Virus (SIV, H1N1 "Sw" Strain)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(1698)  
; OTHER INFORMATION:  
US-09-784-984B-11

Query Match 62.4%; Score 15.6; DB 3; Length 1701;

Best Local Similarity 81.8%; Pred. No. 8.2e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25  
Db 180 GCTGCAGAGTGGCCCGTTATGA 159

RESULT 75

US-08-527-152-1/c  
; Sequence 1, Application US/08527152  
; Patent No. 5827655  
; GENERAL INFORMATION:  
; APPLICANT: Chandy, Kanianthara G.  
; APPLICANT: Cahalan, Michael D.  
; APPLICANT: Grissmer, Stephan  
; APPLICANT: Goldin, Alan L.  
; APPLICANT: Dethlefs, Brent A.  
; APPLICANT: Gutman, George A.  
; APPLICANT: Wasmuth, John J.  
; TITLE OF INVENTION: Assay, Methods and Products Based On n  
; TITLE OF INVENTION: K+ Channel Expression  
; NUMBER OF SEQUENCES: 5  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert,  
; ADDRESSEE: Attn: W.H. Dreger  
; STREET: 4 Embarcadero Center, Suite 3400  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: United States  
; ZIP: 94111-4187  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/527,152  
; FILING DATE: UNKNOWN  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/170,418  
; FILING DATE: 20-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/558,568  
; FILING DATE: 27-JUL-1990  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Dreger, Walter H.  
; REGISTRATION NUMBER: 24,190  
; REFERENCE/DOCKET NUMBER: A-54444-2/WHI  
; TELEPHONE: (415) 781-1989  
; TELEFAX: (415) 398-3249  
; TELEX: 910 277299  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1994 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: linear  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 150..1736  
US-08-527-152-1

Query Match 62.4%; Score 15.6; DB 2; Length 1994;  
Best Local Similarity 81.8%; Pred. No. 8.3e+02;  
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTGGCCCGTTACGA 25  
Db 1669 GCTGTGAGTGGCCCGTTTGA 1648

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RESULT 76
US-09-233-857-2/c
; Sequence 2, Application US/09233857
; Patent No. 6495353
; GENERAL INFORMATION:
; APPLICANT: Plowman, Gregory
; APPLICANT: Flanagan, Peter
; TITLE OF INVENTION: HUMAN ORTHOLOGUES OF WART
; FILE REFERENCE: 239/251
; CURRENT APPLICATION NUMBER: US/09/233,857
; CURRENT FILING DATE: 1999-01-20
; EARLIER APPLICATION NUMBER: USSN 60/072,023
; EARLIER FILING DATE: 1998-01-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 5276
; TYPE: DNA
; ORGANISM: HUMAN
US-09-233-857-2

Query Match          62.4%; Score 15.6; DB 3; Length 5276;
Best Local Similarity 81.8%; Pred. No. 9.4e+02;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      2  CCGCTGCAGAGTTGCCCGTTAC 23
Db      663 CAGCTGCAGAGTTGCCCGATT 642

RESULT 77
US-09-453-702B-39/c
; Sequence 39, Application US/09453702B
; Patent No. 6365723
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6365723el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/453,702B
; FILING DATE: 03-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-114-170-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  TCCGCTGCAGAGTTGCCCGTTA 22
Db      17400 TCGCTCCAGGTTTGGCCGTTA 17379

RESULT 78
US-10-114-170-39/c
; Sequence 39, Application US/10114170
; Patent No. 6855814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-114-170-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  TCCGCTGCAGAGTTGCCCGTTA 22
Db      17400 TCGCTCCAGGTTTGGCCGTTA 17379
```

```
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-09-453-702B-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  TCCGCTGCAGAGTTGCCCGTTA 22
Db      17400 TCGCTCCAGGTTTGGCCGTTA 17379

RESULT 78
US-10-114-170-39/c
; Sequence 39, Application US/10114170
; Patent No. 6855814
; GENERAL INFORMATION:
; APPLICANT: Blattner, Frederick R.
; Burland, Nicole T.
; Perna, Nicole T.
; Plunkett, Guy
; Welch, Rod
; TITLE OF INVENTION: No. 6855814el Sequences of E. coli O157
; NUMBER OF SEQUENCES: 265
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Quarles & Brady
; STREET: 1 South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/114,170
; FILING DATE: 01-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/453,702
; FILING DATE: 03-DEC-1999
; APPLICATION NUMBER: 60/110,955
; FILING DATE: 04-DEC-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 251-5000
; TELEFAX: (608) 251-9166
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 25165
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-114-170-39

Query Match          62.4%; Score 15.6; DB 3; Length 25165;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy      1  TCCGCTGCAGAGTTGCCCGTTA 22
Db      17400 TCGCTCCAGGTTTGGCCGTTA 17379
```

```
RESULT 79
US-09-564-805-28
; Sequence 28, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/564,805
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (910)..(13104)
; OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
; OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
; OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
; OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13756)..(22917)
; OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
; OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
; OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
; OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (910)..(13104)
; OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
; OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
; OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
; OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13756)..(22917)
; OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
; OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
; OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
; OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23045)..(26452)
; OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
; OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
; OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
; OTHER INFORMATION: signal: 26447-26452
; FEATURE:
; NAME/KEY: variation
; LOCATION: (826)..(23879)
; OTHER INFORMATION: s at positions 826 and 23180 is G or C; Y at
; OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
; OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
; OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-564-805-28
Query Match 62.4%; Score 15.6; DB 3; Length 26664;
Best Local Similarity 81.8%; Pred.No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTTGCCGTTACGA 25
||| ||| ||| ||| ||| ||| ||| |||
Db 24888 GCTACGGAGGTGCCCGTTAAGA 24909

RESULT 80
US-09-434-382-28
; Sequence 28, Application US/09434382
; Patent No. 684189
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17q-Linked Prostate Cancer Susceptibility
```

```
; TITLE OF INVENTION: Gene
; FILE REFERENCE: HPC2 Gene
; CURRENT APPLICATION NUMBER: US/09/434,382
; CURRENT FILING DATE: 1999-11-05
; EARLIER APPLICATION NUMBER: US 60/107,468
; EARLIER FILING DATE: 1999-11-06
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 28
; LENGTH: 26664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (910)..(13104)
; OTHER INFORMATION: exon 1: 910-1154; exon 2: 1736-1786; exon 3:
; OTHER INFORMATION: 1925-1995; exon 4: 3025-3089; exon 5: 4361-4418;
; OTHER INFORMATION: exon 6: 5582-5650; exon 7: 7075-7194; exon 8:
; OTHER INFORMATION: 8186-8244; exon 9: 12878-12936; exon 10:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (13756)..(22917)
; OTHER INFORMATION: exon 11: 13756-13868; exon 12: 15283-15378; exon
; OTHER INFORMATION: 13: 16278-16416; exon 14: 16498-16583; exon 15:
; OTHER INFORMATION: 18583-18701; exon 16: 20349-20445; exon 17:
; OTHER INFORMATION: 22172-22310; exon 18: 22879-22917
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (23045)..(26452)
; OTHER INFORMATION: exon 19: 23045-23154; exon 20: 23795-23895; exon
; OTHER INFORMATION: 21: 23973-24093; exon 22: 24354-24432; exon 23:
; OTHER INFORMATION: 25026-25170; exon 24: 25812-26036; polyadenylation
; OTHER INFORMATION: signal: 26447-26452
; FEATURE:
; NAME/KEY: variation
; LOCATION: (826)..(23879)
; OTHER INFORMATION: s at positions 826 and 23180 is G or C; Y at
; OTHER INFORMATION: positions 1914, 5568, 7165, 16431, 1857 and 20486
; OTHER INFORMATION: is C or T; n at position 13128 is t or tgat; r at
; OTHER INFORMATION: positions 22211 and 23879 is A or G.
US-09-434-382-28
Query Match 62.4%; Score 15.6; DB 3; Length 26664;
Best Local Similarity 81.8%; Pred.No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 GCTGCAGAGTTGCCGTTACGA 25
||| ||| ||| ||| ||| ||| ||| |||
Db 24888 GCTACGGAGGTGCCCGTTAAGA 24909

RESULT 81
US-09-949-016-15607
; Sequence 15607, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15607
; LENGTH: 29558
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```
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15607

Query Match      62.4%; Score 15.6; DB 3; Length 29558;
Best Local Similarity 81.8%; Pred. No. 1.1e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCTGCAGAGTTCGCCGTTACGA 25
Db 25979 GCTACGAGGTGCCCGTTAAGA 26000

RESULT 82
US-09-949-016-12968
; Sequence 12968, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12968
; LENGTH: 222452
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12968

Query Match      62.4%; Score 15.6; DB 3; Length 222452;
Best Local Similarity 81.8%; Pred. No. 1.4e+03;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CCGTCGACAGTTCGCCGTTAC 23
Db 21889 CAGTCGACAGTAGACAGTTAC 21910

RESULT 83
US-09-513-999C-3441/c
; Sequence 3441, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 3441
; LENGTH: 267
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 29..265
US-09-513-999C-3441
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```
Query Match      61.6%; Score 15.4; DB 3; Length 267;
Best Local Similarity 76.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
Db 180 TCTCTGCAAAAGTGCCTGTGACGA 156

RESULT 84
US-09-313-294A-2507/c
; Sequence 2507, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 2507
; LENGTH: 268
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700552775H1
; NAME/KEY: unsure
; LOCATION: 26, 132, 191, 211, 239, 245, 266-267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-2507

Query Match      61.6%; Score 15.4; DB 3; Length 268;
Best Local Similarity 76.0%; Pred. No. 8.1e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25
Db 164 TCGGCTGCAAACTGTTCGCTACTA 140

RESULT 85
US-09-313-294A-5359/c
; Sequence 5359, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Lalgudi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 5359
; LENGTH: 282
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700350024H1
; NAME/KEY: unsure
; LOCATION: 44, 150, 262, 267
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-5359

Query Match      61.6%; Score 15.4; DB 3; Length 282;
Best Local Similarity 76.0%; Pred. No. 8.2e+02;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 97 TCGCTGCMAACTTGTCCGCTACTA 73  
|||||

RESULT 86  
US-09-702-705-1202/c  
; Sequence 1202, Application US/09702705  
; Patent No. 6504010  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C14  
; CURRENT APPLICATION NUMBER: US/09/702.705  
; CURRENT FILING DATE: 2000-10-30  
; NUMBER OF SEQ ID NOS: 1833  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-702-705-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 97 TCCGGGAGAGAGCCCGTCACCA 35  
|||||

RESULT 87  
US-09-736-457-1202/c  
; Sequence 1202, Application US/09736457  
; Patent No. 6509448  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; APPLICANT: Wang, Aijun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C15  
; CURRENT APPLICATION NUMBER: US/09/736.457  
; CURRENT FILING DATE: 2000-12-13  
; NUMBER OF SEQ ID NOS: 1864  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-736-457-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 59 TCCGGGAGAGAGCCCGTCACCA 35  
|||||

RESULT 88  
US-09-614-124B-1202/c  
; Sequence 1202, Application US/09614124B  
; Patent No. 6630574  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; FILE REFERENCE: 210121.478C9  
; CURRENT APPLICATION NUMBER: US/09/614.124B  
; CURRENT FILING DATE: 2001-07-11  
; NUMBER OF SEQ ID NOS: 1668  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-614-124B-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 59 TCCGGGAGAGAGCCCGTCACCA 35  
|||||

RESULT 89  
US-09-671-325-1202/c  
; Sequence 1202, Application US/09671325  
; Patent No. 6667154  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedvick, Tom  
; APPLICANT: Carter, Darrick  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND  
; FILE REFERENCE: 210121.478C12  
; CURRENT APPLICATION NUMBER: US/09/671.325  
; CURRENT FILING DATE: 2000-09-26  
; NUMBER OF SEQ ID NOS: 1825  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-671-325-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;  
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25



Db 59 TCCGCGGAGAGAGCCCGTCACCA 35  
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RESULT 90  
US-09-658-824-1202/c  
; Sequence 1202, Application US/09658824  
; Patent No. 6746846  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedwick, Tom  
; APPLICANT: Carter, Darriek  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C11  
; CURRENT APPLICATION NUMBER: US/09/658,824  
; CURRENT FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 1788  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-658-824-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35  
|||||

RESULT 91  
US-10-017-754-1202/c  
; Sequence 1202, Application US/10017754  
; Patent No. 6858204  
; GENERAL INFORMATION:  
; APPLICANT: Henderson, Robert A.  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Watanabe, Yoshihiro  
; APPLICANT: Johnson, Jeffrey C.  
; APPLICANT: Retter, Marc W.  
; APPLICANT: Marnerakis, Margarita  
; APPLICANT: Carter, Darriek  
; APPLICANT: Fanger, Gary R.  
; APPLICANT: Vedwick, Thomas S.  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: McNabb, Andria  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C18  
; CURRENT APPLICATION NUMBER: US/10/017,754  
; CURRENT FILING DATE: 2001-10-29  
; NUMBER OF SEQ ID NOS: 2004  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-017-754-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35  
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RESULT 92  
US-09-651-563-1202/c  
; Sequence 1202, Application US/09651563  
; Patent No. 6914132  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Tongtong  
; APPLICANT: Bangur, Chaitanya S.  
; APPLICANT: Lodes, Michael A.  
; APPLICANT: Fanger, Gary  
; APPLICANT: Vedwick, Tom  
; APPLICANT: Carter, Darriek  
; APPLICANT: Retter, Marc  
; APPLICANT: Mannion, Jane  
; APPLICANT: Fan, Liqun  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND  
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER  
; FILE REFERENCE: 210121.478C10  
; CURRENT APPLICATION NUMBER: US/09/651,563  
; CURRENT FILING DATE: 2000-08-29  
; NUMBER OF SEQ ID NOS: 1679  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 1202  
; LENGTH: 325  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-651-563-1202

Query Match 61.6%; Score 15.4; DB 3; Length 325;  
Best Local Similarity 76.0%; Pred. No. 8.3e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 59 TCCGCGGAGAGAGCCCGTCACCA 35  
|||||

RESULT 93  
US-09-700-820C-25/c  
; Sequence 25, Application US/09700820C  
; Patent No. 6610485  
; GENERAL INFORMATION:  
; APPLICANT: Tsuchiya, Masayuki  
; APPLICANT: Saito, Mikiyoshi  
; APPLICANT: Ohtomo, Toshihiko  
; TITLE OF INVENTION: NOVEL METHOD FOR GENE CLONING  
; FILE REFERENCE: 06501-070001  
; CURRENT APPLICATION NUMBER: US/09/700,820C  
; CURRENT FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: PCT/JP99/02341  
; PRIOR FILING DATE: 1999-04-30  
; PRIOR APPLICATION NUMBER: JP 10/138652  
; PRIOR FILING DATE: 1998-05-20  
; PRIOR APPLICATION NUMBER: JP 10/279876  
; PRIOR FILING DATE: 1998-10-01  
; NUMBER OF SEQ ID NOS: 39  
; SEQ ID NO 25  
; LENGTH: 363  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(363)  
US-09-700-820C-25

Query Match 61.6%; Score 15.4; DB 3; Length 363;  
Best Local Similarity 76.0%; Pred. No. 8.4e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 110 TCCGGGGAGAGAGCCCGTACCA 86  
|||||

## RESULT 94

US-08-754-477A-119/c  
; Sequence 119, Application US/08754477A  
; Patent No. 6518411  
; GENERAL INFORMATION:  
; APPLICANT: Murray, Jeffrey  
; APPLICANT: Semina, Elena  
; TITLE OF INVENTION: RIEG COMPOSITIONS AND THERAPEUTIC  
; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR  
; NUMBER OF SEQUENCES: 139  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
; STREET: One Post Office Square  
; CITY: Boston  
; STATE: MA  
; COUNTRY: USA  
; ZIP: 02109-2170  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/754.477A  
; FILING DATE: 22-NOV-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arnold, Beth E.  
; REGISTRATION NUMBER: 35,430  
; REFERENCE/DOCKET NUMBER: UTA-022.01  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 617-832-1000  
; TELEFAX: 617-832-7000  
; INFORMATION FOR SEQ ID NO: 119:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 515 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-754-477A-119

Query Match 61.6%; Score 15.4; DB 3; Length 515;  
Best Local Similarity 76.0%; Pred. No. 8.8e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 57 TCTGGGGCAGAGTTGCCCACTCCGA 33  
|||||

## RESULT 95

US-09-023-655-1384/c  
; Sequence 1384, Application US/09023655  
; Patent No. 6607879  
; GENERAL INFORMATION:  
; APPLICANT: Cocks, Benjamin G.  
; APPLICANT: Susan G. Stuart  
; APPLICANT: Jeffrey J. Seilhamer  
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE  
; TITLE OF INVENTION: EXPRESSION  
; NUMBER OF SEQUENCES: 1508  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
; STREET: 3174 PORTER DRIVE  
; CITY: PALO ALTO  
; STATE: CALIFORNIA  
; COUNTRY: USA  
; ZIP: 94304

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/023,655  
; FILING DATE: HEREWITH  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Zeller, Karen J.  
; REGISTRATION NUMBER: 37,071  
; REFERENCE/DOCKET NUMBER: PA-0001 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (650) 855-0555  
; TELEFAX: (650) 845-4166  
; INFORMATION FOR SEQ ID NO: 1384:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 540 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; IMMEDIATE SOURCE:  
; LIBRARY: GENBANK  
; CLONE: g38405\_2  
US-09-023-655-1384

Query Match 61.6%; Score 15.4; DB 3; Length 540;  
Best Local Similarity 76.0%; Pred. No. 8.8e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 239 TCCGGGGAGAGAGCCCGTACCA 215  
|||||

## RESULT 96

US-09-533-559-1903/c  
; Sequence 1903, Application US/09533559  
; Patent No. 6902887  
; GENERAL INFORMATION:  
; APPLICANT: Randy M. Berka  
; APPLICANT: Michael W. Rey  
; APPLICANT: Jeffrey R. Shuster  
; APPLICANT: Sakari Kauppinen  
; APPLICANT: Ib Groth Clausen  
; APPLICANT: Peter Bjarke Olsen  
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene  
; TITLE OF INVENTION: Expression  
; FILE REFERENCE: 5849.200-US  
; CURRENT APPLICATION NUMBER: US/09/533,559  
; CURRENT FILING DATE: 2000-03-22  
; EARLIER APPLICATION NUMBER: 09/273,623  
; EARLIER FILING DATE: 1999-03-22  
; NUMBER OF SEQ ID NOS: 7860  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1903  
; LENGTH: 582  
; TYPE: DNA  
; ORGANISM: Fusarium venenatum  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (1)-(582)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-533-559-1903

Query Match 61.6%; Score 15.4; DB 3; Length 582;  
Best Local Similarity 76.0%; Pred. No. 8.9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
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Db 545 TCCGATTCGAATGCCCGTCATGA 521

## RESULT 97

US-09-949-016-47406/c  
; Sequence 47406, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47406  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-47406

Query Match 61.6%; Score 15.4; DB 3; Length 601;  
Best Local Similarity 76.0%; Pred. No. 9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

## RESULT 98

US-09-949-016-47418/c  
; Sequence 47418, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47418  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-47418

Query Match 61.6%; Score 15.4; DB 3; Length 601;  
Best Local Similarity 76.0%; Pred. No. 9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

## RESULT 99

US-09-949-016-47430/c  
; Sequence 47430, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 47430  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-47430

Query Match 61.6%; Score 15.4; DB 3; Length 601;  
Best Local Similarity 76.0%; Pred. No. 9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 262 TCCACAGCAGAGTTGCCCGTGAGA 238

## RESULT 100

US-09-949-002-1736/c  
; Sequence 1736, Application US/09949002  
; Patent No. 6900016  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION  
; AND USES THEREOF  
; FILE REFERENCE: CL000790  
; CURRENT APPLICATION NUMBER: US/09/949,002  
; CURRENT FILING DATE: 2000-01-28  
; PRIOR APPLICATION NUMBER: 60/231,401  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 10823  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1736  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-002-1736

Query Match 61.6%; Score 15.4; DB 3; Length 601;  
Best Local Similarity 76.0%; Pred. No. 9e+02;  
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 376 TCCATTGCAGGATGCCCGTGAGA 352

Search completed: March 8, 2006, 21:08:21  
Job time : 131.903 secs

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:15:52 ; Search time 725.243 Seconds  
(without alignments)  
285.056 Million cell updates/sec

Title: US-10-829-474-4

Perfect score: 25

Sequence: 1 tccgctgcagagtgcccgtaacga 25

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 413489005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 500 summaries

Database : Published Applications\_NA\_Main:

- 1: /cgn2\_6/ptodata/1/pubna/US07\_PUBCOMB.seq\*
- 2: /cgn2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq\*
- 3: /cgn2\_6/ptodata/1/pubna/US09A\_PUBCOMB.seq\*
- 4: /cgn2\_6/ptodata/1/pubna/US09B\_PUBCOMB.seq\*
- 5: /cgn2\_6/ptodata/1/pubna/US10A\_PUBCOMB.seq\*
- 6: /cgn2\_6/ptodata/1/pubna/US10B\_PUBCOMB.seq\*
- 7: /cgn2\_6/ptodata/1/pubna/US10C\_PUBCOMB.seq\*
- 8: /cgn2\_6/ptodata/1/pubna/US10D\_PUBCOMB.seq\*
- 9: /cgn2\_6/ptodata/1/pubna/US10E\_PUBCOMB.seq\*
- 10: /cgn2\_6/ptodata/1/pubna/US11\_PUBCOMB.seq\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	25	9	US-10-829-474-4
2	25	100.0	26	9	US-10-829-474-4
3	25	100.0	26	9	US-10-829-474-4
4	25	100.0	69	9	US-10-295-787D-27
5	25	100.0	70	9	US-10-295-787D-6
6	25	100.0	70	9	US-10-295-787D-7
7	25	100.0	70	9	US-10-295-787D-9
8	25	100.0	70	9	US-10-295-787D-12
9	25	100.0	70	9	US-10-295-787D-14
10	25	100.0	70	9	US-10-295-787D-16
11	25	100.0	70	9	US-10-295-787D-18
12	25	100.0	70	9	US-10-295-787D-19
13	25	100.0	70	9	US-10-295-787D-20
14	25	100.0	70	9	US-10-295-787D-22
15	25	100.0	70	9	US-10-295-787D-35
16	25	100.0	107	9	US-10-760-048-53
17	25	100.0	126	9	US-10-760-048-18
18	25	100.0	237	9	US-10-760-048-32
19	25	100.0	238	9	US-10-760-048-13
20	25	100.0	238	9	US-10-760-048-14
21	25	100.0	238	9	US-10-760-048-15
22	25	100.0	238	9	US-10-760-048-19
23	25	100.0	238	9	US-10-760-048-22

Sequence 24, Appl	238	9	US-10-760-048-24
Sequence 25, Appl	238	9	US-10-760-048-25
Sequence 26, Appl	238	9	US-10-760-048-26
Sequence 27, Appl	238	9	US-10-760-048-27
Sequence 28, Appl	238	9	US-10-760-048-28
Sequence 29, Appl	238	9	US-10-760-048-29
Sequence 30, Appl	238	9	US-10-760-048-30
Sequence 31, Appl	238	9	US-10-760-048-31
Sequence 42, Appl	238	9	US-10-760-048-42
Sequence 43, Appl	238	9	US-10-760-048-43
Sequence 46, Appl	238	9	US-10-760-048-46
Sequence 47, Appl	238	9	US-10-760-048-47
Sequence 48, Appl	238	9	US-10-760-048-48
Sequence 54, Appl	238	9	US-10-760-048-54
Sequence 67, Appl	660	9	US-10-760-048-67
Sequence 1, Appl	709	9	US-10-614-283-1
Sequence 7, Appl	7399	6	US-10-136-819-7
Sequence 42, Appl	24	9	US-10-829-474-42
Sequence 43, Appl	24	9	US-10-829-474-43
Sequence 28, Appl	66	9	US-10-295-787D-28
Sequence 4, Appl	70	9	US-10-295-787D-4
Sequence 15, Appl	70	9	US-10-295-787D-15
Sequence 5, Appl	25	9	US-10-829-474-5
Sequence 56, Appl	26	9	US-10-829-474-56
Sequence 57, Appl	26	9	US-10-829-474-57
Sequence 21, Appl	70	9	US-10-295-787D-21
Sequence 23, Appl	70	9	US-10-295-787D-23
Sequence 31, Appl	70	9	US-10-295-787D-31
Sequence 112, Appl	70	9	US-10-295-787D-112
Sequence 17, Appl	71	9	US-10-295-787D-17
Sequence 8, Appl	75	9	US-10-295-787D-8
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Sequence 40, Appl	117	9	US-10-760-048-40
Sequence 37, Appl	236	9	US-10-760-048-37
Sequence 49, Appl	236	9	US-10-760-048-49
Sequence 50, Appl	236	9	US-10-760-048-50
Sequence 51, Appl	236	9	US-10-760-048-51
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Sequence 33, Appl	238	9	US-10-760-048-33
Sequence 55, Appl	525	7	US-10-332-123-55
Sequence 38, Appl	23	9	US-10-829-474-38
Sequence 39, Appl	23	9	US-10-829-474-39
Sequence 41, Appl	23	9	US-10-829-474-41
Sequence 2, Appl	58	6	US-10-408-519-2
Sequence 52, Appl	24	9	US-10-829-474-52
Sequence 53, Appl	24	9	US-10-829-474-53
Sequence 5, Appl	62	6	US-10-366-823-5
Sequence 13, Appl	70	9	US-10-295-787D-13
Sequence 44, Appl	22	9	US-10-829-474-44
Sequence 45, Appl	22	9	US-10-829-474-45
Sequence 48, Appl	23	9	US-10-829-474-48
Sequence 49, Appl	23	9	US-10-829-474-49
Sequence 51, Appl	23	9	US-10-829-474-51
Sequence 26, Appl	70	9	US-10-295-787D-26
Sequence 29, Appl	70	9	US-10-295-787D-29
Sequence 52, Appl	110	9	US-10-760-048-52
Sequence 21, Appl	235	9	US-10-760-048-21
Sequence 41, Appl	237	9	US-10-760-048-41
Sequence 23, Appl	238	9	US-10-760-048-23
Sequence 34, Appl	238	9	US-10-760-048-34
Sequence 35, Appl	238	9	US-10-760-048-35
Sequence 36, Appl	238	9	US-10-760-048-36
Sequence 40, Appl	21	9	US-10-829-474-40
Sequence 54, Appl	22	9	US-10-829-474-54
Sequence 55, Appl	22	9	US-10-829-474-55
Sequence 24, Appl	69	9	US-10-295-787D-24
Sequence 25, Appl	70	9	US-10-295-787D-25
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Sequence 38, Appl	238	9	US-10-760-048-38
Sequence 50, Appl	21	9	US-10-829-474-50
Sequence 62, Appl	238	9	US-10-760-048-62

c 97	18.6	74.4	521	7	US-10-332-123-53	Sequence 53, Appl	c 170	17	68.0	237	9	US-10-760-048-56	Sequence 56, Appl
c 98	18.2	72.8	1499	7	US-10-425-114-9634	Sequence 9634, Ap	c 171	17	68.0	237	9	US-10-760-048-57	Sequence 57, Appl
c 99	18.2	72.8	1645	7	US-10-424-599-2070	Sequence 2070, Ap	c 172	17	68.0	237	9	US-10-760-048-59	Sequence 59, Appl
c 100	17.6	70.4	1182	3	US-09-738-626-2740	Sequence 2740, Ap	c 173	17	68.0	237	9	US-10-760-048-60	Sequence 60, Appl
c 101	17.6	70.4	2692	10	US-11-097-143-25478	Sequence 25478, A	c 174	17	68.0	237	9	US-10-760-048-63	Sequence 63, Appl
c 102	17.6	70.4	3663	10	US-11-097-143-23542	Sequence 23542, A	c 175	17	68.0	237	9	US-10-760-048-64	Sequence 64, Appl
c 103	17.6	70.4	6051	10	US-11-097-143-25477	Sequence 25477, A	c 176	17	68.0	237	9	US-10-760-048-66	Sequence 66, Appl
c 104	17.6	70.4	6462	8	US-10-775-169-329	Sequence 329, App	c 177	17	68.0	238	9	US-10-760-048-17	Sequence 17, Appl
c 105	17.6	70.4	3309400	3	US-09-738-626-1	Sequence 1, Appli	c 178	17	68.0	238	9	US-10-760-048-58	Sequence 58, Appl
c 106	17.4	69.6	919	5	US-10-228-794-45	Sequence 45, Appl	c 179	17	68.0	238	9	US-10-760-048-55	Sequence 55, Appl
c 107	17.2	68.8	514	4	US-09-925-065A-465485	Sequence 465485,	c 180	17	68.0	294	7	US-10-424-599-132735	Sequence 132735,
c 108	17.2	68.8	584	4	US-09-925-065A-696948	Sequence 696948,	c 181	17	68.0	537	3	US-09-864-761-20582	Sequence 20582, A
c 109	17.2	68.8	606	3	US-09-974-300-6658	Sequence 6658, Ap	c 182	17	68.0	548	3	US-09-864-761-12453	Sequence 12453, A
c 110	17	68.0	25	9	US-10-829-474-3	Sequence 3, Appli	c 183	17	68.0	603	6	US-10-156-761-1419	Sequence 1419, Ap
c 111	17	68.0	26	9	US-10-829-474-36	Sequence 36, Appl	c 184	17	68.0	743	8	US-10-839-729-21	Sequence 21, Appl
c 112	17	68.0	26	9	US-10-829-474-37	Sequence 37, Appl	c 185	17	68.0	745	8	US-10-489-136-10	Sequence 10, Appl
c 113	17	68.0	66	6	US-10-157-305A-54	Sequence 54, Appl	c 186	17	68.0	1575	6	US-10-369-493-32283	Sequence 32283, A
c 114	17	68.0	66	6	US-10-157-305A-57	Sequence 57, Appl	c 187	17	68.0	1604	8	US-10-425-115-82479	Sequence 82479, A
c 115	17	68.0	66	6	US-10-157-391-54	Sequence 54, Appl	c 188	17	68.0	1782	8	US-10-800-023-37	Sequence 37, Appl
c 116	17	68.0	66	6	US-10-157-391-57	Sequence 57, Appl	c 189	17	68.0	1823	5	US-10-194-163-435	Sequence 435, App
c 117	17	68.0	66	6	US-10-157-096-54	Sequence 54, Appl	c 190	17	68.0	1823	5	US-10-194-163-435	Sequence 435, App
c 118	17	68.0	66	6	US-10-157-096-57	Sequence 57, Appl	c 191	17	68.0	1950	3	US-09-864-761-3816	Sequence 3816, Ap
c 119	17	68.0	66	6	US-10-157-302-54	Sequence 54, Appl	c 192	17	68.0	2076	3	US-09-884-586A-3	Sequence 3, Appli
c 120	17	68.0	66	6	US-10-157-302-57	Sequence 57, Appl	c 193	17	68.0	2337	3	US-09-938-842A-1123	Sequence 1123, Ap
c 121	17	68.0	66	6	US-10-157-215A-54	Sequence 54, Appl	c 194	17	68.0	2337	3	US-09-938-842A-1123	Sequence 1123, Ap
c 122	17	68.0	66	6	US-10-157-215A-57	Sequence 57, Appl	c 195	17	68.0	2544	6	US-10-157-305A-3	Sequence 3, Appli
c 123	17	68.0	66	6	US-10-157-215A-57	Sequence 57, Appl	c 196	17	68.0	2544	6	US-10-157-391-3	Sequence 3, Appli
c 124	17	68.0	66	6	US-10-157-299-54	Sequence 54, Appl	c 197	17	68.0	2544	6	US-10-157-096-3	Sequence 3, Appli
c 125	17	68.0	66	6	US-10-157-299-57	Sequence 57, Appl	c 198	17	68.0	2544	6	US-10-157-302-3	Sequence 3, Appli
c 126	17	68.0	66	6	US-10-154-951B-54	Sequence 54, Appl	c 199	17	68.0	2544	6	US-10-157-215A-3	Sequence 3, Appli
c 127	17	68.0	66	6	US-10-156-831-54	Sequence 54, Appl	c 200	17	68.0	2544	6	US-10-157-299-3	Sequence 3, Appli
c 128	17	68.0	66	6	US-10-156-831-57	Sequence 57, Appl	c 201	17	68.0	2544	6	US-10-154-951B-3	Sequence 3, Appli
c 129	17	68.0	66	6	US-10-157-147-54	Sequence 54, Appl	c 202	17	68.0	2544	6	US-10-156-831-3	Sequence 3, Appli
c 130	17	68.0	66	6	US-10-157-147-57	Sequence 57, Appl	c 203	17	68.0	2544	6	US-10-157-147-3	Sequence 3, Appli
c 131	17	68.0	66	6	US-10-157-166-54	Sequence 54, Appl	c 204	17	68.0	2544	6	US-10-157-166-3	Sequence 3, Appli
c 132	17	68.0	66	6	US-10-157-166-57	Sequence 57, Appl	c 205	17	68.0	2544	6	US-10-156-902-3	Sequence 3, Appli
c 133	17	68.0	66	6	US-10-156-902-54	Sequence 54, Appl	c 206	17	68.0	2544	6	US-10-157-318-3	Sequence 3, Appli
c 134	17	68.0	66	6	US-10-156-902-57	Sequence 57, Appl	c 207	17	68.0	2544	6	US-10-157-178-3	Sequence 3, Appli
c 135	17	68.0	66	6	US-10-157-318-54	Sequence 54, Appl	c 208	17	68.0	2544	6	US-10-156-792A-3	Sequence 3, Appli
c 136	17	68.0	66	6	US-10-157-318-57	Sequence 57, Appl	c 209	17	68.0	2544	6	US-10-157-213-3	Sequence 3, Appli
c 137	17	68.0	66	6	US-10-157-178-54	Sequence 54, Appl	c 210	17	68.0	2544	6	US-10-156-811-3	Sequence 3, Appli
c 138	17	68.0	66	6	US-10-157-178-57	Sequence 57, Appl	c 211	17	68.0	2544	6	US-10-157-073-3	Sequence 3, Appli
c 139	17	68.0	66	6	US-10-156-792A-54	Sequence 54, Appl	c 212	17	68.0	2544	6	US-10-157-106A-3	Sequence 3, Appli
c 140	17	68.0	66	6	US-10-156-792A-57	Sequence 57, Appl	c 213	17	68.0	2544	6	US-10-157-320A-3	Sequence 3, Appli
c 141	17	68.0	66	6	US-10-157-213-54	Sequence 54, Appl	c 214	17	68.0	2544	6	US-10-157-418A-3	Sequence 3, Appli
c 142	17	68.0	66	6	US-10-157-213-57	Sequence 57, Appl	c 215	17	68.0	2544	6	US-10-157-171-3	Sequence 3, Appli
c 143	17	68.0	66	6	US-10-156-811-54	Sequence 54, Appl	c 216	17	68.0	2544	6	US-10-157-491-3	Sequence 3, Appli
c 144	17	68.0	66	6	US-10-156-811-57	Sequence 57, Appl	c 217	17	68.0	2544	6	US-10-157-317-3	Sequence 3, Appli
c 145	17	68.0	66	6	US-10-157-073-54	Sequence 54, Appl	c 218	17	68.0	2785	3	US-09-764-891-7798	Sequence 7798, Ap
c 146	17	68.0	66	6	US-10-157-073-57	Sequence 57, Appl	c 219	17	68.0	4203	3	US-09-764-891-7800	Sequence 7800, Ap
c 147	17	68.0	66	6	US-10-157-106A-54	Sequence 54, Appl	c 220	17	68.0	4203	3	US-09-764-891-7801	Sequence 7801, Ap
c 148	17	68.0	66	6	US-10-157-106A-57	Sequence 57, Appl	c 221	17	68.0	49646	9	US-09-764-891-7801	Sequence 7801, Ap
c 149	17	68.0	66	6	US-10-157-320A-54	Sequence 54, Appl	c 222	17	68.0	9242716	9	US-10-915-740A-5	Sequence 5, Appli
c 150	17	68.0	66	6	US-10-157-320A-57	Sequence 57, Appl	c 223	17	68.0	2025608	6	US-10-915-740A-1068	Sequence 1068, Ap
c 151	17	68.0	66	6	US-10-157-418A-54	Sequence 54, Appl	c 224	16.8	67.2	285	3	US-10-156-761-1	Sequence 1, Appli
c 152	17	68.0	66	6	US-10-157-418A-57	Sequence 57, Appl	c 225	16.8	67.2	294	3	US-09-294-093B-4801	Sequence 4801, Ap
c 153	17	68.0	66	6	US-10-157-171-54	Sequence 54, Appl	c 226	16.8	67.2	294	3	US-09-728-445-347	Sequence 347, App
c 154	17	68.0	66	6	US-10-157-171-57	Sequence 57, Appl	c 227	16.8	67.2	294	3	US-10-964-549-347	Sequence 347, App
c 155	17	68.0	66	6	US-10-157-491-54	Sequence 54, Appl	c 228	16.8	67.2	398	8	US-10-357-930-649	Sequence 649, App
c 156	17	68.0	66	6	US-10-157-491-57	Sequence 57, Appl	c 229	16.8	67.2	399	8	US-10-357-930-9818	Sequence 9818, Ap
c 157	17	68.0	66	6	US-10-157-317-54	Sequence 54, Appl	c 230	16.8	67.2	450	8	US-10-357-930-31019	Sequence 31019, A
c 158	17	68.0	66	6	US-10-157-317-57	Sequence 57, Appl	c 231	16.8	67.2	450	8	US-10-357-930-39988	Sequence 39988, A
c 159	17	68.0	66	6	US-10-157-339-54	Sequence 54, Appl	c 232	16.8	67.2	787	3	US-09-917-800A-1428	Sequence 1428, Ap
c 160	17	68.0	66	6	US-10-157-339-57	Sequence 57, Appl	c 233	16.8	67.2	787	3	US-10-151-803-228	Sequence 228, App
c 161	17	68.0	66	6	US-10-295-787D-30	Sequence 30, Appl	c 234	16.8	67.2	787	3	US-10-152-319A-1963	Sequence 1963, Ap
c 162	17	68.0	70	9	US-10-295-787D-2	Sequence 2, Appli	c 235	16.8	67.2	1130	7	US-10-425-114-5	Sequence 5, Appli
c 163	17	68.0	70	9	US-10-295-787D-3	Sequence 3, Appli	c 236	16.8	67.2	1192	7	US-10-425-114-18401	Sequence 18401, A
c 164	17	68.0	70	9	US-10-295-787D-5	Sequence 5, Appli	c 237	16.8	67.2	1281	6	US-10-369-493-42497	Sequence 42497, A
c 165	17	68.0	70	9	US-10-295-787D-110	Sequence 110, App	c 238	16.8	67.2	1538	7	US-10-425-114-32940	Sequence 32940, A
c 166	17	68.0	70	9	US-10-295-787D-113	Sequence 113, App	c 239	16.8	67.2	1873	8	US-10-425-115-146374	Sequence 146374, A
c 167	17	68.0	73	9	US-10-295-787D-1	Sequence 1, Appli	c 240	16.8	67.2	1891	6	US-10-316-253-108	Sequence 108, App
c 168	17	68.0	74	9	US-10-295-787D-80	Sequence 80, Appl	c 241	16.6	66.4	180227	7	US-10-322-281-308	Sequence 308, App
c 169	17	68.0	236	9	US-10-760-048-55	Sequence 55, Appl	c 242	16.6	66.4	272	8	US-10-425-115-180307	Sequence 180307, A
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C 243	16.6	65.4	415	3	US-09-864-761-18894	Sequence 18894, A	C 316	16	64.0	25	10	US-11-036-317-630624	Sequence 630624,
C 244	16.6	65.4	443	3	US-09-918-995-32266	Sequence 32266, A	317	16	64.0	32	3	US-09-891-735-5	Sequence 5, Appli
C 245	16.6	65.4	455	3	US-09-864-761-2152	Sequence 2152, A	318	16	64.0	50	6	US-10-131-827-4079	Sequence 4079, Ap
C 246	16.6	65.4	584	4	US-09-925-065A-696949	Sequence 696949, A	C 319	16	64.0	204	7	US-10-437-963-56934	Sequence 56934, A
C 247	16.6	65.4	589	4	US-09-925-065A-52347	Sequence 52347, A	C 320	16	64.0	283	8	US-10-357-930-12772	Sequence 12772, A
C 248	16.6	65.4	615	4	US-09-925-065A-148871	Sequence 148871, A	C 321	16	64.0	290	8	US-10-357-930-22359	Sequence 22359, A
C 249	16.6	65.4	683	9	US-10-487-901-2125	Sequence 2125, Ap	C 322	16	64.0	290	8	US-10-357-930-28201	Sequence 28201, A
C 250	16.6	65.4	820	7	US-10-260-238-4789	Sequence 4789, Ap	C 323	16	64.0	307	5	US-10-198-846-12777	Sequence 12777, A
C 251	16.6	65.4	848	5	US-10-027-632-160688	Sequence 160688, A	C 324	16	64.0	319	7	US-10-424-599-125473	Sequence 125473, A
C 252	16.6	65.4	848	6	US-10-027-632-160688	Sequence 160688, A	C 325	16	64.0	321	8	US-10-357-930-3603	Sequence 3603, Ap
C 253	16.6	65.4	1762	9	US-10-450-763-22719	Sequence 22719, A	C 326	16	64.0	339	7	US-10-437-963-12819	Sequence 12819, A
C 254	16.6	65.4	1878	7	US-10-282-132A-13742	Sequence 13742, A	C 327	16	64.0	369	7	US-10-282-122A-33432	Sequence 33432, A
C 255	16.6	65.4	1894	6	US-10-094-749-1535	Sequence 1535, Ap	C 328	16	64.0	419	7	US-10-631-467-250	Sequence 250, App
C 256	16.6	65.4	2358	9	US-10-450-763-22717	Sequence 22717, A	C 329	16	64.0	430	8	US-10-357-930-33928	Sequence 33928, A
C 257	16.6	65.4	2746	6	US-10-108-260A-2234	Sequence 2234, Ap	C 330	16	64.0	430	8	US-10-357-930-42805	Sequence 42805, A
C 258	16.6	65.4	3335	8	US-10-739-930-314	Sequence 314, App	C 331	16	64.0	430	8	US-10-424-599-51763	Sequence 51763, A
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C 260	16.6	65.4	12104	6	US-09-764-877-2761	Sequence 2761, Ap	C 333	16	64.0	495	5	US-10-027-632-221364	Sequence 221364, A
C 261	16.6	65.4	12104	6	US-10-242-515-2761	Sequence 2761, Ap	C 334	16	64.0	506	5	US-10-027-632-221365	Sequence 221365, A
C 262	16.6	65.4	23229	6	US-10-017-161-2003	Sequence 2003, Ap	C 335	16	64.0	506	6	US-10-027-632-221364	Sequence 221364, A
C 263	16.6	65.4	23229	6	US-10-292-798-1649	Sequence 1649, Ap	C 336	16	64.0	530	8	US-10-357-930-15891	Sequence 15891, A
C 264	16.6	65.4	91141	5	US-10-087-192-649	Sequence 649, App	C 337	16	64.0	540	5	US-10-198-846-9203	Sequence 9203, Ap
C 265	16.6	65.4	2731748	7	US-10-297-465A-1	Sequence 1, Appli	C 338	16	64.0	559	5	US-10-027-632-221364	Sequence 221364, A
C 266	16.4	65.6	517	4	US-09-925-065A-814933	Sequence 814933, A	C 339	16	64.0	559	5	US-10-027-632-221365	Sequence 221365, A
C 267	16.4	65.6	2061	7	US-10-282-122A-41544	Sequence 41544, A	C 340	16	64.0	559	6	US-10-027-632-221364	Sequence 221364, A
C 268	16.4	65.6	96598	7	US-10-394-948-25	Sequence 25, Appl	C 341	16	64.0	559	6	US-10-027-632-221365	Sequence 221365, A
C 269	16.4	65.6	96598	7	US-10-052-482-115	Sequence 115, App	C 342	16	64.0	559	6	US-10-767-701-37983	Sequence 37983, A
C 270	16.4	65.6	2731748	7	US-10-297-465A-1	Sequence 1, Appli	C 343	16	64.0	561	3	US-09-918-995-28616	Sequence 28616, A
C 271	16.2	64.8	274	6	US-10-393-840-854	Sequence 854, App	C 344	16	64.0	593	4	US-09-925-065A-154453	Sequence 154453, A
C 272	16.2	64.8	288	7	US-10-437-963-24655	Sequence 24655, A	C 345	16	64.0	596	9	US-10-450-763-10679	Sequence 10679, A
C 273	16.2	64.8	323	6	US-10-393-840-812	Sequence 812, App	C 346	16	64.0	618	8	US-10-357-930-45719	Sequence 45719, A
C 274	16.2	64.8	359	6	US-10-393-840-851	Sequence 851, App	C 347	16	64.0	638	4	US-09-925-065A-88728	Sequence 88728, A
C 275	16.2	64.8	400	6	US-10-393-840-774	Sequence 774, App	C 348	16	64.0	738	7	US-10-322-281-640	Sequence 640, App
C 276	16.2	64.8	403	6	US-10-393-840-773	Sequence 773, App	C 349	16	64.0	778	8	US-10-425-115-63943	Sequence 63943, A
C 277	16.2	64.8	412	3	US-09-960-352-11235	Sequence 11235, A	C 350	16	64.0	820	7	US-10-260-238-4789	Sequence 4789, Ap
C 278	16.2	64.8	417	6	US-10-393-840-848	Sequence 848, App	C 351	16	64.0	828	7	US-10-282-122A-6927	Sequence 6927, Ap
C 279	16.2	64.8	430	6	US-10-393-840-813	Sequence 813, App	C 352	16	64.0	918	5	US-10-198-846-5399	Sequence 5399, Ap
C 280	16.2	64.8	442	3	US-09-918-995-5137	Sequence 5137, App	C 353	16	64.0	941	9	US-10-450-763-15002	Sequence 15002, A
C 281	16.2	64.8	460	6	US-10-393-840-822	Sequence 822, App	C 354	16	64.0	942	7	US-10-302-172-300	Sequence 300, App
C 282	16.2	64.8	463	3	US-09-732-627A-1531	Sequence 1531, Ap	C 355	16	64.0	950	3	US-09-974-300-1143	Sequence 1143, Ap
C 283	16.2	64.8	477	4	US-09-925-065A-500218	Sequence 500218, A	C 356	16	64.0	960	3	US-09-974-300-1086	Sequence 1086, Ap
C 284	16.2	64.8	508	5	US-10-194-163-301	Sequence 301, App	C 357	16	64.0	975	7	US-10-282-122A-39509	Sequence 39509, A
C 285	16.2	64.8	524	4	US-09-925-065A-418795	Sequence 418795, A	C 358	16	64.0	1004	7	US-10-282-122A-36877	Sequence 36877, A
C 286	16.2	64.8	524	4	US-09-925-065A-418796	Sequence 418796, A	C 359	16	64.0	1098	3	US-09-954-456-740	Sequence 740, App
C 287	16.2	64.8	524	4	US-09-925-065A-418797	Sequence 418797, A	C 360	16	64.0	1098	5	US-10-198-846-5485	Sequence 5485, Ap
C 288	16.2	64.8	527	4	US-09-925-065A-606466	Sequence 606466, A	C 361	16	64.0	1098	9	US-10-843-641A-3767	Sequence 3767, Ap
C 289	16.2	64.8	593	4	US-09-925-065A-404208	Sequence 404208, A	C 362	16	64.0	1144	8	US-10-856-499-154	Sequence 154, App
C 290	16.2	64.8	593	4	US-09-925-065A-404209	Sequence 404209, A	C 363	16	64.0	1149	10	US-11-097-143-18662	Sequence 18662, A
C 291	16.2	64.8	599	9	US-10-972-079-9670	Sequence 9670, Ap	C 364	16	64.0	1157	9	US-10-450-763-17882	Sequence 17882, A
C 292	16.2	64.8	599	9	US-10-972-079-9671	Sequence 9671, Ap	C 365	16	64.0	1159	3	US-09-891-735-1	Sequence 1, Appli
C 293	16.2	64.8	600	9	US-10-972-079-9672	Sequence 9672, Ap	C 366	16	64.0	1233	6	US-10-369-493-46565	Sequence 46565, A
C 294	16.2	64.8	754	3	US-10-424-599-131436	Sequence 131436, A	C 367	16	64.0	1242	7	US-10-424-599-27799	Sequence 27799, A
C 295	16.2	64.8	1233	3	US-09-925-298-256	Sequence 256, App	C 368	16	64.0	1346	9	US-10-450-763-17919	Sequence 17919, A
C 296	16.2	64.8	1233	5	US-10-102-806-256	Sequence 256, App	C 369	16	64.0	1376	10	US-11-097-143-2627	Sequence 2627, Ap
C 297	16.2	64.8	1254	8	US-10-484-788-13	Sequence 43, Appl	C 370	16	64.0	1417	7	US-10-282-122A-24031	Sequence 24031, A
C 298	16.2	64.8	1317	9	US-10-492-782-1	Sequence 1, Appli	C 371	16	64.0	1629	10	US-11-097-143-23900	Sequence 23900, A
C 299	16.2	64.8	1473	3	US-09-815-242-5960	Sequence 5960, Ap	C 372	16	64.0	1649	7	US-10-425-114-16108	Sequence 16108, A
C 300	16.2	64.8	1473	6	US-10-369-493-24407	Sequence 24407, A	C 373	16	64.0	1734	5	US-10-198-846-10103	Sequence 10103, A
C 301	16.2	64.8	1473	7	US-10-282-122A-20254	Sequence 20254, A	C 374	16	64.0	1734	8	US-10-357-930-30216	Sequence 30216, A
C 302	16.2	64.8	1697	9	US-10-492-782-43	Sequence 43, Appl	C 375	16	64.0	1822	8	US-10-425-115-118423	Sequence 118423, A
C 303	16.2	64.8	1733	6	US-10-397-635-13	Sequence 13, Appl	C 376	16	64.0	2015	6	US-10-369-493-35038	Sequence 35038, A
C 304	16.2	64.8	2442	7	US-10-027-632-115534	Sequence 40322, A	C 377	16	64.0	2101	9	US-10-450-763-28905	Sequence 28905, A
C 305	16.2	64.8	3313	5	US-10-027-632-115534	Sequence 115534, A	C 378	16	64.0	2322	9	US-10-450-763-28905	Sequence 28905, A
C 306	16.2	64.8	3313	6	US-10-027-632-115534	Sequence 115534, A	C 379	16	64.0	2323	9	US-10-450-763-24813	Sequence 24813, A
C 307	16.2	64.8	3391	3	US-09-968-007A-990	Sequence 990, App	C 380	16	64.0	2326	9	US-10-450-763-26188	Sequence 26188, A
C 308	16.2	64.8	3391	9	US-10-843-641A-7460	Sequence 7460, Ap	C 381	16	64.0	2346	6	US-10-369-493-24645	Sequence 24645, A
C 309	16.2	64.8	3994	7	US-10-764-425-20	Sequence 20, Appl	C 382	16	64.0	2415	7	US-10-282-122A-18994	Sequence 18994, A
C 310	16.2	64.8	4253	8	US-10-723-860-5312	Sequence 5312, Ap	C 383	16	64.0	2577	10	US-11-097-143-36076	Sequence 36076, A
C 311	16.2	64.8	5824	10	US-11-097-143-8608	Sequence 8608, Ap	C 384	16	64.0	2766	10	US-11-097-143-37163	Sequence 37163, A
C 312	16.2	64.8	7513	3	US-09-880-107-3869	Sequence 3869, Ap	C 385	16	64.0	2940	5	US-10-171-229-1	Sequence 1, Appli
C 313	16	64.0	24	9	US-10-829-474-32	Sequence 32, Appl	C 386	16	64.0	2940	6	US-10-429-398-1	Sequence 1, Appli
C 314	16	64.0	24	9	US-10-829-474-33	Sequence 33, Appl	C 387	16	64.0	2949	5	US-10-114-893-59	Sequence 59, Appli
C 315	16	64.0	25	10	US-11-036-317-99351	Sequence 99351, A	C 388	16	64.0	3149	10	US-11-097-143-18661	Sequence 18661, A





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RESULT 2
US-10-829-474-46
; Sequence 46, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-46
Query Match      100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 3
US-10-829-474-47
; Sequence 47, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-47
Query Match      100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||||
Db 2 TCCGCTGCAGAGTTGCCCGTTACGA 26

RESULT 4
US-10-829-787D-27
; Sequence 27, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 8
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-787D-27
Query Match      100.0%; Score 25; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||||
Db 2 TCCGCTGCAGAGTTGCCCGTTACGA 26
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; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 27
; LENGTH: 69
; TYPE: DNA
; ORGANISM: Echovirus 7
US-10-295-787D-27
Query Match      100.0%; Score 25; DB 9; Length 69;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 5
US-10-295-787D-6
; Sequence 6, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 30
US-10-295-787D-6
Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   |||||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 6
US-10-295-787D-7
; Sequence 7, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 7
; LENGTH: 70
; TYPE: DNA
; ORGANISM: echovirus 8
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## US-10-295-787D-7

Query Match 100.0%; Score 25; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

## RESULT 7

US-10-295-787D-9  
; Sequence 9, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 9  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Ev Yambian Virus  
US-10-295-787D-9

Query Match 100.0%; Score 25; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

## RESULT 8

US-10-295-787D-12  
; Sequence 12, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 12  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: echovirus 8  
US-10-295-787D-12

Query Match 100.0%; Score 25; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

## RESULT 9

US-10-295-787D-14  
; Sequence 14, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 14  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Coxsackie virus B2  
US-10-295-787D-14

Query Match 100.0%; Score 25; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

## RESULT 10

US-10-295-787D-16  
; Sequence 16, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 16  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Coxsackie Virus B5  
US-10-295-787D-16

Query Match 100.0%; Score 25; DB 9; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.041;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

## RESULT 11

US-10-295-787D-18  
; Sequence 18, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu

```

; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 18
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie Virus A9
; US-10-295-787D-18

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred.No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   ||||||||||||||||||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 12
US-10-295-787D-19
; Sequence 19, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 70
; TYPE: DNA
; ORGANISM: Coxsackie Virus B4
; US-10-295-787D-19

Query Match      100.0%; Score 25; DB 9; Length 70;
Best Local Similarity 100.0%; Pred.No. 0.041;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
   ||||||||||||||||||||
Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 13
US-10-295-787D-20
; Sequence 20, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
; NUMBER OF SEQ ID NOS: 113

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RESOL 18  
US-10-760-048-32/c

; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 14  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-14

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 21

US-10-760-048-15/c  
; Sequence 15, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 15  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-15

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 22

US-10-760-048-19/c  
; Sequence 19, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 19  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-19

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 23

US-10-760-048-22/c  
; Sequence 22, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 22  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-22

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 24

US-10-760-048-24/c  
; Sequence 24, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 24  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-24

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 25

US-10-760-048-25/c  
; Sequence 25, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 25  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-25

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 26

US-10-760-048-26/c  
; Sequence 26, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 26  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-26

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 27

US-10-760-048-27/c  
; Sequence 27, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 27  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-27

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 28

US-10-760-048-28/c  
; Sequence 28, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 28  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-28

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 29

US-10-760-048-29/c  
; Sequence 29, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 29

```

; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
;   OTHER INFORMATION: Description of Unknown Organism: Viral
;   OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-29

```

Query Match	100.0%	Score 25;	DB 9;	Length 238;
Best Local Similarity	100.0%;	Mism.No. 0.04;		
Matches	25;	Conservative 0;	Mismatches 0;	Indels
Qy	1	TCCGCTGCAGAGTTGCCCGTTACGA	25	
Db	75	TCCGCTGCAGAGTTGCCCGTTACGA	51	

```

RESULT 30
US-10-760-048-30/c
; Sequence 30, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187, 0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 30
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-30

```

```

Query Match      100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pident.No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels

QY  1  TCCGCTGCAGAGTTGCCCGTTACGA  25
      |||||
Db   75  TCCGCTGCAGAGTTGCCCGTTACGA  51

```

```

RESULT 31
US-10-760-048-31/c
; Sequence 31, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE REFERENCE: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 31
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-31

```

Query Match

```

Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  TCGCGTCGACAGTTGCCCGTTACGA 25
         |||||
Db       75  TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT: 32
US-10-760-048-42/c
; Sequence 42, Application US/10760048
; Publication No. US20050158710A1
; GENERAL INFORMATION:
; APPLICANT: TSANG, SHIRLEY
; APPLICANT: PRICE, JAMES A.
; APPLICANT: HELLYER, TOBIN J.
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID
; FILE OF INVENTION: 020187.0187PTUS
; CURRENT APPLICATION NUMBER: US/10/760,048
; CURRENT FILING DATE: 2004-01-16
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 42
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-42

```

```

Query Match      100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. NO. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGCAGAGTTGCCGTTACGA 25
Db 75 TCGCTGCAGAGTTGCCGTTACGA 51

```

RESULT 33  
US-10-760-048-43/c  
; Sequence 43, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 43  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-43

```

Query Match      100.0%; Score 25; DB 9; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCTGCAGAGTTGCCCGTTACGA 25
Db 75 TCGCTGCAGAGTTGCCCGTTACGA 51

```

RESULT 34

US-10-760-048-46/c  
; Sequence 46, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 46  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence

US-10-760-048-46  
Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 35

US-10-760-048-47/c  
; Sequence 47, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 47  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence

## US-10-760-048-47

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 36

US-10-760-048-48/c  
; Sequence 48, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS

; CURRENT APPLICATION NUMBER: US/10760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 48  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence

## US-10-760-048-48

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 37

US-10-760-048-54/c  
; Sequence 54, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 54  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence

## US-10-760-048-54

Query Match 100.0%; Score 25; DB 9; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 38

US-10-760-048-67/c  
; Sequence 67, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:

; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10760.048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 67  
; LENGTH: 660  
; TYPE: DNA  
; ORGANISM: Coxsackievirus B3

## US-10-760-048-67



```
Query Match      100.0%; Score 25; DB 9; Length 660;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 457 TCCGCTGCAGAGTTGCCCGTTACGA 433

RESULT 39
US-10-614-283-1/c
; Sequence 1, Application US/10614283
; Publication No. US20050112095A1
; GENERAL INFORMATION:
; APPLICANT: HSU, TSU-AN
; APPLICANT: WU, TZONG-YUAN
; APPLICANT: LEE, JIN-CHING
; TITLE OF INVENTION: INTERNAL RIBOSOME ENTRY SITES FOR RECOMBINANT PROTEIN
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: 08842.0002-00000
; CURRENT APPLICATION NUMBER: US/10/614,283
; CURRENT FILING DATE: 2003-07-08
; PRIOR APPLICATION NUMBER: 60/394,269
; PRIOR FILING DATE: 2002-07-09
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 1
; LENGTH: 709
; TYPE: DNA
; ORGANISM: Enterovirus 71
US-10-614-283-1

Query Match      100.0%; Score 25; DB 9; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 504 TCCGCTGCAGAGTTGCCCGTTACGA 480

RESULT 40
US-10-136-819-7/c
; Sequence 7, Application US/10136819
; Publication No. US20030166593A1
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Hoshijima, Masahiko
; TITLE OF INVENTION: No. US20030166593A1-viral vesicle vector for cardiac specific gen
; FILE REFERENCE: 6627-PAL198
; CURRENT APPLICATION NUMBER: US/10/136,819
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: 60/287,423
; PRIOR FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 7
; LENGTH: 7399
; TYPE: DNA
; ORGANISM: Coxsackievirus B3
US-10-136-819-7

Query Match      100.0%; Score 25; DB 6; Length 7399;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 538 TCCGCTGCAGAGTTGCCCGTTACGA 514

RESULT 41
```

```
US-10-829-474-42
; Sequence 42, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 42
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-42

Query Match      96.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24

RESULT 42
US-10-829-474-43
; Sequence 43, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 43
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-43

Query Match      96.0%; Score 24; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24
Db 1 TCCGCTGCAGAGTTGCCCGTTACG 24

RESULT 43
US-10-295-787D-28
; Sequence 28, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
```

; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 28  
 ; LENGTH: 66  
 ; TYPE: DNA  
 ; ORGANISM: Echovirus 27  
 US-10-295-787D-28

Query Match 96.0%; Score 24; DB 9; Length 66;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24

RESULT 44  
 US-10-295-787D-4  
 ; Sequence 4, Application US/10295787D  
 ; Publication No. US20050202414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Regents of The University of California  
 ; APPLICANT: Jia, Xi Yu  
 ; APPLICANT: Berger, Martina M  
 ; APPLICANT: Tilles, Jeremiah G  
 ; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
 ; FILE REFERENCE: UCIWN--015A  
 ; CURRENT APPLICATION NUMBER: US/10/295,787D  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/335,539  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 4  
 ; LENGTH: 70  
 ; TYPE: DNA  
 ; ORGANISM: enterovirus 71  
 US-10-295-787D-4

Query Match 96.0%; Score 24; DB 9; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24

RESULT 45  
 US-10-295-787D-15  
 ; Sequence 15, Application US/10295787D  
 ; Publication No. US20050202414A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The Regents of The University of California  
 ; APPLICANT: Jia, Xi Yu  
 ; APPLICANT: Berger, Martina M  
 ; APPLICANT: Tilles, Jeremiah G  
 ; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
 ; FILE REFERENCE: UCIWN--015A  
 ; CURRENT APPLICATION NUMBER: US/10/295,787D  
 ; CURRENT FILING DATE: 2002-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/335,539  
 ; PRIOR FILING DATE: 2001-11-15  
 ; NUMBER OF SEQ ID NOS: 113  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 15  
 ; LENGTH: 70  
 ; TYPE: DNA  
 ; ORGANISM: Echovirus 11  
 US-10-295-787D-15

Query Match 96.0%; Score 24; DB 9; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24

RESULT 46  
 US-10-829-474-5  
 ; Sequence 5, Application US/10829474  
 ; Publication No. US20050239055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genetics & IVP  
 ; APPLICANT: MARIANI, Brian D.  
 ; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
 ; FILE REFERENCE: 043956-0121  
 ; CURRENT APPLICATION NUMBER: US/10/829,474  
 ; CURRENT FILING DATE: 2004-04-22  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 5  
 ; LENGTH: 25  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Chemically synthesized probe for enteroviral RNA  
 ; NAME/KEY: misc feature  
 ; LOCATION: (9)..(9)  
 ; OTHER INFORMATION: r = a or g  
 ; FEATURE: misc feature  
 ; NAME/KEY: misc feature  
 ; LOCATION: (15)..(15)  
 ; OTHER INFORMATION: r = a or g  
 ; FEATURE: misc feature  
 ; NAME/KEY: misc feature  
 ; LOCATION: (19)..(19)  
 ; OTHER INFORMATION: r = a or g  
 ; US-10-829-474-5

Query Match 95.2%; Score 23.8; DB 9; Length 25;  
 Best Local Similarity 88.0%; Pred. No. 0.16;  
 Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 TCCGCTGCGAGTTGCCCGTTACGA 25

RESULT 47  
 US-10-829-474-56  
 ; Sequence 56, Application US/10829474  
 ; Publication No. US20050239055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genetics & IVP  
 ; APPLICANT: MARIANI, Brian D.  
 ; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
 ; FILE REFERENCE: 043956-0121  
 ; CURRENT APPLICATION NUMBER: US/10/829,474  
 ; CURRENT FILING DATE: 2004-04-22  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 56  
 ; LENGTH: 26  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE: Chemically synthesized probe for enteroviral RNA  
 ; NAME/KEY: misc feature  
 ; LOCATION: (9)..(9)

; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (15)..(15)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-56

Query Match 95.2%; Score 23.8; DB 9; Length 26;  
Best Local Similarity 88.0%; Pred. No. 0.16;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:||||:  
Db 1 TCCGCTGCGAGTTTCCCRTTACGA 25

## RESULT 48

US-10-829-474-57  
; Sequence 57, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22

; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 57  
; LENGTH: 26  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (10)..(10)  
; OTHER INFORMATION: r = a or g

; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (16)..(16)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (20)..(20)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-57

Query Match 95.2%; Score 23.8; DB 9; Length 26;  
Best Local Similarity 88.0%; Pred. No. 0.16;  
Matches 22; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:||||:  
Db 2 TCCGCTGCGAGTTTCCCRTTACGA 26

## RESULT 49

US-10-295-787D-21  
; Sequence 21, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A

; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 21  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Echovirus 12  
US-10-295-787D-21

Query Match 93.6%; Score 23.4; DB 9; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:||||:  
Db 1 TCCGCTGCAGAGTTGCCCAATTACGA 25

## RESULT 50

US-10-295-787D-23  
; Sequence 23, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A

; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 23  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Coxsackie A16  
US-10-295-787D-23

Query Match 93.6%; Score 23.4; DB 9; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:||||:  
Db 1 TCCGCTGCAGAGTTACCCGTTACGA 25

## RESULT 51

US-10-295-787D-31  
; Sequence 31, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A

; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: Patent in version 3.3  
; SEQ ID NO 31  
; LENGTH: 70  
; TYPE: DNA

; ORGANISM: Ev sp virus  
US-10-295-787D-31

Query Match 93.6%; Score 23.4; DB 9; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCTGCAGAGTTGCCCATTTACGA 25

## RESULT 52

US-10-295-787D-112  
; Sequence 112, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 112  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Coxsackie virus B6  
US-10-295-787D-112

Query Match 93.6%; Score 23.4; DB 9; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 1 TCCGCCGCGAGAGTTGCCCGTTACGA 25

## RESULT 53

US-10-295-787D-17  
; Sequence 17, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 17  
; LENGTH: 71  
; TYPE: DNA  
; ORGANISM: Echovirus 9  
US-10-295-787D-17

Query Match 93.6%; Score 23.4; DB 9; Length 71;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||

Db 1 TCCGCTGCAGAGTTACCCGTTACGA 25

## RESULT 54

US-10-295-787D-8  
; Sequence 8, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 8  
; LENGTH: 75  
; TYPE: DNA  
; ORGANISM: Echovirus 3  
US-10-295-787D-8

Query Match 93.6%; Score 23.4; DB 9; Length 75;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 6 TCCGCTGCAGAGTTACCCGTTACGA 30

## RESULT 55

US-10-760-048-39/c  
; Sequence 39, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 39  
; LENGTH: 117  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-39

Query Match 93.6%; Score 23.4; DB 9; Length 117;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCATTTACGA 51

## RESULT 56

US-10-760-048-40/c  
; Sequence 40, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 40  
; LENGTH: 117  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-40

Query Match 93.6%; Score 23.4; DB 9; Length 117;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 57  
US-10-760-048-37/c  
; Sequence 37, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 37  
; LENGTH: 236  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-37

Query Match 93.6%; Score 23.4; DB 9; Length 236;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 58  
US-10-760-048-49/c  
; Sequence 49, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 49

; LENGTH: 236  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-49

Query Match 93.6%; Score 23.4; DB 9; Length 236;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 59  
US-10-760-048-50/c  
; Sequence 50, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 50  
; LENGTH: 236  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-50

Query Match 93.6%; Score 23.4; DB 9; Length 236;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 60  
US-10-760-048-51/c  
; Sequence 51, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 51  
; LENGTH: 236  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-51

Query Match 93.6%; Score 23.4; DB 9; Length 236;

Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 61

US-10-760-048-44/c  
; Sequence 44, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 44  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-44

Query Match 93.6%; Score 23.4; DB 9; Length 237;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 62

US-10-760-048-45/c  
; Sequence 45, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 45  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-45

Query Match 93.6%; Score 23.4; DB 9; Length 237;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 63

US-10-760-048-33/c  
; Sequence 33, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 33  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-33

Query Match 93.6%; Score 23.4; DB 9; Length 238;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 64

US-10-332-123-55/c  
; Sequence 55, Application US/10332123  
; Publication No. US20040072239A1  
; GENERAL INFORMATION:  
; APPLICANT: RENAUD, Patricia  
; APPLICANT: GUILLOT, Emmanuelle  
; APPLICANT: MABILAT, Claude  
; APPLICANT: VACHON, Carole  
; APPLICANT: LACROIX, Bruno  
; APPLICANT: VERNET, Guy  
; APPLICANT: ARMAND, Marie-Astrid  
; APPLICANT: LAFFAIRE, Philippe  
; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
; FILE REFERENCE: 114502  
; CURRENT APPLICATION NUMBER: US/10/332,123  
; CURRENT FILING DATE: 2003-09-24  
; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
; PRIOR FILING DATE: 2001-07-06  
; PRIOR APPLICATION NUMBER: FR00-08839  
; PRIOR FILING DATE: 2000-07-06  
; NUMBER OF SEQ ID NOS: 108  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 55  
; LENGTH: 525  
; TYPE: DNA  
; ORGANISM: Echovirus (X77708)  
US-10-332-123-55

Query Match 93.6%; Score 23.4; DB 7; Length 525;  
Best Local Similarity 96.0%; Pred. No. 0.24;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 475 TCCGCTGCAGAGTTGCCCGTTACGA 451

RESULT 65

US-10-829-474-38  
; Sequence 38, Application US/10829474

```
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 38
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-38

Query Match          92.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTAC 23
Db 1 TCCGCTGCAGAGTTGCCCGTTAC 23

RESULT 66
US-10-829-474-39
; Sequence 39, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-39

Query Match          92.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTACGA 25
Db 1 CGCTGCAGAGTTGCCCGTTACGA 23

RESULT 67
US-10-829-474-41
; Sequence 41, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 41
; LENGTH: 23
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-41

Query Match          92.0%; Score 23; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.4;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACG 24
Db 1 CCGCTGCAGAGTTGCCCGTTACG 23

RESULT 68
US-10-408-519-2/c
; Sequence 2, Application US/10408519
; Publication No. US20030228683A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Kan-Hung
; APPLICANT: Shih, Yu-Hau
; APPLICANT: Tsai, Chuan-Mei
; APPLICANT: Wang, Yih-Weng
; APPLICANT: Hsiao, Hsiung
; APPLICANT: Bair, Chi-Horng
; APPLICANT: Wang, Shin-Hwan
; TITLE OF INVENTION: BIOMOLECULE-BOUND SUBSTRATES
; FILE REFERENCE: 12674-002002
; CURRENT APPLICATION NUMBER: US/10/408,519
; CURRENT FILING DATE: 2003-04-07
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe from 5' ends of enterovirus genes
US-10-408-519-2

Query Match          92.0%; Score 23; DB 6; Length 58;
Best Local Similarity 80.0%; Pred. No. 0.39;
Matches 20; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 52 TCCGCTGCAGAGTTGCCCGTTACGA 28

RESULT 69
US-10-829-474-52
; Sequence 52, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
; NAME/KEY: misc feature
; LOCATION: (8)..(8)
```

; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (14)..(14)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (18)..(18)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-52

Query Match 91.2%; Score 22.8; DB 9; Length 24;  
Best Local Similarity 87.5%; Pred. No. 0.5;  
Matches 21; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:|||||  
Db 1 CCGCTGCRGAGTTRCCCRTTACGA 24

## RESULT 70

US-10-829-474-53  
; Sequence 53, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 53  
; LENGTH: 24  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15)..(15)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-53

Query Match 91.2%; Score 22.8; DB 9; Length 24;  
Best Local Similarity 87.5%; Pred. No. 0.5;  
Matches 21; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACG 24  
|||||:||||:||||:|||||  
Db 1 TCCGCTGCRGAGTTRCCCRTTACG 24

## RESULT 71

US-10-366-823-5/c  
; Sequence 5, Application US/10366823  
; Publication No. US20030211526A1  
; GENERAL INFORMATION:  
; APPLICANT: Juang, Jyh-Lyh  
; APPLICANT: Hsiung, Chao Agnes  
; APPLICANT: Lin, Chung-Yen  
; TITLE OF INVENTION: CROSS-SPECIES NUCLEIC ACID PROBES  
; FILE REFERENCE: 12563-006001  
; CURRENT APPLICATION NUMBER: US/10/366,823

; CURRENT FILING DATE: 2003-02-14  
; PRIOR APPLICATION NUMBER: US 60/357,541  
; PRIOR FILING DATE: 2002-02-15  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5  
; LENGTH: 62  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Probe  
US-10-366-823-5

Query Match 90.4%; Score 22.6; DB 6; Length 62;  
Best Local Similarity 76.0%; Pred. No. 0.61;  
Matches 19; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:|||||  
Db 27 TCCGTCRCGASITGCSCTTACGA 3

## RESULT 72

US-10-295-787D-13  
; Sequence 13, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCI-VN-015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 13  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: echovirus 2  
US-10-295-787D-13

Query Match 89.6%; Score 22.4; DB 9; Length 70;  
Best Local Similarity 95.8%; Pred. No. 0.76;  
Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
|||||:||||:||||:|||||  
Db 1 CCGCTGCAGAGTTGCCCATACGA 24

## RESULT 73

US-10-829-474-44  
; Sequence 44, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVF  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 44  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA



## US-10-829-474-44

Query Match 88.0%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTACG 24  
|||||:|||||:|||||:|||||  
Db 1 CGCTGCAGAGTTGCCCGTTACG 22

## RESULT 74

US-10-829-474-45  
; Sequence 45, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVP  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 45  
; LENGTH: 22  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
US-10-829-474-45

Query Match 88.0%; Score 22; DB 9; Length 22;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTAC 23  
|||||:|||||:|||||:|||||  
Db 1 CCGCTGCAGAGTTGCCCGTTAC 22

## RESULT 75

US-10-829-474-48  
; Sequence 48, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVP  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (9)..(9)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (15)..(15)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (19)..(19)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-48

## US-10-829-474-44

Query Match 87.2%; Score 21.8; DB 9; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.5;  
Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTAC 23  
|||||:|||||:|||||:|||||  
Db 1 TCCGCTGCAGAGTTCCCRITAC 23

## RESULT 76

US-10-829-474-49  
; Sequence 49, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVP  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 49  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (13)..(13)  
; OTHER INFORMATION: r = a or g  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (17)..(17)  
; OTHER INFORMATION: r = a or g  
US-10-829-474-49

Query Match 87.2%; Score 21.8; DB 9; Length 23;  
Best Local Similarity 87.0%; Pred. No. 1.5;  
Matches 20; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTACGA 25  
|||||:|||||:|||||:|||||  
Db 1 CGCTGCAGAGTTCCCRITACGA 23

## RESULT 77

US-10-829-474-51  
; Sequence 51, Application US/10829474  
; Publication No. US20050239055A1  
; GENERAL INFORMATION:  
; APPLICANT: Genetics & IVP  
; APPLICANT: MARIANI, Brian D.  
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
; FILE REFERENCE: 043956-0121  
; CURRENT APPLICATION NUMBER: US/10/829,474  
; CURRENT FILING DATE: 2004-04-22  
; NUMBER OF SEQ ID NOS: 57  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 51  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
; FEATURE:  
; NAME/KEY: misc feature  
US-10-829-474-51



Db 75 TCCGCTGCAGAGTTACCCATTACGA 51

## RESULT 82

US-10-760-048-21/c  
; Sequence 21, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 21  
; LENGTH: 237  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-21

Query Match 87.2%; Score 21.8; DB 9; Length 237;

Best Local Similarity 92.0%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTACCCATTACGA 51

## RESULT 83

US-10-760-048-23/c  
; Sequence 23, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 23  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-23

Query Match 87.2%; Score 21.8; DB 9; Length 238;

Best Local Similarity 92.0%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

## RESULT 84

US-10-760-048-34/c  
; Sequence 34, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY

; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 34  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-34

Query Match 87.2%; Score 21.8; DB 9; Length 238;

Best Local Similarity 92.0%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

## RESULT 85

US-10-760-048-35/c  
; Sequence 35, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 35  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-35

Query Match 87.2%; Score 21.8; DB 9; Length 238;

Best Local Similarity 92.0%; Pred. No. 1.4;  
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25

Db 75 TCCGCTGCAGAGTTCCCGTTACGA 51

## RESULT 86

US-10-760-048-36/c  
; Sequence 36, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELLYER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 36

```
; LENGTH: 238
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Viral
; OTHER INFORMATION: 5'untranslated polynucleotide sequence
US-10-760-048-36

Query Match      87.2%; Score 21.8; DB 9; Length 238;
Best Local Similarity 92.0%; Pred. No. 1.4;
Matches 23; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
    |||||:|||||:|||||:|||||
Db 75 TCCGCTGCGGAGTTGCCCATACGA 51

RESULT 87
US-10-829-474-40
; Sequence 40, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-40

Query Match      84.0%; Score 21; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTAC 23
    |||||:|||||:|||||:|||||
Db 1 CGCTGCAGAGTTGCCCGTTAC 21

RESULT 88
US-10-829-474-54
; Sequence 54, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-54

Query Match      87.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTAC 23
    |||||:|||||:|||||:|||||
Db 1 CCGCTGCRGAGTTCCCRTTAC 22

RESULT 89
US-10-829-474-55
; Sequence 55, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-55

Query Match      83.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTAC 23
    |||||:|||||:|||||:|||||
Db 1 CCGCTGCRGAGTTCCCRTTAC 22

RESULT 90
US-10-295-787D-24
; Sequence 24, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
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; OTHER INFORMATION: r = a or g
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (17)..(17)
; OTHER INFORMATION: r = a or g
US-10-829-474-54

Query Match      83.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 3 CGCTGCAGAGTTGCCCGTTACG 24
    |||||:|||||:|||||:|||||
Db 1 CGCTGCRGAGTTCCCRTTACG 22

RESULT 89
US-10-829-474-55
; Sequence 55, Application US/10829474
; Publication No. US20050239055A1
; GENERAL INFORMATION:
; APPLICANT: Genetics & IVF
; APPLICANT: MARIANI, Brian D.
; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES
; FILE REFERENCE: 043956-0121
; CURRENT APPLICATION NUMBER: US/10/829,474
; CURRENT FILING DATE: 2004-04-22
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA
US-10-829-474-55

Query Match      83.2%; Score 20.8; DB 9; Length 22;
Best Local Similarity 86.4%; Pred. No. 4.7;
Matches 19; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 CCGCTGCAGAGTTGCCCGTTAC 23
    |||||:|||||:|||||:|||||
Db 1 CCGCTGCRGAGTTCCCRTTAC 22

RESULT 90
US-10-295-787D-24
; Sequence 24, Application US/10295787D
; Publication No. US20050202414A1
; GENERAL INFORMATION:
; APPLICANT: The Regents of The University of California
; APPLICANT: Jia, Xi Yu
; APPLICANT: Berger, Martina M
; APPLICANT: Tilles, Jeremiah G
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE
; FILE REFERENCE: UCIVN--015A
; CURRENT APPLICATION NUMBER: US/10/295,787D
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/335,539
; PRIOR FILING DATE: 2001-11-15
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; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 24  
; LENGTH: 69  
; TYPE: DNA  
; ORGANISM: Echovirus 5  
US-10-295-787D-24

Query Match 83.2%; Score 20.8; DB 9; Length 69;  
Best Local Similarity 91.7%; Pred. No. 4.6;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
DB 1 CCGCTGCAGAGTTACCCATTACGA 24

## RESULT 91

US-10-295-787D-25  
; Sequence 25, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 25  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Porcine ev virus 9  
US-10-295-787D-25

Query Match 83.2%; Score 20.8; DB 9; Length 70;  
Best Local Similarity 91.7%; Pred. No. 4.6;  
Matches 22; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
DB 1 CGCCACAGAGTTGCCCGTTACGA 24

## RESULT 92

US-10-295-787D-11  
; Sequence 11, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 11  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: echovirus 25  
US-10-295-787D-11

Query Match 80.8%; Score 20.2; DB 9; Length 70;

Best Local Similarity 88.0%; Pred. No. 8.9;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
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DB 1 TCCGCCGAGAGTTACCCATTACGA 25

## RESULT 93

US-10-295-787D-111  
; Sequence 111, Application US/10295787D  
; Publication No. US20050202414A1  
; GENERAL INFORMATION:  
; APPLICANT: The Regents of The University of California  
; APPLICANT: Jia, Xi Yu  
; APPLICANT: Berger, Martina M  
; APPLICANT: Tilles, Jeremiah G  
; TITLE OF INVENTION: APPARATUS AND METHODS FOR DETECTING A PATHOGEN IN A SAMPLE  
; FILE REFERENCE: UCIVN--015A  
; CURRENT APPLICATION NUMBER: US/10/295,787D  
; CURRENT FILING DATE: 2002-11-15  
; PRIOR APPLICATION NUMBER: US 60/335,539  
; PRIOR FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 113  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 111  
; LENGTH: 70  
; TYPE: DNA  
; ORGANISM: Echo virus 4  
US-10-295-787D-111

Query Match 80.8%; Score 20.2; DB 9; Length 70;  
Best Local Similarity 88.0%; Pred. No. 8.9;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
DB 1 TCCGCTGCAGAGTTACCCATTACGA 25

## RESULT 94

US-10-760-048-38/c  
; Sequence 38, Application US/10760048  
; Publication No. US20050158710A1  
; GENERAL INFORMATION:  
; APPLICANT: TSANG, SHIRLEY  
; APPLICANT: PRICE, JAMES A.  
; APPLICANT: HELDIER, TOBIN J.  
; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
; FILE REFERENCE: 020187.0187PTUS  
; CURRENT APPLICATION NUMBER: US/10/760,048  
; CURRENT FILING DATE: 2004-01-16  
; NUMBER OF SEQ ID NOS: 67  
; SOFTWARE: PatentIn ver. 3.2  
; SEQ ID NO 38  
; LENGTH: 238  
; TYPE: DNA  
; ORGANISM: Unknown Organism  
; FEATURE:  
; OTHER INFORMATION: Description of Unknown Organism: Viral  
; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
US-10-760-048-38

Query Match 80.8%; Score 20.2; DB 9; Length 238;  
Best Local Similarity 88.0%; Pred. No. 8.7;  
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
DB 75 TCCGCTGCAGAGTTACCCATTACGA 51

## RESULT 95

US-10-829-474-50  
 ; Sequence 50, Application US/10829474  
 ; Publication No. US20050239055A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Genetics & IVF  
 ; APPLICANT: MARIANI, Brian D.  
 ; TITLE OF INVENTION: ENTEROVIRUS PRIMERS AND PROBES  
 ; FILE REFERENCE: 043956-0121  
 ; CURRENT APPLICATION NUMBER: US/10/829,474  
 ; CURRENT FILING DATE: 2004-04-22  
 ; NUMBER OF SEQ ID NOS: 57  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 50  
 ; LENGTH: 21  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chemically synthesized probe for enteroviral RNA  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (7)..(7)  
 ; OTHER INFORMATION: r = a or g  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (13)..(13)  
 ; OTHER INFORMATION: r = a or g  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (17)..(17)  
 ; OTHER INFORMATION: r = a or g  
 US-10-829-474-50

Query Match 79.2%; Score 19.8; DB 9; Length 21;  
 Best Local Similarity 85.7%; Pred. No. 14;  
 Matches 18; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Oy 3 CGCTGCAGAGTTGCCGTTAC 23  
 Db 1 CGCTGCGAGTTCCCTTAC 21

RESULT 96  
 US-10-760-048-62/c  
 ; Sequence 62, Application US/10760048  
 ; Publication No. US20050158710A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: TSANG, SHIRLEY  
 ; APPLICANT: PRICE, JAMES A.  
 ; APPLICANT: HELLYER, TOBIN J.  
 ; TITLE OF INVENTION: DETECTION OF ENTEROVIRUS NUCLEIC ACID  
 ; FILE REFERENCE: 020187.0187PTUS  
 ; CURRENT APPLICATION NUMBER: US/10/760,048  
 ; CURRENT FILING DATE: 2004-01-16  
 ; NUMBER OF SEQ ID NOS: 67  
 ; SOFTWARE: PatentIn Ver. 3.2  
 ; SEQ ID NO 62  
 ; LENGTH: 238  
 ; TYPE: DNA  
 ; ORGANISM: Unknown Organism  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Unknown Organism: Viral  
 ; OTHER INFORMATION: 5'untranslated polynucleotide sequence  
 US-10-760-048-62

Query Match 74.4%; Score 18.6; DB 9; Length 238;  
 Best Local Similarity 84.0%; Pred. No. 52;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 TCCGCTGCAGAGTTGCCGTTAC 25  
 Db 75 TCCGCCACAGACTTGCCTTAC 51

RESULT 97  
 US-10-332-123-53/c  
 ; Sequence 53, Application US/10332123  
 ; Publication No. US20040072239A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: RENAUD, Patricia  
 ; APPLICANT: GUILLOT, Emmanuelle  
 ; APPLICANT: MABILAT, Claude  
 ; APPLICANT: VACHON, Carole  
 ; APPLICANT: LACROIX, Bruno  
 ; APPLICANT: VERNET, Guy  
 ; APPLICANT: ARMAND, Marie-Astrid  
 ; APPLICANT: LAFFAIRE, Philippe  
 ; TITLE OF INVENTION: METHOD FOR CONTROLLING THE MICROBIOLOGICAL QUALITY OF AN AQUEOUS  
 ; FILE REFERENCE: 114502  
 ; CURRENT APPLICATION NUMBER: US/10/332,123  
 ; CURRENT FILING DATE: 2003-09-24  
 ; PRIOR APPLICATION NUMBER: PCT/FR01/02191  
 ; PRIOR FILING DATE: 2001-07-06  
 ; PRIOR APPLICATION NUMBER: FR00-08839  
 ; PRIOR FILING DATE: 2000-07-06  
 ; NUMBER OF SEQ ID NOS: 108  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 53  
 ; LENGTH: 521  
 ; TYPE: DNA  
 ; ORGANISM: Poliovirus (X00595)  
 US-10-332-123-53

Query Match 74.4%; Score 18.6; DB 7; Length 521;  
 Best Local Similarity 84.0%; Pred. No. 51;  
 Matches 21; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 Oy 1 TCCGCTGCAGAGTTGCCGTTAC 25  
 Db 471 TCCGCCACAGACTTGCCTTAC 447

RESULT 98  
 US-10-425-114-9634/c  
 ; Sequence 9634, Application US/10425114  
 ; Publication No. US20040034888A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liu, Jingdong  
 ; APPLICANT: Zhou, Yihua  
 ; APPLICANT: Kovalic, David K.  
 ; APPLICANT: Screen, Steven E.  
 ; APPLICANT: Tabaska, Jack E.  
 ; APPLICANT: Cao, Yongwei  
 ; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with  
 ; FILE REFERENCE: 38-21(53313)B  
 ; CURRENT APPLICATION NUMBER: US/10/425,114  
 ; CURRENT FILING DATE: 2003-04-28  
 ; NUMBER OF SEQ ID NOS: 73128  
 ; SEQ ID NO 9634  
 ; LENGTH: 1499  
 ; TYPE: DNA  
 ; ORGANISM: Glycine max  
 ; FEATURE:  
 ; OTHER INFORMATION: Clone ID: 700854421\_FLI  
 US-10-425-114-9634

Query Match 72.8%; Score 18.2; DB 7; Length 1499;  
 Best Local Similarity 87.0%; Pred. No. 78;  
 Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 3 CGCTGCAGAGTTGCCGTTAC 25  
 Db 761 CGCTGCAGTGTGCCAGTTAC 739

Search completed: March 9, 2006, 08:34:16  
Job time : 741.243 secs

RESULT 99  
US-10-424-599-2070/c  
; Sequence 2070, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa Thomas J  
; APPLICANT: Kovalic David K  
; APPLICANT: Zhou Yihua  
; APPLICANT: Cao Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424,599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 2070  
; LENGTH: 1645  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_101874C.1  
US-10-424-599-2070

Query Match 72.8%; Score 18.2; DB 7; Length 1645;  
Best Local Similarity 87.0%; Pred. No. 78;  
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
Qy 3 CGCTGCAGAGTTGCCCGTTACGA 25  
Db 905 CGCTGCAGTTGCCAGTTACCA 883

RESULT 100  
US-09-738-626-2740  
; Sequence 2740, Application US/09738626  
; Publication No. US20020197605A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAGAWA, SATOSHI  
; APPLICANT: MIZOGUCHI, HIROSHI  
; APPLICANT: ANDO, SEIKO  
; APPLICANT: HAYASHI, MIKIRO  
; APPLICANT: OCHIAI, KEIKO  
; APPLICANT: YOKOI, HARUHIKO  
; APPLICANT: TATEISHI, NAOKO  
; APPLICANT: SENOH, AKIHIRO  
; APPLICANT: IKEDA, MASATO  
; APPLICANT: OZAKI, AKIO  
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES  
; FILE REFERENCE: 249-125  
; CURRENT APPLICATION NUMBER: US/09/738,626  
; CURRENT FILING DATE: 2000-12-18  
; PRIOR APPLICATION NUMBER: JP 99/377484  
; PRIOR FILING DATE: 1999-12-16  
; PRIOR APPLICATION NUMBER: JP 00/159162  
; PRIOR FILING DATE: 2000-04-07  
; PRIOR APPLICATION NUMBER: JP 00/280988  
; PRIOR FILING DATE: 2000-08-03  
; NUMBER OF SEQ ID NOS: 7059  
; SOFTWARE: PatentIn ver. 3.0  
; SEQ ID NO 2740  
; LENGTH: 1182  
; TYPE: DNA  
; ORGANISM: Corynebacterium glutamicum  
US-09-738-626-2740

Query Match 70.4%; Score 17.6; DB 3; Length 1182;  
Best Local Similarity 83.3%; Pred. No. 1.5e+02;  
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
Qy 2 CGCTGCAGAGTTGCCCGTTACGA 25  
Db 116 CGCGCAAGTTGCTCGCTACGA 139

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 9, 2006, 00:06:59 ; Search time 250.485 Seconds  
(without alignments)  
665.178 Million cell updates/sec

Title: US-10-829-474-4

Perfect score: 25

Sequence: 1 tccgctgcagagttgccggttaaca 25

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing 'first 500 summaries

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1: geneseqn1980s.\*  
2: geneseqn1990s.\*  
3: geneseqn2000s.\*  
4: geneseqn2001as.\*  
5: geneseqn2001bs.\*  
6: geneseqn2002as.\*  
7: geneseqn2002bs.\*  
8: geneseqn2003as.\*  
9: geneseqn2003bs.\*  
10: geneseqn2003cs.\*  
11: geneseqn2003ds.\*  
12: geneseqn2004as.\*  
13: geneseqn2004bs.\*  
14: geneseqn2005s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25	100.0	69	12	ADP05526 Novel mic
2	25	100.0	70	12	ADP05510 Novel mic
3	25	100.0	70	12	ADP05515 Novel mic
4	25	100.0	70	12	ADP05513 Novel mic
5	25	100.0	70	12	ADP05521 Novel mic
6	25	100.0	70	12	ADP05504 Novel mic
7	25	100.0	70	12	ADP05507 Novel mic
8	25	100.0	70	12	ADP05517 Novel mic
9	25	100.0	70	12	ADP05534 Novel mic
10	25	100.0	70	12	ADP05503 Novel mic
11	25	100.0	70	12	ADP05519 Novel mic
12	25	100.0	70	12	ADP05518 Novel mic
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C 14	25	100.0	107	14	ABE56814 Viral 5'
C 15	25	100.0	126	14	ABE56779 Viral 5'
C 16	25	100.0	180	14	ABE56834 Human cox
C 17	25	100.0	198	14	ABE56858 Human ech
C 18	25	100.0	198	14	ABE56863 Human ech
C 19	25	100.0	237	14	ABE56848 Human:cox

C 20	25	100.0	237	14	ABE56862	Ab556862 Human ech
C 21	25	100.0	237	14	ABE56793	Ab556793 Viral 5'
C 22	25	100.0	238	14	ABE56840	Ab556840 Human cox
C 23	25	100.0	238	14	ABE56791	Ab556791 Viral 5'
C 24	25	100.0	238	14	ABE56846	Ab556846 Human cox
C 25	25	100.0	238	14	ABE56847	Ab556847 Human cox
C 26	25	100.0	238	14	ABE56789	Ab556789 Viral 5'
C 27	25	100.0	238	14	ABE56775	Ab556775 Viral 5'
C 28	25	100.0	238	14	ABE56807	Ab556807 Viral 5'
C 29	25	100.0	238	14	ABE56815	Ab556815 Viral 5'
C 30	25	100.0	238	14	ABE56838	Ab556838 Human cox
C 31	25	100.0	238	14	ABE56842	Ab556842 Human cox
C 32	25	100.0	238	14	ABE56785	Ab556785 Viral 5'
C 33	25	100.0	238	14	ABE56835	Ab556835 Human cox
C 34	25	100.0	238	14	ABE56780	Ab556780 Viral 5'
C 35	25	100.0	238	14	ABE56803	Ab556803 Viral 5'
C 36	25	100.0	238	14	ABE56829	Ab556829 Consensus
C 37	25	100.0	238	14	ABE56843	Ab556843 Human cox
C 38	25	100.0	238	14	ABE56845	Ab556845 Human cox
C 39	25	100.0	238	14	ABE56774	Ab556774 Viral 5'
C 40	25	100.0	238	14	ABE56788	Ab556788 Viral 5'
C 41	25	100.0	238	14	ABE56792	Ab556792 Viral 5'
C 42	25	100.0	238	14	ABE56783	Ab556783 Viral 5'
C 43	25	100.0	238	14	ABE56786	Ab556786 Viral 5'
C 44	25	100.0	238	14	ABE56787	Ab556787 Viral 5'
C 45	25	100.0	238	14	ABE56870	Ab556870 Human cox
C 46	25	100.0	238	14	ABE56830	Ab556830 Human cox
C 47	25	100.0	238	14	ABE56864	Ab556864 Human ech
C 48	25	100.0	238	14	ABE56859	Ab556859 Human ech
C 49	25	100.0	238	14	ABE56776	Ab556776 Viral 5'
C 50	25	100.0	238	14	ABE56790	Ab556790 Viral 5'
C 51	25	100.0	238	14	ABE56841	Ab556841 Human cox
C 52	25	100.0	238	14	ABE56809	Ab556809 Viral 5'
C 53	25	100.0	238	14	ABE56831	Ab556831 Human cox
C 54	25	100.0	238	14	ABE56808	Ab556808 Viral 5'
C 55	25	100.0	238	14	ABE56844	Ab556844 Human cox
C 56	25	100.0	238	14	ABE56804	Ab556804 Viral 5'
C 57	25	100.0	502	8	ABX12451	Abx12451 Cxsackie
C 58	25	100.0	548	8	ABX12448	Abx12448 Cxsackie
C 59	25	100.0	551	8	ABX12453	Abx12453 Cxsackie
C 60	25	100.0	552	8	ABX12452	Abx12452 Cxsackie
C 61	25	100.0	660	4	AAC85174	Aac85174 Cxsackie
C 62	25	100.0	660	14	ABE56828	Ab556828 Cxsackie
C 63	25	100.0	709	14	Aea00424	Aea00424 Enterovir
C 64	25	100.0	745	4	AAC85152	Aac85152 Cxsackie
C 65	25	100.0	810	12	ADP82873	Adp82873 Human cox
C 66	25	100.0	1560	13	ADU47469	Adu47469 Enterovir
C 67	25	100.0	7392	8	ABX12440	Abx12440 Diabetoge
C 68	25	100.0	7399	2	AAQ11816	Aaq11816 RNA encod
C 69	25	100.0	7399	10	ABV76134	Abv76134 Cxsackie
C 70	24	96.0	66	12	ADP05527	Adp05527 Novel mic
C 71	24	96.0	70	12	ADP05501	Adp05501 Novel mic
C 72	24	96.0	70	12	ADP05514	Adp05514 Novel mic
C 73	23.4	93.6	70	12	ADP05512	Adp05512 Novel mic
C 74	23.4	93.6	70	12	ADP05530	Adp05530 Novel mic
C 75	23.4	93.6	70	12	ADP05506	Adp05506 Novel mic
C 76	23.4	93.6	70	12	ADP05522	Adp05522 Novel mic
C 77	23.4	93.6	70	12	ADP05520	Adp05520 Novel mic
C 78	23.4	93.6	71	12	ADP05516	Adp05516 Novel mic
C 79	23.4	93.6	117	14	ABE56800	Ab556800 Viral 5'
C 80	23.4	93.6	117	14	ABE56801	Ab556801 Viral 5'
C 81	23.4	93.6	173	14	ABE56856	Ab556856 Human ech
C 82	23.4	93.6	173	14	ABE56855	Ab556855 Human ech
C 83	23.4	93.6	198	14	ABE56865	Ab556865 Human ech
C 84	23.4	93.6	198	14	ABE56853	Ab556853 Human ech
C 85	23.4	93.6	198	14	ABE56860	Ab556860 Human ech
C 86	23.4	93.6	236	14	ABE56811	Ab556811 Viral 5'
C 87	23.4	93.6	236	14	ABE56810	Ab556810 Viral 5'
C 88	23.4	93.6	236	14	ABE56812	Ab556812 Viral 5'
C 89	23.4	93.6	236	14	ABE56798	Ab556798 Viral 5'
C 90	23.4	93.6	237	14	ABE56805	Ab556805 Viral 5'
C 91	23.4	93.6	237	14	ABE56806	Ab556806 Viral 5'
C 92	23.4	93.6	237	14	ABE56861	Ab556861 Human ech

C 93	23.4	93.6	238	14	AEBS56849	Aeb56849 Human cox	166	17	68.0	66	10	ADG25387	Adg25387 Chromosom
C 94	23.4	93.6	238	14	AEBS56794	Aeb56794 Viral 5'	167	17	68.0	66	10	ADG25390	Adg25390 Chromosom
C 95	23.4	93.6	238	14	AEBS56867	Aeb56867 Human ech	168	17	68.0	66	10	ADJ47786	Adj47786 E. coli f
C 96	23.4	93.6	238	14	AEBS56866	Aeb56866 Human ech	169	17	68.0	66	10	ADJ47789	Adj47789 E. coli f
C 97	23.4	93.6	525	6	ABL53113	AbL53113 Micro-org	170	17	68.0	66	10	ADJ61978	Adj61978 Novel min
C 98	23.4	93.6	646	4	AAC85153	Aac85153 Echo viru	171	17	68.0	66	10	ADJ61981	Adj61981 Novel min
C 99	23.4	93.6	7400	3	AAZ98719	Aaz98719 Swine ves	172	17	68.0	66	11	ADP70556	Adp70556 Minicell
C 100	23.4	93.6	7400	3	AAZ98717	Aaz98717 Swine ves	173	17	68.0	66	11	ADP70553	Adp70553 Minicell
C 101	23.4	93.6	7400	3	AAZ98718	Aaz98718 Swine ves	174	17	68.0	66	12	ADP56223	Adp56223 E. coli f
C 102	23.4	93.6	7400	3	AAZ29863	Aaz29863 Swine ves	175	17	68.0	66	12	ADP56220	Adp56220 E. coli f
C 103	23.4	93.6	7421	3	AAZ98720	Aaz98720 Swine ves	176	17	68.0	66	12	ADG43251	Adg43251 E. coli f
C 104	23	92.0	33	8	ACDU26710	Acd26710 Enterovir	177	17	68.0	66	12	ADG43248	Adg43248 E. coli f
C 105	23	92.0	33	13	ADU47463	Adu47463 p2 probe	178	17	68.0	66	12	ADG43508	Adg43508 E. coli f
C 106	22.6	90.4	62	12	AECK67516	Aec67516 Picornavi	179	17	68.0	66	12	ADG43505	Adg43505 E. coli f
C 107	22.6	90.4	62	14	AEC05511	Aec05511 Novel mic	180	17	68.0	66	12	ADG68569	Adg68569 E. coli f
C 108	22.4	89.6	70	12	ADP05525	Adp05525 Novel mic	181	17	68.0	66	12	ADG68572	Adg68572 E. coli f
C 109	21.8	87.2	70	12	ADP05528	Adp05528 Novel mic	182	17	68.0	66	12	ADH56709	Adh56709 Primer to
C 110	21.8	87.2	70	12	ADP05528	Adp05528 Novel mic	183	17	68.0	66	12	ADH56712	Adh56712 Primer to
C 111	21.8	87.2	106	14	AEBS6868	Aeb56868 Human ech	184	17	68.0	66	12	ADH56712	Adh56712 Primer to
C 112	21.8	87.2	110	14	AEBS6813	Aeb56813 Viral 5'	185	17	68.0	66	12	ADJ112801	Adj112801 Primer to
C 113	21.8	87.2	235	14	AEBS6802	Aeb56802 Viral 5'	186	17	68.0	66	12	ADJ112804	Adj112804 Primer to
C 114	21.8	87.2	237	14	AEBS6837	Aeb56837 Human cox	187	17	68.0	66	12	ADI27706	Adi27706 Primer to
C 115	21.8	87.2	237	14	AEBS6857	Aeb56857 Human ech	188	17	68.0	66	12	ADI27703	Adi27703 Primer to
C 116	21.8	87.2	237	14	AEBS6782	Aeb56782 Viral 5'	189	17	68.0	66	12	ADI33772	Adi33772 E. coli f
C 117	21.8	87.2	238	14	AEBS6782	Aeb56782 Viral 5'	190	17	68.0	66	12	ADI33775	Adi33775 E. coli f
C 118	21.8	87.2	238	14	AEBS6839	Aeb56839 Human cox	191	17	68.0	66	12	ADK51506	Adk51506 Primer to
C 119	21.8	87.2	238	14	AEBS6797	Aeb56797 Viral 5'	192	17	68.0	66	12	ADK51509	Adk51509 Primer to
C 120	21.8	87.2	238	14	AEBS6851	Aeb56851 Human cox	193	17	68.0	66	12	ADM17991	Adm17991 E. coli f
C 121	21.8	87.2	238	14	AEBS6852	Aeb56852 Human cox	194	17	68.0	66	12	ADM17988	Adm17988 E. coli f
C 122	21.8	87.2	238	14	AEBS6784	Aeb56784 Viral 5'	195	17	68.0	66	12	ADL82586	Adl82586 Primer to
C 123	21.8	87.2	238	14	AEBS6795	Aeb56795 Viral 5'	196	17	68.0	66	12	ADL82589	Adl82589 Primer to
C 124	21.8	87.2	238	14	AEBS6796	Aeb56796 Viral 5'	197	17	68.0	66	12	ADM46224	Adm46224 Primer to
C 125	21.8	87.2	654	4	AAC85173	Aac85173 Coxsackie	198	17	68.0	69	12	ADP05529	Adp05529 Novel mic
C 126	20.8	83.2	69	12	ADP05523	Adp05523 Novel mic	C 199	17	68.0	70	2	AAV58283	Av58283 Type 3 Sa
C 127	20.8	83.2	70	12	ADP05524	Adp05524 Novel mic	200	17	68.0	70	12	ADP05500	Adp05500 Novel mic
C 128	20.2	80.8	70	12	ADP05505	Adp05505 Novel mic	201	17	68.0	70	12	ADP05499	Adp05499 Novel mic
C 129	20.2	80.8	70	12	ADP05509	Adp05509 Novel mic	202	17	68.0	70	12	ADP05502	Adp05502 Novel mic
C 130	20.2	80.8	198	14	AEBS6854	Aeb56854 Human ech	203	17	68.0	70	12	ADP05497	Adp05497 Novel mic
C 131	20.2	80.8	238	14	AEBS6799	Aeb56799 Viral 5'	204	17	68.0	70	12	ADP05498	Adp05498 Novel mic
C 132	18.8	75.2	366	11	ACH94885	Ach94885 Klebsiell	205	17	68.0	70	12	ADP05496	Adp05496 Novel mic
C 133	18.6	74.4	238	14	AEBS6878	Aeb56878 Human pol	C 206	17	68.0	74	12	ADP05579	Adp05579 Novel mic
C 134	18.6	74.4	238	14	AEBS6882	Aeb56882 Viral 5'	C 207	17	68.0	176	3	AAZ58488	Aaz58488 Recombina
C 135	18.6	74.4	521	6	ABL53111	AbL53111 Micro-org	C 208	17	68.0	195	10	ABZ69931	Abz69931 Polioviru
C 136	18.4	73.6	497	8	ABX12446	Abx12446 Coxsackie	C 209	17	68.0	236	14	AEBS6816	Aeb56816 Viral 5'
C 137	18.2	72.8	1499	13	ADX15059	Adx15059 Plant ful	C 210	17	68.0	237	14	AEBS6879	Aeb56879 Human pol
C 138	18.2	72.8	11000	4	AAI96883_03	Continuation (4 of	C 211	17	68.0	237	14	AEBS6881	Aeb56881 Human pol
C 139	17.6	70.4	1137	8	ACA01486	Aca01486 C. glutam	C 212	17	68.0	237	14	AEBS6827	Aeb56827 Viral 5'
C 140	17.6	70.4	1182	5	AH67705	Aah67705 C. glutami	C 213	17	68.0	237	14	AEBS6875	Aeb56875 Human pol
C 141	17.6	70.4	2381	12	ADP71896	Adp71896 Renal tox	C 214	17	68.0	237	14	AEBS6876	Aeb56876 Human pol
C 142	17.6	70.4	2692	4	ABL18825	AbL18825 Drosophil	C 215	17	68.0	237	14	AEBS6880	Aeb56880 Human pol
C 143	17.6	70.4	3663	4	ABL17534	AbL17534 Drosophil	C 216	17	68.0	237	14	AEBS6825	Aeb56825 Viral 5'
C 144	17.6	70.4	6051	4	ABL18824	AbL18824 Drosophil	C 217	17	68.0	237	14	AEBS6818	Aeb56818 Viral 5'
C 145	17.6	70.4	6462	6	ABK83473	AbK83473 Human cdn	C 218	17	68.0	237	14	AEBS6873	Aeb56873 Human pol
C 146	17.6	70.4	6462	13	ADR52978	Adr52978 Drug ther	C 219	17	68.0	237	14	AEBS6817	Aeb56817 Viral 5'
C 147	17.6	70.4	34980	5	AAH68532	Aah68532 C. glutami	C 220	17	68.0	237	14	AEBS6820	Aeb56820 Viral 5'
C 148	17.4	69.6	919	2	AAV06125	Av06125 Viral inf	C 221	17	68.0	237	14	AEBS6871	Aeb56871 Human ent
C 149	17.4	69.6	919	12	ADJ74131	Adj74131 Rat cdna	C 222	17	68.0	237	14	AEBS6821	Aeb56821 Viral 5'
C 150	17.2	68.8	606	6	ABK79367	Abk79367 Bacillus	C 223	17	68.0	237	14	AEBS6872	Aeb56872 Human pol
C 151	17.2	68.8	824	2	ADR01831	AdR01831 A. gosseyp	C 224	17	68.0	237	14	AEBS6824	Aeb56824 Viral 5'
C 152	17	68.0	66	10	ADB89060	Adb89060 E. coli ft	C 225	17	68.0	237	14	AEBS6826	Aeb56826 Viral 5'
C 153	17	68.0	66	10	ADB89063	Adb89063 E. coli ft	C 226	17	68.0	238	14	AEBS6819	Aeb56819 Viral 5'
C 154	17	68.0	66	10	ADC24410	Adc24410 E. coli ft	C 227	17	68.0	238	14	AEBS6874	Aeb56874 Human pol
C 155	17	68.0	66	10	ADC24407	Adc24407 E. coli ft	C 228	17	68.0	238	14	AEBS6833	Aeb56833 Human cox
C 156	17	68.0	66	10	ADD67680	Add67680 E. coli f	C 229	17	68.0	238	14	AEBS6778	Aeb56778 Viral 5'
C 157	17	68.0	66	10	ADD67677	Add67677 E. coli f	C 230	17	68.0	238	14	AEBS6682	Aeb56682 Human pol
C 158	17	68.0	66	10	ADE10390	Ade10390 E. coli f	C 231	17	68.0	319	2	AAV28515	Aav28515 Phosphate
C 159	17	68.0	66	10	ADE10393	Ade10393 E. coli f	C 232	17	68.0	514	3	AAZ58487	Aaz58487 Polioviru
C 160	17	68.0	66	10	ADE11315	Ade11315 E. coli f	C 233	17	68.0	537	4	AAI23152	Aai23152 Probe #13
C 161	17	68.0	66	10	ADE11312	Ade11312 E. coli f	C 234	17	68.0	537	4	ABM68253	Abm68253 Human foe
C 162	17	68.0	66	10	ADE12490	Ade12490 E. coli f	C 235	17	68.0	537	4	AAI48468	Aai48468 Probe #17
C 163	17	68.0	66	10	ADE12493	Ade12493 E. coli f	C 236	17	68.0	537	4	ABA50309	AbA50309 Human bre
C 164	17	68.0	66	10	ADE12253	Ade12253 E. coli f	C 237	17	68.0	537	4	ABA35262	AbA35262 Probe #13
C 165	17	68.0	66	10	ADE12256	Ade12256 E. coli f	C 238	17	68.0	537	4	AAK42389	Aak42389 Human bon

C 239	17	68.0	537	4	AAK16630	Aak16630 Human bra	C 312	17	68.0	7431	2	AAQ30148	Aeq30148 Attenuate
C 240	17	68.0	537	4	AB541999	Ab541999 Human liv	C 313	17	68.0	7432	2	AAQ22965	Aa22965 True type
C 241	17	68.0	537	5	Aai08808	Aai08808 Probe #87	C 314	17	68.0	7440	1	AA200042	Aan20042 Sequence
C 242	17	68.0	537	6	ABa16444	AbA16444 Human gen	C 315	17	68.0	7441	1	AA26152	Aax26152 DNA seque
C 243	17	68.0	548	4	ABa60784	AbA60784 Human foe	C 316	17	68.0	7473	8	ACC43138	Acc43138 Nucleotid
C 244	17	68.0	548	4	AAI40677	Aai40677 Probe #93	C 317	17	68.0	7925	12	ADP74702	Adp74702 Novel bic
C 245	17	68.0	548	4	AAK34960	Aak34960 Human bon	C 318	17	68.0	7925	12	ADP74702	Adp74702 Novel bic
C 246	17	68.0	548	4	AAK09069	Aak09069 Human bon	C 319	17	68.0	7943	8	ACC43139	Acc43139 Nucleotid
C 247	17	68.0	548	4	AB534715	Ab534715 Human liv	C 320	17	68.0	8298	2	AAV18096	Aav18096 pMCDHAP
C 248	17	68.0	628	2	AAQ58715	Aaq58715 Polioviru	C 321	17	68.0	11326	12	ADP7660	Adp7660 Viral vec
C 249	17	68.0	628	2	AAQ58726	Aaq58726 Polioviru	C 322	17	68.0	11326	12	AAV12373	Aav12373 Chimeric
C 250	17	68.0	639	12	ADP74707	Adp74707 Novel bic	C 323	17	68.0	11746	12	ADP7659	Adp7659 Viral vec
C 251	17	68.0	743	14	ADM37919	Adm37919 Polioviru	C 324	17	68.0	38246	12	ADP7662	Adp7662 Viral vec
C 252	17	68.0	745	8	ACC48197	Acc48197 Polioviru	C 325	17	68.0	40352	2	AAV02032	Aav02032 MAGS-B cl
C 253	17	68.0	1575	13	ADS56609	Ads56609 Bacterial	C 326	17	68.0	49646	3	AAA81457	Aaa81457 N. mening
C 254	17	68.0	1782	14	ADV85656	Adv85656 Human Mel	C 327	17	68.0	110000	3	AAA81490	Aaa81490 .06
C 255	17	68.0	1866	2	AAI41492	Aai41492 DNA encod	C 328	17	68.0	349980	3	AAF21608	Aaf21608 Neisseria
C 256	17	68.0	1866	2	ABQ76213	Abq76213 Human tum	C 329	16.8	67.2	285	6	ABL75427	AbL75427 Corn taas
C 257	17	68.0	1927	3	AAQ45906	Aaq45906 Arabidops	C 330	16.8	67.2	294	6	AB569284	Ab569284 Novel mur
C 258	17	68.0	1930	3	AAI13969	Aai13969 Arabidops	C 331	16.8	67.2	398	5	ABV00658	Abv00658 Human pro
C 259	17	68.0	1950	4	AAI13936	Aai13936 Probe #38	C 332	16.8	67.2	399	5	ABV09827	Abv09827 Human pro
C 260	17	68.0	1950	4	AB556555	Ab556555 Human foe	C 333	16.8	67.2	450	5	ABV31001	Abv31001 Human pro
C 261	17	68.0	1950	4	AAI35311	Aai35311 Probe #39	C 334	16.8	67.2	450	5	ABV39969	Abv39969 Human pro
C 262	17	68.0	1950	4	AB445173	Ab445173 Human bre	C 335	16.8	67.2	787	6	ABK63521	Abk63521 Rat seque
C 263	17	68.0	1950	4	ABK25350	Abk25350 Probe #38	C 336	16.8	67.2	787	10	ADB58686	Adb58686 Toxicity-
C 264	17	68.0	1950	4	AAK29349	Aak29349 Human bon	C 337	16.8	67.2	787	10	ABT42261	Abt42261 Toxicity
C 265	17	68.0	1950	4	AAK03880	Aak03880 Human bra	C 338	16.8	67.2	787	12	ADP72725	Adp72725 Renal tox
C 266	17	68.0	1950	4	AB528971	Ab528971 Human liv	C 339	16.8	67.2	787	13	ADT66606	Adt66606 Rat heat
C 267	17	68.0	1950	5	AAI03805	Aai03805 Probe #37	C 340	16.8	67.2	787	13	ADV41475	Adv41475 Rat cardi
C 268	17	68.0	1950	6	AB503309	Ab503309 Human gen	C 341	16.8	67.2	1130	13	ADO81285	Ado81285 Plant ful
C 269	17	68.0	2076	6	ABK14791	Abk14791 Platelet-	C 342	16.8	67.2	1192	13	ADX35581	Adx35581 Plant ful
C 270	17	68.0	2313	3	AAQ45979	Aaq45979 Arabidops	C 343	16.8	67.2	1281	13	ADT44059	Adt44059 Bacterial
C 271	17	68.0	2337	6	ABZ13318	Abz13318 Arabidops	C 344	16.8	67.2	1538	13	ADG62097	Adg62097 Plant ful
C 272	17	68.0	2337	8	ADA68290	Ada68290 Arabidops	C 345	16.8	67.2	1891	10	ADF30545	Adf30545 Rat angio
C 273	17	68.0	2544	10	ADB89267	Adb89267 E. coli f	C 346	16.8	67.2	3468	13	ADP06762	Adp06762 Full leng
C 274	17	68.0	2544	10	ADC24614	Adc24614 E. coli ft	C 347	16.6	66.4	180227	13	ABD33268	Abd33268 Human can
C 275	17	68.0	2544	10	ADP67891	Adp67891 E. coli f	C 348	16.6	66.4	297	10	ADC64938	Adc64938 Camellia
C 276	17	68.0	2544	10	ADE10339	Ade10339 Minicell	C 349	16.6	66.4	297	10	ADC63449	Adc63449 Camellia
C 277	17	68.0	2544	10	ADE11518	Ade11518 E. coli f	C 350	16.6	66.4	415	4	AAI21430	Aai21430 Probe #11
C 278	17	68.0	2544	10	ADE12696	Ade12696 E. coli f	C 351	16.6	66.4	415	4	ABA66510	AbA66510 Human foe
C 279	17	68.0	2544	10	ADE12202	Ade12202 E. coli f	C 352	16.6	66.4	415	4	AAI46719	Aai46719 Probe #15
C 280	17	68.0	2544	10	ADG25336	Adg25336 Minicell	C 353	16.6	66.4	415	4	ABA48601	AbA48601 Human bre
C 281	17	68.0	2544	10	ADJ47735	Adj47735 E. coli f	C 354	16.6	66.4	415	4	ABA33574	AbA33574 Probe #12
C 282	17	68.0	2544	11	ADP70502	Adp70502 Fusion po	C 355	16.6	66.4	415	4	AAK40667	Aak40667 Human bon
C 283	17	68.0	2544	12	ADF56169	Adf56169 E. coli f	C 356	16.6	66.4	415	4	AAK14934	Aak14934 Human bra
C 284	17	68.0	2544	12	ADG43197	Adg43197 E. coli f	C 357	16.6	66.4	415	4	AB540235	Ab540235 Human liv
C 285	17	68.0	2544	12	ADG43454	Adg43454 E. coli f	C 358	16.6	66.4	415	5	AAI07125	Aai07125 Probe #71
C 286	17	68.0	2544	12	ADG68518	Adg68518 E. coli f	C 359	16.6	66.4	415	6	AB514627	Ab514627 Human gen
C 287	17	68.0	2544	12	ADH56658	Adh56658 Fusion pr	C 360	16.6	66.4	443	9	ACH46054	Ach46054 Human inf
C 288	17	68.0	2544	12	ADI12751	Adi12751 Fusion pr	C 361	16.6	66.4	455	4	AAI12232	Aai12232 Probe #21
C 289	17	68.0	2544	12	ADI27652	Adi27652 Fusion pr	C 362	16.6	66.4	455	4	ABA53935	AbA53935 Human foe
C 290	17	68.0	2544	12	ADI33721	Adi33721 E. coli f	C 363	16.6	66.4	455	4	AAI33586	Aai33586 Probe #22
C 291	17	68.0	2544	12	ADK51455	Adk51455 Fusion pr	C 364	16.6	66.4	455	4	ABA43488	AbA43488 Human bre
C 292	17	68.0	2544	12	ADM17937	Adm17937 E. coli f	C 365	16.6	66.4	455	4	ABA23686	AbA23686 Probe #21
C 293	17	68.0	2544	12	ADL82535	Adl82535 Fusion pr	C 366	16.6	66.4	455	4	AAK27652	Aak27652 Human bon
C 294	17	68.0	2544	12	ADM46173	Adm46173 Fusion pr	C 367	16.6	66.4	455	4	AB527224	Ab527224 Human liv
C 295	17	68.0	2785	4	AAK75530	Aak75530 Human imm	C 368	16.6	66.4	455	5	AAI02145	Aai02145 Probe #21
C 296	17	68.0	2785	4	AAI05110	Aai05110 Human rep	C 369	16.6	66.4	455	5	AAI02113	Aai02113 Human gen
C 297	17	68.0	2785	4	ABL98002	AbL98002 Human tes	C 370	16.6	66.4	459	8	ACF03941	Acf03941 Rice endo
C 298	17	68.0	2843	10	ADE07614	Ade07614 Novel cod	C 371	16.6	66.4	683	10	ADK54742	Adk54742 Plant DNA
C 299	17	68.0	4203	4	AAK75532	Aak75532 Human imm	C 372	16.6	66.4	820	12	ADJ43789	Adj43789 Plant CDN
C 300	17	68.0	4203	4	AAK75531	Aak75531 Human imm	C 373	16.6	66.4	997	4	AAAD08303	Aad08303 Human eec
C 301	17	68.0	4203	4	AAI05112	Aai05112 Human rep	C 374	16.6	66.4	1762	5	AA586915	Aa586915 DNA encod
C 302	17	68.0	4203	4	AAI05113	Aai05113 Human rep	C 375	16.6	66.4	1762	5	AA586915	Aa586915 DNA encod
C 303	17	68.0	4203	4	ABL98004	AbL98004 Human tes	C 376	16.6	66.4	1878	8	ACA25872	AcA25872 Prokaryot
C 304	17	68.0	4203	4	ABL98005	AbL98005 Human tes	C 377	16.6	66.4	1894	10	ADA53967	Ada53967 Human cod
C 305	17	68.0	5252	12	ADO07652	Ado07652 Tricistaro	C 378	16.6	66.4	2358	5	AAA86913	Aaa86913 DNA encod
C 306	17	68.0	7185	12	ADP74699	Adp74699 Novel bic	C 379	16.6	66.4	2746	11	ADM03549	Adm03549 Human CDN
C 307	17	68.0	7185	12	ADP74701	Adp74701 Novel bic	C 380	16.6	66.4	2997	4	AAK94769	Aak94769 Human ful
C 308	17	68.0	7235	12	ADP74714	Adp74714 Novel bic	C 381	16.6	66.4	2997	12	ADL31827	Adl31827 Full leng
C 309	17	68.0	7235	12	ADP74715	Adp74715 Novel bic	C 382	16.6	66.4	3056	12	ADP10452	Adp10452 Reference
C 310	17	68.0	7235	12	ADP74700	Adp74700 Novel bic	C 383	16.6	66.4	3235	12	ADQ62861	Adq62861 Novel hum
C 311	17	68.0	7235	12	ADP74713	Adp74713 Novel bic	C 384	16.6	66.4	3335	13	ADT14988	Adt14988 Plant CDN
										3342	8	ABV93961	Abv93961 Human col

C 385	16.6	66.4	12104	4	AAL36396	Aal36396 Human mus	16	64.0	738	13	ABD33481	Abd33481 Murine ca
C 386	16.6	66.4	12104	8	ABX59384	ABX59384 cDNA enco	16	64.0	738	14	AD213480	Ad213480 Murine ca
C 387	16.6	66.4	12104	12	ADJ30134	ADJ30134 Human mus	16	64.0	757	4	ADJ14285	Adj14285 Human bre
C 388	16.6	66.4	13226	14	ACL46669	ACL46669 M. xanthu	16	64.0	820	12	ADJ43789	Adj43789 Plant CDN
C 389	16.6	66.4	23229	10	ADC87196	ADC87196 Human GPC	C 461	64.0	828	8	ACA19057	AcA19057 Prokaryot
C 390	16.6	66.4	32376	4	AAK66113	AAK66113 Human imm	C 462	64.0	918	11	ACN84249	Acn84249 Breast ca
C 391	16.6	66.4	91141	11	ACN44280	ACN44280 Mouse gen	C 463	64.0	931	10	ADG32951	AdG32951 Human DNA
C 392	16.6	66.4	110000	4	RAI19682_03	Continuation (4 of	C 464	64.0	941	5	AAS79198	Aas79198 DNA enco
C 393	16.4	65.6	2061	8	ACA53674	ACA53674 Prokaryot	C 465	64.0	942	6	ABZ11418	Abz11418 Human pol
C 394	16.4	65.6	96598	9	ADA02609	ADA02609 Mouse Nfk	C 466	64.0	942	12	ADM43936	AdM43936 Novel hum
C 395	16.4	65.6	96598	10	ADB72347	ADB72347 Mouse Nfk	C 467	64.0	950	6	ABK73852	Abk73852 Bacillus
C 396	16.4	65.6	96598	10	ADE82941	ADE82941 Mouse Nfk	C 468	64.0	960	6	ABK73795	Abk73795 Bacillus
C 397	16.4	65.6	96598	10	ADE95857	ADE95857 Mouse Nfk	C 469	64.0	975	8	ACA51639	AcA51639 Prokaryot
C 398	16.2	64.8	274	3	AAA67853	AAA67853 Pinus rad	C 470	64.0	1004	8	ACA49007	AcA49007 Prokaryot
C 399	16.2	64.8	323	3	AAA67811	AAA67811 Pinus rad	C 471	64.0	1008	6	ABL65430	AbL65430 Lung canc
C 400	16.2	64.8	359	3	AAA67850	AAA67850 Pinus rad	C 472	64.0	1098	6	ABL65430	AbL65430 Lung canc
C 401	16.2	64.8	400	3	AAA67773	AAA67773 Pinus rad	C 473	64.0	1098	11	ACN84335	Acn84335 Breast ca
C 402	16.2	64.8	403	3	AAA67772	AAA67772 Pinus rad	C 474	64.0	1144	3	ACSA56023	AcS56023 Eucalyptu
C 403	16.2	64.8	412	8	ABX46070	ABX46070 Bovine ES	C 475	64.0	1149	4	ABL14281	AbL14281 Drosophil
C 404	16.2	64.8	417	3	AAA67847	AAA67847 Pinus rad	C 476	64.0	1157	5	AAS82078	Aas82078 DNA enco
C 405	16.2	64.8	430	3	AAA67812	AAA67812 Pinus rad	C 477	64.0	1159	6	ABK27922	Abk27922 DNA enco
C 406	16.2	64.8	442	9	ACH17925	ACH17925 Human adu	C 478	64.0	1233	13	ADT48127	AdT48127 Bacterial
C 407	16.2	64.8	460	3	AAA67821	AAA67821 Pinus rad	C 479	64.0	1346	5	AAS82115	Aas82115 DNA enco
C 408	16.2	64.8	463	12	ADP92520	ADP92520 Cotton ex	C 480	64.0	1376	4	ABL03591	AbL03591 Drosophil
C 409	16.2	64.8	1002	10	ACF72193	ACF72193 Photorhab	C 481	64.0	1417	8	ACA36161	AcA36161 Prokaryot
C 410	16.2	64.8	1233	3	AAF21869	AAF21869 Human bre	C 482	64.0	1431	11	ACH97135	Ach97135 Klebsiell
C 411	16.2	64.8	1254	10	ABS57853	ABS57853 Rabbit cd	C 483	64.0	1629	4	ABL17773	AbL17773 Drosophil
C 412	16.2	64.8	1317	8	ACC78408	ACC78408 P. chryso	C 484	64.0	1629	13	ADX33288	AdX33288 Plant ful
C 413	16.2	64.8	1473	4	AAS52323	AAS52323 E. coli D	C 485	64.0	1734	5	ABV30198	Abv30198 Human pro
C 414	16.2	64.8	1473	8	ACA32384	ACA32384 Prokaryot	C 486	64.0	1734	11	ACN88953	Acn88953 Breast ca
C 415	16.2	64.8	1473	13	ADS45977	ADS45977 Bacterial	C 487	64.0	1794	14	ADW16458	AdW16458 Eucalyptu
C 416	16.2	64.8	1697	8	ACC78415	ACC78415 P. chryso	C 488	64.0	1938	11	ADN97356	Adn97356 B. lichen
C 417	16.2	64.8	1733	10	ADF28972	ADF28972 Influenza	C 489	64.0	1974	8	ACC46725	Acc46725 Human dit
C 418	16.2	64.8	3391	6	ABL69123	ABL69123 Kidney ca	C 490	64.0	2015	13	ADS59364	AdS59364 Bacterial
C 419	16.2	64.8	3552	4	AAK51875	AAK51875 Human pol	C 491	64.0	2101	5	AAS88998	Aas88998 DNA enco
C 420	16.2	64.8	3679	4	AAK52859	AAK52859 Human pol	C 492	64.0	2285	14	ADY19023	AdY19023 DNA enco
C 421	16.2	64.8	3968	12	ADQ84976	ADQ84976 Human tum	C 493	64.0	2322	5	AAS93101	Aas93101 DNA enco
C 422	16.2	64.8	3968	12	ADQ87257	ADQ87257 Human tum	C 494	64.0	2323	5	AAS89009	Aas89009 DNA enco
C 423	16.2	64.8	3968	13	ADQ83799	ADQ83799 Human tum	C 495	64.0	2326	5	AAS90384	Aas90384 DNA enco
C 424	16.2	64.8	4253	12	ADQ22492	ADQ22492 Human sof	C 496	64.0	2346	13	ADS46215	AdS46215 Bacterial
C 425	16.2	64.8	5824	4	ABL07578	ABL07578 Drosophil	C 497	64.0	2415	8	ACA31124	AcA31124 Prokaryot
C 426	16.2	64.8	7513	6	ABK84767	ABK84767 Human CDN	C 498	64.0	2577	4	ABL25890	AbL25890 Drosophil
C 427	16.2	64.8	7513	6	ABN97374	ABN97374 Gene #387	C 499	64.0	2766	4	ABL26615	AbL26615 Drosophil
C 428	16.2	64.8	70665	6	ABT10716	ABT10716 Human bre	C 500	64.0	2940	6	ABK27919	Abk27919 DNA enco
C 429	16.2	64.8	70665	11	ADN95672	ADN95672 Human BEC						
C 430	16.2	64.8	96798	10	ACF65387_6	Continuation (7 of						
C 431	16.2	64.8	110000	10	ACF67367_54	Continuation (55 o						
C 432	16.2	64.8	110000	10	ACF65387_5	Continuation (6 of						
C 433	16.2	64.0	32	6	ABK27956	ABK27956 Lipolytic						
C 434	16.2	64.0	50	6	ABZ04088	ABZ04088 Human leu						
C 435	16.2	64.0	50	10	ADG33453	ADG33453 Human DNA						
C 436	16.2	64.0	281	4	AAL14197	AAL14197 Human bre						
C 437	16.2	64.0	281	4	AAL23059	AAL23059 Human bre						
C 438	16.2	64.0	283	5	ABV12781	ABV12781 Human pro						
C 439	16.2	64.0	290	5	ABV22366	ABV22366 Human pro						
C 440	16.2	64.0	290	5	ABV28188	ABV28188 Human pro						
C 441	16.2	64.0	307	11	ACN91627	ACN91627 Breast ca						
C 442	16.2	64.0	321	5	ABV03612	ABV03612 Human pro						
C 443	16.2	64.0	369	8	ACA45562	ACA45562 Prokaryot						
C 444	16.2	64.0	372	11	ABD06168	ABD06168 Pseudomon						
C 445	16.2	64.0	390	12	ADJ74998	ADJ74998 Marker ge						
C 446	16.2	64.0	430	5	ABV42786	ABV42786 Human pro						
C 447	16.2	64.0	430	5	ABV33910	ABV33910 Human pro						
C 448	16.2	64.0	447	11	ABD06132	ABD06132 Pseudomon						
C 449	16.2	64.0	495	4	AAH33458	AAH33458 Human col						
C 450	16.2	64.0	509	10	ADB57386	ADB57386 Toxicity-						
C 451	16.2	64.0	509	10	ADB51933	ADB51933 Primaty r						
C 452	16.2	64.0	530	5	ABV15900	ABV15900 Human pro						
C 453	16.2	64.0	540	11	ACN88053	ACN88053 Breast ca						
C 454	16.2	64.0	561	9	ACH41404	ACH41404 Human foe						
C 455	16.2	64.0	596	5	AAS74875	AAS74875 DNA enco						
C 456	16.2	64.0	618	5	ABV45700	ABV45700 Human pro						
C 457	16.2	64.0	718	2	ADR02269	ADR02269 A. gossyp						

## ALIGNMENTS

## RESULT 1

ID ADP05526 standard; DNA; 69 BP.

XX ADP05526;

XX AC ADP05526;

XX DT 26-AUG-2004 (first entry)

XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID31.

XX KW microbe detection; microbe identification; virus; viral particle;

XX KW pathogenic bacterium; cellular microbe; acellular microbe;

XX KW clinical diagnosis; research; epidemiological surveillance;

XX KW bioterrorism countermeasure; environmental pathogen survey;

XX KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX OS Viruses.

XX PN WO2004045365-A2.

XX PD 03-JUN-2004.

XX XX 23-MAY-2003; 2003WO-US016461.

XX XX 15-NOV-2002; 2002US-00295787.

XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Jia XY, Berger MA, Tilles JG;  
 XX DR WPI; 2004-449626/42.  
 XX DR  
 XX PT New (microarray) apparatus comprising a substrate with attached nucleic  
 XX PT acid probes, useful for detecting one or more microbes in a sample.  
 XX PS Claim 16; SEQ ID NO 31; 89pp; English.  
 XX CC This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX SQ Sequence 69 BP; 11 A; 20 C; 20 G; 18 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 12; Length 69;  
 Best Local Similarity 100.0%; Pred. No. 0.042;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
 DB 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
 RESULT 2  
 ADP05510  
 ID ADP05510 standard; DNA; 70 BP.  
 AC ADP05510;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID15.  
 XX KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX OS Viruses.  
 XX PN WO2004045365-A2.  
 XX PD 03-JUN-2004.  
 XX PF 23-MAY-2003; 2003WO-US016461.  
 XX PR 15-NOV-2002; 2002US-00295787.  
 XX PA (REGC ) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;  
 XX DR WPI; 2004-449626/42.  
 XX DR  
 XX PT New (microarray) apparatus comprising a substrate with attached nucleic  
 XX PT acid probes, useful for detecting one or more microbes in a sample.  
 XX PS Claim 16; SEQ ID NO 15; 89pp; English.  
 XX CC This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX SQ Sequence 70 BP; 12 A; 22 C; 20 G; 16 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
 DB 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
 RESULT 3  
 ADP05515  
 ID ADP05515 standard; DNA; 70 BP.  
 AC ADP05515;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID20.  
 XX KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX OS Viruses.  
 XX PN WO2004045365-A2.  
 XX PD 03-JUN-2004.  
 XX PF 23-MAY-2003; 2003WO-US016461.  
 XX PR 15-NOV-2002; 2002US-00295787.  
 XX PA (REGC ) UNIV CALIFORNIA.  
 XX PI Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.  
 XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 XX Claim 16; SEQ ID NO 20; 89pp; English.  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX SQ Sequence 70 BP; 13 A; 23 C; 20 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 DB 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 4  
 ADP05513  
 ID ADP05513 standard; DNA; 70 BP.  
 XX AC ADP05513;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID18.  
 XX microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX Viruses.  
 OS WO2004045365-A2.  
 XX PN 03-JUN-2004.  
 XX PD 23-MAY-2003; 2003WO-US016461.  
 XX PF 15-NOV-2002; 2002US-00295787.  
 XX PR (REGC ) UNIV CALIFORNIA.  
 XX PA Jia XY, Berger MA, Tilles JG;  
 XX WPI; 2004-449626/42.  
 XX DR

XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 XX Claim 16; SEQ ID NO 18; 89pp; English.  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX SQ Sequence 70 BP; 10 A; 21 C; 21 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 DB 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 5  
 ADP05521  
 ID ADP05521 standard; DNA; 70 BP.  
 XX AC ADP05521;  
 XX DT 26-AUG-2004 (first entry)  
 XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID26.  
 XX microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX Viruses.  
 OS WO2004045365-A2.  
 XX PN 03-JUN-2004.  
 XX PD 23-MAY-2003; 2003WO-US016461.  
 XX PF 15-NOV-2002; 2002US-00295787.  
 XX PR (REGC ) UNIV CALIFORNIA.  
 XX PA Jia XY, Berger MA, Tilles JG;  
 XX WPI; 2004-449626/42.  
 XX DR  
 XX PT New (microarray) apparatus comprising a substrate with attached nucleic

acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 26; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 11 A; 21 C; 21 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 6  
 ADP05504  
 ID ADP05504 standard; DNA; 70 BP.  
 AC ADP05504;  
 XX  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID9.  
 XX  
 KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX  
 OS Viruses.  
 XX  
 WO2004045365-A2.  
 XX  
 PN 03-JUN-2004.  
 XX  
 PD 23-MAY-2003; 2003WO-US016461.  
 XX  
 PF 15-NOV-2002; 2002US-00295787.  
 XX  
 PR (REGC ) UNIV CALIFORNIA.  
 XX  
 PA Jia XY, Berger MA, Tilles JG;  
 XX  
 FI WPI; 2004-449626/42.  
 XX  
 DR New (microarray) apparatus comprising a substrate with attached nucleic  
 XX acid probes, useful for detecting one or more microbes in a sample.  
 PT  
 PS Claim 16; SEQ ID NO 26; 89pp; English.

Claim 16; SEQ ID NO 9; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 14 A; 22 C; 18 G; 16 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 7  
 ADP05507  
 ID ADP05507 standard; DNA; 70 BP.  
 AC ADP05507;  
 XX  
 XX  
 DT 26-AUG-2004 (first entry)  
 XX  
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID12.  
 XX  
 KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX  
 OS Viruses.  
 XX  
 WO2004045365-A2.  
 XX  
 PN 03-JUN-2004.  
 XX  
 PD 23-MAY-2003; 2003WO-US016461.  
 XX  
 PF 15-NOV-2002; 2002US-00295787.  
 XX  
 PR (REGC ) UNIV CALIFORNIA.  
 XX  
 PA Jia XY, Berger MA, Tilles JG;  
 XX  
 FI WPI; 2004-449626/42.  
 XX  
 DR New (microarray) apparatus comprising a substrate with attached nucleic  
 XX acid probes, useful for detecting one or more microbes in a sample.  
 PT  
 PS Claim 16; SEQ ID NO 12; 89pp; English.

CC This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at a target nucleic acid to provide a detectable signal at  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.

SQ Sequence 70 BP; 13 A; 21 C; 19 G; 17 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 8  
 ADP05517  
 ID ADP05517 standard; DNA; 70 BP.  
 AC ADP05517;  
 XX 26-AUG-2004 (first entry)  
 DT XX  
 DE XX  
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID22.  
 KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX Viruses.  
 OS  
 XX WO2004045365-A2.  
 FN  
 XX 03-JUN-2004.  
 PD  
 XX 23-MAY-2003; 2003WO-US016461.  
 PF  
 XX 15-NOV-2002; 2002US-00295787.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Jia XY, Berger MA, Tilles JG;  
 PI  
 XX WPI; 2004-449626/42.  
 DR  
 XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 FT  
 XX Claim 16; SEQ ID NO 22; 89pp; English.  
 PS  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification

CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at a target nucleic acid to provide a detectable signal at  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.

SQ Sequence 70 BP; 8 A; 21 C; 23 G; 18 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.043;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

RESULT 9  
 ADP05534  
 ID ADP05534 standard; DNA; 70 BP.  
 AC ADP05534;  
 XX 26-AUG-2004 (first entry)  
 DT XX  
 DE XX  
 DE Novel microbe detection apparatus-related oligonucleotide probe SeqID39.  
 KW microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX Viruses.  
 OS  
 XX WO2004045365-A2.  
 FN  
 XX 03-JUN-2004.  
 PD  
 XX 23-MAY-2003; 2003WO-US016461.  
 PF  
 XX 15-NOV-2002; 2002US-00295787.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Jia XY, Berger MA, Tilles JG;  
 PI  
 XX WPI; 2004-449626/42.  
 DR  
 XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 FT  
 XX Claim 16; SEQ ID NO 39; 89pp; English.  
 PS  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid



CC probes disposed at the microbe identification sites, each group being  
CC complementary to a target nucleic acid to provide a detectable signal at  
CC one or more microbe identification sites. The apparatus is useful for  
CC detecting the presence of one or more microbes in a sample, such as virus  
CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
CC microbe. The apparatus is particularly useful for clinical diagnosis,  
CC research, epidemiological surveillance, bioterrorism countermeasures,  
CC environmental pathogen surveys, and monitoring food contaminants. Current  
CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
CC difficult to implement, time consuming, expensive, outdated, and  
CC typically rely on the use of agents that recognise and bind to membrane  
CC bound proteins or carbohydrates of the pathogen. These further cannot  
CC assay multiple pathogens. The new apparatus or device for detecting  
CC microbes overcomes these disadvantages. The apparatus is compact,  
CC sensitive, and quick to detect the presence of any of a number of  
CC pathogens present in a sample. The present sequence is that of an  
CC oligonucleotide probe which is related to the micorbe detection apparatus  
CC of the invention.

SQ Sequence 70 BP; 11 A; 20 C; 20 G; 19 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

#### RESULT 10

ADP05503  
ID ADP05503 standard; DNA; 70 BP.

XX AC ADP05503;

DT 26-AUG-2004 (first entry)

DE Novel microbe detection apparatus-related oligonucleotide probe SeqID8.

XX microbe detection; microbe identification; virus; viral particle;  
KW pathogenic bacterium; cellular microbe; acellular microbe;  
KW clinical diagnosis; research; epidemiological surveillance;  
KW bioterrorism countermeasure; environmental pathogen survey;  
KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic  
XX acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 8; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a  
XX sample which comprises a substrate having multiple microbe identification  
XX sites, each having a unique address indicative of the position of that  
XX microbe identification site on the substrate and groups of nucleic acid  
XX probes disposed at the microbe identification sites, each group being  
XX complementary to a target nucleic acid to provide a detectable signal at

CC one or more microbe identification sites. The apparatus is useful for  
CC detecting the presence of one or more microbes in a sample, such as virus  
CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
CC microbe. The apparatus is particularly useful for clinical diagnosis,  
CC research, epidemiological surveillance, bioterrorism countermeasures,  
CC environmental pathogen surveys, and monitoring food contaminants. Current  
CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
CC difficult to implement, time consuming, expensive, outdated, and  
CC typically rely on the use of agents that recognise and bind to membrane  
CC bound proteins or carbohydrates of the pathogen. These further cannot  
CC assay multiple pathogens. The new apparatus or device for detecting  
CC microbes overcomes these disadvantages. The apparatus is compact,  
CC sensitive, and quick to detect the presence of any of a number of  
CC pathogens present in a sample. The present sequence is that of an  
CC oligonucleotide probe which is related to the micorbe detection apparatus  
CC of the invention.

SQ Sequence 70 BP; 12 A; 21 C; 19 G; 18 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

#### RESULT 11

ADP05519  
ID ADP05519 standard; DNA; 70 BP.

XX AC ADP05519;

DT 26-AUG-2004 (first entry)

DE Novel microbe detection apparatus-related oligonucleotide probe SeqID24.

XX microbe detection; microbe identification; virus; viral particle;  
KW pathogenic bacterium; cellular microbe; acellular microbe;  
KW clinical diagnosis; research; epidemiological surveillance;  
KW bioterrorism countermeasure; environmental pathogen survey;  
KW food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX PD 03-JUN-2004.

XX PF 23-MAY-2003; 2003WO-US016461.

XX PR 15-NOV-2002; 2002US-00295787.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Jia XY, Berger MA, Tilles JG;

XX DR WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic  
XX acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 24; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a  
XX sample which comprises a substrate having multiple microbe identification  
XX sites, each having a unique address indicative of the position of that  
XX microbe identification site on the substrate and groups of nucleic acid  
XX probes disposed at the microbe identification sites, each group being  
XX complementary to a target nucleic acid to provide a detectable signal at  
XX one or more microbe identification sites. The apparatus is useful for  
XX detecting the presence of one or more microbes in a sample, such as virus

or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus of the invention.

Sequence 70 BP; 11 A; 20 C; 19 G; 20 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

## RESULT 12

ADP05518  
ID ADF05518 standard; DNA; 70 BP.

XX  
AC ADP05518;

DT 26-AUG-2004 (first entry)

XX Novel microbe detection apparatus-related oligonucleotide probe SeqID23.

XX microbe detection; microbe identification; virus; viral particle;  
XX pathogenic bacterium; cellular microbe; acellular microbe;  
XX clinical diagnosis; research; epidemiological surveillance;  
XX bioterrorism countermeasure; environmental pathogen survey;  
XX food contaminant; radioimmunoassay; ELISA; probe; ss.

XX Viruses.

XX WO2004045365-A2.

XX 03-JUN-2004.

XX 23-MAY-2003; 2003WO-US016461.

XX 15-NOV-2002; 2002US-00295787.

XX (REGC ) UNIV CALIFORNIA.

XX Jia XY, Berger MA, Tilles JG;

XX WPI; 2004-449626/42.

XX New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

XX Claim 16; SEQ ID NO 23; 89pp; English.

XX This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis,

CC research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the micorbe detection apparatus of the invention.

Sequence 70 BP; 12 A; 22 C; 19 G; 17 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 12; Length 70;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTCGCCGTTACGA 25  
Db 1 TCCGCTGCAGAGTTCGCCGTTACGA 25

## RESULT 13

AEB56869/C  
ID AEB56869 standard; DNA; 105 BP.

XX  
AC AEB56869;

DT 22-SEP-2005 (first entry)

XX Human echovirus 30 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human echovirus 30.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; S76769.

XX Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequences. (I), (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 105 BP; 22 A; 27 C; 27 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 105;  
 Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 70 TCCGCTGCAGAGTTGCCCGTTACGA 46

RESULT 14  
 AEB56814/c  
 ID AEB56814 standard; DNA; 107 BP.

XX AC AEB56814;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:53.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN//) TSANG S.

XX PA (PRIC//) PRICE J A.

XX PA (HELL//) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 53; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 target binding sequence of an oligonucleotide chosen from any one of the  
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 selected amplification or detection reaction. Also described: (1) a kit  
 (KI) comprising (I), and one or more container that contains (I); and (2)  
 detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 the target sequence using first amplification primer having a sequence  
 consisting essentially of target binding sequence of any one of AEB56764  
 to AEB56771 and optionally a sequence required for selected amplification  
 reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
 (KI) are useful for detecting enterovirus target sequences. (I)  
 specifically and selectively recognizes the enterovirus genome. (I)  
 sensitively and rapidly detects fewer than 500 copies of enteroviral  
 genome and allows detection of broad range of enterovirus serotypes. The  
 present sequence represents a viral 5' untranslated polynucleotide  
 sequence given in the exemplification of the present invention.

XX SQ Sequence 107 BP; 22 A; 28 C; 28 G; 29 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 107;  
 Best Local Similarity 100.0%; Pred. No. 0.045; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 72 TCCGCTGCAGAGTTGCCCGTTACGA 48

RESULT 15

AEB56779/c

ID AEB56779 standard; DNA; 126 BP.

XX AC AEB56779;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:18.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN//) TSANG S.

XX PA (PRIC//) PRICE J A.

XX PA (HELL//) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 18; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 target binding sequence of an oligonucleotide chosen from any one of the  
 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 selected amplification or detection reaction. Also described: (1) a kit  
 (KI) comprising (I), and one or more container that contains (I); and (2)  
 detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 the target sequence using first amplification primer having a sequence  
 consisting essentially of target binding sequence of any one of AEB56764  
 to AEB56771 and optionally a sequence required for selected amplification  
 reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
 (KI) are useful for detecting enterovirus target sequences. (I)  
 specifically and selectively recognizes the enterovirus genome. (I)  
 sensitively and rapidly detects fewer than 500 copies of enteroviral  
 genome and allows detection of broad range of enterovirus serotypes. The  
 present sequence represents a viral 5' untranslated polynucleotide  
 sequence given in the exemplification of the present invention.

XX SQ Sequence 126 BP; 26 A; 36 C; 31 G; 33 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 126;  
 Best Local Similarity 100.0%; Pred. No. 0.046; Mismatches 0; Indels 0; Gaps 0;  
 Matches 25; Conservative 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 16

AEB56834/c

ID AEB56834 standard; DNA; 180 BP.

XX AC AEB56834;

XX 22-SEP-2005 (first entry)  
 XX Human coxsackievirus B1 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human coxsackievirus B1.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; S76767.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I), (MI) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 180 BP; 37 A; 48 C; 47 G; 48 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 14; Length 180;  
 Best Local Similarity 100.0%; Pred. No. 0.047;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 129 TCCGCTGCAGAGTTGCCCGTTACGA 105  
 RESULT 17  
 AEB56858/C  
 ID AEB56858 standard; DNA; 198 BP.  
 AC AEB56858;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 6 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human echovirus 6.  
 OS  
 XX

PN US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 DR GENBANK; U11709.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I), (MI) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 198 BP; 37 A; 47 C; 55 G; 59 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 25; DB 14; Length 198;  
 Best Local Similarity 100.0%; Pred. No. 0.048;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 91 TCCGCTGCAGAGTTGCCCGTTACGA 67  
 RESULT 18  
 AEB56863/C  
 ID AEB56863 standard; DNA; 198 BP.  
 XX AEB56863;  
 AC AEB56863;  
 XX 22-SEP-2005 (first entry)  
 XX Human echovirus 11 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 XX Human echovirus 11.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA

PA (PRIC/) PRICE J A.  
XX (HELL/) HELLYER T J.  
PI Tsang S, Price JA, Hellyer TJ;  
XX WPI; 2005-512251/52.  
DR GENBANK; U11705.  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
PS Disclosure; Fig 1A-D; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 25; DB 14; Length 198;  
Best Local Similarity 100.0%; Pred. No. 0.048;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
DB 91 TCCGCTGCAGAGTTGCCCGTTACGA 67  
XX  
RESULT 19  
AEB56848/C  
ID AEB56848 standard; DNA; 237 BP.  
XX  
AC AEB56848;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human coxsackievirus B5 5' untranslated polynucleotide sequence.  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
OS Human coxsackievirus B5.  
XX  
PN US2005158710-A1.  
XX  
PD 21-JUL-2005.  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
DR WPI; 2005-512251/52.  
DR GENBANK; AF114383.  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
PS Disclosure; Fig 1A-D; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 237 BP; 48 A; 52 C; 66 G; 71 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 25; DB 14; Length 237;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107  
XX  
RESULT 20  
AEB56862/C  
ID AEB56862 standard; DNA; 237 BP.  
XX  
AC AEB56862;  
XX  
DT 22-SEP-2005 (first entry)  
XX  
DE Human echovirus 9 5' untranslated polynucleotide sequence.  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
OS Human echovirus 9.  
XX  
PN US2005158710-A1.  
XX  
PD 21-JUL-2005.  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
DR WPI; 2005-512251/52.  
DR GENBANK; X92886.  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
PS Disclosure; Fig 1A-D; 34pp; English.  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 51 A; 55 C; 62 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 130 TCCGCTGCAGAGTTGCCCGTTACGA 106

RESULT 21  
 AEB56793/c  
 ID AEB56793 standard; DNA; 237 BP.

AC AEB56793;

XX  
 DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:32.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 32; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 237 BP; 52 A; 52 C; 59 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 237;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 22

AEB56840/c

ID AEB56840 standard; DNA; 238 BP.

XX AC AEB56840;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX FN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; AH008164.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 23  
AEB56791/c  
ID AEB56791 standard; DNA; 238 BP.  
XX  
XX  
AC AEB56791;  
XX  
XX  
DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Vital 5' untranslated polynucleotide sequence SEQ ID NO:30.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX  
OS Unidentified.  
XX  
XX  
PN US2005158710-A1.  
XX  
XX  
PD 21-JUL-2005.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX  
DR WPI; 2005-512251/52.  
XX  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX  
PS Disclosure; SEQ ID NO 30; 34pp; English.  
XX  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 24  
AEB56846/c  
ID AEB56846 standard; DNA; 238 BP.  
XX  
XX  
AC AEB56846;  
XX  
XX

DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX  
OS Human coxsackievirus B4.  
XX  
XX  
PN US2005158710-A1.  
XX  
XX  
PD 21-JUL-2005.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX  
DR WPI; 2005-512251/52.  
DR GENBANK; D00149.  
XX  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX  
PS Disclosure; Fig 1A-D; 34pp; English.  
XX  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
CC (KI) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
|||||  
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 25  
AEB56847/c  
ID AEB56847 standard; DNA; 238 BP.  
XX  
XX  
AC AEB56847;  
XX  
XX  
DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Human coxsackievirus B4 5' untranslated polynucleotide sequence.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX  
OS Human coxsackievirus B4.  
XX  
XX  
PN US2005158710-A1.

XX PD 21-JUL-2005.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.  
 XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX DR GENBANK; X05690.  
 XX PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX FT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; Fig 1A-D; 34pp; English.  
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 50 A; 55 C; 65 G; 68 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107  
 RESULT 26  
 AEB56789/c  
 ID AEB56789 standard; DNA; 238 BP.  
 AC AEB56789;  
 XX 22-SEP-2005 (first entry)  
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:28.  
 DE DNA detection; enteroviral detection; ds.  
 XX Unidentified.  
 XX OS US2005158710-A1.  
 XX PN 21-JUL-2005.  
 XX PD 16-JAN-2004; 2004US-00760048.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.

PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; SEQ ID NO 28; 34pp; English.  
 XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
 RESULT 27  
 AEB56775/c  
 ID AEB56775 standard; DNA; 238 BP.  
 XX AEB56775;  
 AC 22-SEP-2005 (first entry)  
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:14.  
 DE DNA detection; enteroviral detection; ds.  
 XX Unidentified.  
 XX OS US2005158710-A1.  
 XX PN 21-JUL-2005.  
 XX PD 16-JAN-2004; 2004US-00760048.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; SEQ ID NO 14; 34pp; English.



XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 56 A; 55 C; 58 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 28  
 AEB56807/C  
 ID AEB56807 standard; DNA; 238 BP.  
 XX  
 AC AEB56807;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:46.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 XN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.  
 XX (PRIC//) PRICE J A.  
 XX (HELL//) HELLYER T J.  
 XX  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 XX Disclosure; SEQ ID NO 46; 34pp; English.  
 XX  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enterovirus  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 53 A; 53 C; 58 G; 74 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 29  
 AEB56815/C  
 ID AEB56815 standard; DNA; 238 BP.  
 XX  
 AC AEB56815;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:54.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 XN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.  
 XX (PRIC//) PRICE J A.  
 XX (HELL//) HELLYER T J.  
 XX  
 XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 XX Disclosure; SEQ ID NO 54; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 53 A; 53 C; 55 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 30  
 AEB56838/c  
 ID AEB56838 standard; DNA; 238 BP.  
 XX  
 AC AEB56838;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B3.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Teang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; AF169665.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 50 A; 56 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 32  
 AEB56785/c  
 ID AEB56785 standard; DNA; 238 BP.  
 XX  
 AC AEB56785;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:24.

RESULT 31  
 AEB56842/c  
 ID AEB56842 standard; DNA; 238 BP.  
 XX  
 AC AEB56842;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Human coxsackievirus B3.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX  
 PI Teang S, Price JA, Hellyer TJ;  
 XX  
 DR WPI; 2005-512251/52.  
 DR GENBANK; M16572.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 32  
 AEB56785/c  
 ID AEB56785 standard; DNA; 238 BP.  
 XX  
 AC AEB56785;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:24.

```

KW DNA detection; enteroviral detection; ds.
XX Unidentified.
XX OS
XX US2005158710-A1.
XX PN
XX PD
XX 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX XX
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX XX
XX PI Teang S, Price JA, Hellyer TJ;
XX XX
XX DR WPI; 2005-512251/52.
XX XX
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX XX
XX PI Teang S, Price JA, Hellyer TJ;
XX XX
XX DR WPI; 2005-512251/52.
XX XX
XX PR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PT Disclosure; SEQ ID NO 24; 34pp; English.
XX XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABB56764
XX CC to ABB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 51 A; 51 C; 59 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCGTTACGA 51

RESULT 33
ABB56835/c
ID ABB56835 standard; DNA; 238 BP.
XX AC
XX ABB56835;
XX XX
XX DT 22-SEP-2005 (first entry)
XX XX
XX DE Human coxsackievirus B1 5' untranslated polynucleotide sequence.
XX XX
XX KW DNA detection; enteroviral detection; ds.
XX XX
XX OS Human coxsackievirus B1.
XX XX
XX PN US2005158710-A1.
XX XX
XX PD 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX XX

KW DNA detection; enteroviral detection; ds.
XX OS
XX US2005158710-A1.
XX PN
XX PD
XX 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX XX
XX PR (TSAN/) TSANG S.
XX PR (PRIC/) PRICE J A.
XX PR (HELL/) HELLYER T J.
XX XX
XX PI Teang S, Price JA, Hellyer TJ;
XX XX
XX DR WPI; 2005-512251/52.
XX XX
XX PR Novel oligonucleotide comprising sequences for binding and amplifying or
XX PT detecting target, useful for detecting enterovirus nucleic acids.
XX PT Disclosure; SEQ ID NO 24; 34pp; English.
XX XX
XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the
XX CC target binding sequence of an oligonucleotide chosen from any one of the
XX CC 10 sequence of ABB56762 to ABB56771; and (b) a sequence required for
XX CC selected amplification or detection reaction. Also described: (1) a kit
XX CC (K1) comprising (I), and one or more container that contains (I); and (2)
XX CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX CC the target sequence using first amplification primer having a sequence
XX CC consisting essentially of target binding sequence of any one of ABB56764
XX CC to ABB56771 and optionally a sequence required for selected amplification
XX CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and
XX CC (K1) are useful for detecting enterovirus target sequences. (I)
XX CC specifically and selectively recognizes the enterovirus genome. (I)
XX CC sensitively and rapidly detects fewer than 500 copies of enteroviral
XX CC genome and allows detection of broad range of enterovirus serotypes. The
XX CC present sequence represents a viral 5' untranslated polynucleotide
XX CC sequence given in the exemplification of the present invention.
XX SQ Sequence 238 BP; 51 A; 51 C; 59 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
Db 75 TCCGCTGCAGAGTTGCCGTTACGA 51

RESULT 34
ABB56780/c
ID ABB56780 standard; DNA; 238 BP.
XX AC
XX ABB56780;
XX XX
XX DT 22-SEP-2005 (first entry)
XX XX
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:19.
XX XX
XX KW DNA detection; enteroviral detection; ds.
XX XX
XX OS Unidentified.
XX XX
XX PN US2005158710-A1.
XX XX
XX PD 21-JUL-2005.
XX XX
XX PF 16-JAN-2004; 2004US-00760048.
XX XX
XX PR 16-JAN-2004; 2004US-00760048.
XX XX
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX XX
XX PI Teang S, Price JA, Hellyer TJ;
XX XX
```

DR WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 19; 34pp; English.  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 57 A; 51 C; 58 G; 72 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. NO. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 35  
 AEB56803/c  
 ID AEB56803 standard; DNA; 238 BP.  
 XX  
 AC AEB56803;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:42.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Unidentified.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.  
 XX  
 PA (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

PI Teang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX  
 PT Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX  
 PS Disclosure; SEQ ID NO 42; 34pp; English.  
 XX  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 49 A; 52 C; 60 G; 77 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. NO. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 36  
 AEB56829/c  
 ID AEB56829 standard; DNA; 238 BP.  
 XX  
 AC AEB56829;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Consensus viral 5' untranslated polynucleotide sequence.  
 XX  
 KW DNA detection; enteroviral detection; ds.  
 XX  
 OS Synthetic.  
 XX  
 PN US2005158710-A1.  
 XX  
 PD 21-JUL-2005.  
 XX  
 PF 16-JAN-2004; 2004US-00760048.  
 XX  
 PR 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.  
 XX (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 XX  
 PI Teang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a consensus viral 5' untranslated  
 CC polynucleotide sequence given in the exemplification of the present  
 CC invention.

XX SQ Sequence 238 BP; 51 A; 55 C; 65 G; 67 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;

Best Local Similarity 100.0%; Pred. No. 0.049;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25

Db 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 37

ABE56843/c

ID ABE56843 standard; DNA; 238 BP.

XX AC ABE56843;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX TSANG S.

PA (PRIC/) PRICE J A.

PA (HELL/) HELLYER T J.

XX TSang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

DR GENBANK; M33854.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of ABE56762 to ABE56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of ABE56764  
 CC to ABE56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I), (MI) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 58 C; 64 G; 63 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 25; DB 14; Length 238;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25

Db 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 38

ABE56845/c

ID ABE56845 standard; DNA; 238 BP.

XX AC ABE56845;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus B3.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX TSANG S.

PA (PRIC/) PRICE J A.

PA (HELL/) HELLYER T J.

XX TSang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

DR GENBANK; U57056.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of ABE56762 to ABE56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of ABE56764  
 CC to ABE56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I), (MI) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 54 A; 57 C; 62 G; 65 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Score 25; DB 14; Length 238;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25

Db 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 39

ABE56774/c

ID AEB56774 standard; DNA; 238 BP.  
AC AEB56774;  
XX  
XX  
DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:13.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX  
OS Unidentified.  
XX  
XX  
PN US2005158710-A1.  
XX  
XX  
PD 21-JUL-2005.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX  
DR WPI; 2005-512251/52.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX  
DR WPI; 2005-512251/52.  
XX  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
XX  
XX  
PS Detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX  
XX Disclosure; SEQ ID NO 13; 34pp; English.  
XX  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I) and  
CC (K1) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 238 BP; 59 A; 51 C; 54 G; 74 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
RESULT 40  
AEB56788/c  
ID AEB56788 standard; DNA; 238 BP.  
AC AEB56788;  
XX  
XX  
DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:27.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX

OS Unidentified.  
XX  
XX  
PN US2005158710-A1.  
XX  
XX  
PD 21-JUL-2005.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
PI Tsang S, Price JA, Hellyer TJ;  
XX  
XX  
DR WPI; 2005-512251/52.  
XX  
XX  
PT Novel oligonucleotide comprising sequences for binding and amplifying or  
XX  
XX  
PS Detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX  
XX Disclosure; SEQ ID NO 27; 34pp; English.  
XX  
XX  
CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequences. (I) and  
CC (K1) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 238 BP; 57 A; 53 C; 58 G; 70 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
RESULT 41  
AEB56792/c  
ID AEB56792 standard; DNA; 238 BP.  
AC AEB56792;  
XX  
XX  
DT 22-SEP-2005 (first entry)  
XX  
XX  
DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:31.  
XX  
XX  
KW DNA detection; enteroviral detection; ds.  
XX  
XX  
OS Unidentified.  
XX  
XX  
PN US2005158710-A1.  
XX  
XX  
PD 21-JUL-2005.  
XX  
XX  
PF 16-JAN-2004; 2004US-00760048.  
XX  
XX  
PR 16-JAN-2004; 2004US-00760048.  
XX  
XX

PA (TSAN/) TSANG S.  
PA (PRIC/) PRICE J A.  
PA (HELL/) HELLYER T J.  
XX  
XX  
XX Tsang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.  
XX  
XX Disclosure; SEQ ID NO 31; 34pp; English.  
XX  
XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC (KI) specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX Sequence 238 BP; 54 A; 52 C; 58 G; 74 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 25; DB 14; Length 238;  
XX Best Local Similarity 100.0%; Pred. No. 0.049;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
XX ||||||||||||||||||||||||||||  
XX 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
XX  
XX RESULT 42  
XX AEB56783/c  
XX ID AEB56783 standard; DNA; 238 BP.  
XX  
XX AC AEB56783;  
XX  
XX XX 22-SEP-2005 (first entry)  
XX  
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:22.  
XX  
XX KW DNA detection; enteroviral detection; ds.  
XX  
XX OS Unidentified.  
XX  
XX XX US2005158710-A1.  
XX  
XX PD 21-JUL-2005.  
XX  
XX PF 16-JAN-2004; 2004US-00760048.  
XX  
XX PR 16-JAN-2004; 2004US-00760048.  
XX  
XX PA (TSAN/) TSANG S.  
XX PA (PRIC/) PRICE J A.  
XX PA (HELL/) HELLYER T J.  
XX  
XX TSang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 22; 34pp; English.  
XX  
XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC (KI) specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX Sequence 238 BP; 51 A; 51 C; 59 G; 77 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 25; DB 14; Length 238;  
XX Best Local Similarity 100.0%; Pred. No. 0.049;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
XX ||||||||||||||||||||||||||||  
XX 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
XX  
XX RESULT 43  
XX AEB56786/c  
XX ID AEB56786 standard; DNA; 238 BP.  
XX  
XX AC AEB56786;  
XX  
XX XX 22-SEP-2005 (first entry)  
XX  
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:25.  
XX  
XX KW DNA detection; enteroviral detection; ds.  
XX  
XX OS Unidentified.  
XX  
XX XX US2005158710-A1.  
XX  
XX PD 21-JUL-2005.  
XX  
XX PF 16-JAN-2004; 2004US-00760048.  
XX  
XX PR 16-JAN-2004; 2004US-00760048.  
XX  
XX PA (TSAN/) TSANG S.  
XX PA (PRIC/) PRICE J A.  
XX PA (HELL/) HELLYER T J.  
XX  
XX TSang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 25; 34pp; English.  
XX  
XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
CC target binding sequence of an oligonucleotide chosen from any one of the  
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
CC selected amplification or detection reaction. Also described: (1) a kit  
CC (KI) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I) and  
CC (KI) are useful for detecting enterovirus target sequences. (I) and  
CC (KI) specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
XX Sequence 238 BP; 51 A; 51 C; 59 G; 77 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 25; DB 14; Length 238;  
XX Best Local Similarity 100.0%; Pred. No. 0.049;  
XX Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
XX ||||||||||||||||||||||||||||  
XX 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
XX  
XX RESULT 44  
XX AEB56786/c  
XX ID AEB56786 standard; DNA; 238 BP.  
XX  
XX AC AEB56786;  
XX  
XX XX 22-SEP-2005 (first entry)  
XX  
XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:25.  
XX  
XX KW DNA detection; enteroviral detection; ds.  
XX  
XX OS Unidentified.  
XX  
XX XX US2005158710-A1.  
XX  
XX PD 21-JUL-2005.  
XX  
XX PF 16-JAN-2004; 2004US-00760048.  
XX  
XX PR 16-JAN-2004; 2004US-00760048.  
XX  
XX PA (TSAN/) TSANG S.  
XX PA (PRIC/) PRICE J A.  
XX PA (HELL/) HELLYER T J.  
XX  
XX TSang S, Price JA, Hellyer TJ;  
XX  
XX WPI; 2005-512251/52.  
XX  
XX Novel oligonucleotide comprising sequences for binding and amplifying or  
PT detecting target, useful for detecting enterovirus nucleic acids.

CC consisting essentially of target binding sequence of any one of AEB56764  
CC to AEB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I), (M1) and  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.  
XX  
SQ Sequence 238 BP; 55 A; 53 C; 59 G; 71 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 44  
AEB56787/c  
ID AEB56787 standard; DNA; 238 BP.

AC AEB56787;

DT 22-SEP-2005 (first entry)

DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:26.

KW DNA detection; enteroviral detection; ds.

OS Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 26; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (I), and one or more container that contains (I); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
XX (K1) are useful for detecting enterovirus target sequences. (I)  
XX specifically and selectively recognizes the enterovirus genome. (I)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The  
XX present sequence represents a viral 5' untranslated polynucleotide  
XX sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 57 A; 52 C; 58 G; 71 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 45  
AEB56870/c  
ID AEB56870 standard; DNA; 238 BP.

XX AEB56870;

DT 22-SEP-2005 (first entry)

DE Human echovirus 30 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

OS Human echovirus 30.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Teang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; AF162711.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
XX target binding sequence of an oligonucleotide chosen from any one of the  
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
XX selected amplification or detection reaction. Also described: (1) a kit  
XX (K1) comprising (I), and one or more container that contains (I); and (2)  
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
XX the target sequence using first amplification primer having a sequence  
XX consisting essentially of target binding sequence of any one of AEB56764  
XX to AEB56771 and optionally a sequence required for selected amplification  
XX reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
XX (K1) are useful for detecting enterovirus target sequences. (I)  
XX specifically and selectively recognizes the enterovirus genome. (I)  
XX sensitively and rapidly detects fewer than 500 copies of enteroviral  
XX genome and allows detection of broad range of enterovirus serotypes. The  
XX present sequence represents a viral 5' untranslated polynucleotide  
XX sequence given in the exemplification of the present invention.

SQ Sequence 238 BP; 51 A; 56 C; 61 G; 70 T; 0 U; 0 Other;  
Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107



RESULT 46  
 AEB56830/c  
 ID AEB56830 standard; DNA; 238 BP.  
 XX AC AEB56830;  
 XX DT 22-SEP-2005 (first entry)  
 XX DE Human coxsackievirus A9 5' untranslated polynucleotide sequence.  
 XX KW DNA detection; enteroviral detection; ds.  
 XX OS Human coxsackievirus A9.  
 XX PN US2005158710-A1.  
 XX PD 21-JUL-2005.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.  
 XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX DR GENBANK; D00627.  
 XX DT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 50 A; 58 C; 66 G; 64 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 47  
 AEB56864/c  
 ID AEB56864 standard; DNA; 238 BP.  
 XX AC AEB56864;  
 XX DT 22-SEP-2005 (first entry)

XX DE Human echovirus 11 5' untranslated polynucleotide sequence.  
 XX KW DNA detection; enteroviral detection; ds.  
 XX OS Human echovirus 11.  
 XX PN US2005158710-A1.  
 XX PD 21-JUL-2005.  
 XX PF 16-JAN-2004; 2004US-00760048.  
 XX PR 16-JAN-2004; 2004US-00760048.  
 XX PA (TSAN/) TSANG S.  
 XX PA (PRIC/) PRICE J A.  
 XX PA (HELL/) HELLYER T J.  
 XX PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX DR GENBANK; X80059.  
 XX DT Novel oligonucleotide comprising sequences for binding and amplifying or  
 detecting target, useful for detecting enterovirus nucleic acids.  
 XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 48  
 AEB56859/c  
 ID AEB56859 standard; DNA; 238 BP.  
 XX AC AEB56859;  
 XX DT 22-SEP-2005 (first entry)  
 XX DE Human echovirus 6 5' untranslated polynucleotide sequence.  
 XX KW DNA detection; enteroviral detection; ds.  
 XX OS Human echovirus 6.  
 XX PN US2005158710-A1.



CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 57 A; 51 C; 57 G; 73 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 51  
 AEB56841/c  
 ID AEB56841 standard; DNA; 238 BP.  
 XX  
 AC AEB56841;  
 XX  
 DT 22-SEP-2005 (first entry)  
 XX  
 DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX DNA detection; enteroviral detection; ds.

XX Human coxsackievirus B3.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.  
 XX (PRIC//) PRICE J A.  
 XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; M74567.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX  
 SQ Sequence 238 BP; 52 A; 58 C; 65 G; 63 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 52  
 AEB56809/c  
 ID AEB56809 standard; DNA; 238 BP.

XX AC AEB56809;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:48.

XX DNA detection; enteroviral detection; ds.

XX Unidentified.

XX US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN//) TSANG S.

XX (PRIC//) PRICE J A.

XX (HELL//) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; SEQ ID NO 48; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I)  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 53

ABB56831/c  
ID AEB56831 standard; DNA; 238 BP.

XX AC AEB56831;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus A16 5' untranslated polynucleotide sequence.

XX KW DNA detection; enteroviral detection; ds.

XX OS Human coxsackievirus A16.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX DR GENBANK; U05876.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; Fig 1A-D; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 51 A; 55 C; 64 G; 68 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

## RESULT 54

ABB56808/c

ID AEB56808 standard; DNA; 238 BP.

XX AC AEB56808;

XX DT 22-SEP-2005 (first entry)

XX DE Viral 5' untranslated polynucleotide sequence SEQ ID NO:47.

XX KW DNA detection; enteroviral detection; ds.

XX OS Unidentified.

XX PN US2005158710-A1.

XX PD 21-JUL-2005.

XX PF 16-JAN-2004; 2004US-00760048.

XX PR 16-JAN-2004; 2004US-00760048.

XX PA (TSAN/) TSANG S.

XX PA (PRIC/) PRICE J A.

XX PA (HELL/) HELLYER T J.

XX PI Tsang S, Price JA, Hellyer TJ;

XX DR WPI; 2005-512251/52.

XX PT Novel oligonucleotide comprising sequences for binding and amplifying or detecting target, useful for detecting enterovirus nucleic acids.

XX PS Disclosure; SEQ ID NO 47; 34pp; English.

XX CC The invention relates to an oligonucleotide (I) consisting of: (a) the target binding sequence of an oligonucleotide chosen from any one of the 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for selected amplification or detection reaction. Also described: (1) a kit (K1) comprising (I), and one or more container that contains (I); and (2) detecting (M1) an enterovirus target sequence, involving: (a) amplifying the target sequence using first amplification primer having a sequence consisting essentially of target binding sequence of any one of AEB56764 to AEB56771 and optionally a sequence required for selected amplification reaction; and (b) detecting the amplified target sequence. (I) (M1) and (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 53 A; 54 C; 55 G; 76 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 14; Length 238;  
Best Local Similarity 100.0%; Pred. No. 0.049;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

## RESULT 55

ABB56844/c

ID AEB56844 standard; DNA; 238 BP.

XX AC AEB56844;

XX DT 22-SEP-2005 (first entry)

XX DE Human coxsackievirus B3 5' untranslated polynucleotide sequence.

XX XX

KW DNA detection; enteroviral detection; ds.  
 OS Human coxsackievirus B3.  
 XX US2005158710-A1.  
 PN 21-JUL-2005.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 PF (TSAN//) TSANG S.  
 PA (PRIC//) PRICE J A.  
 XX (HELL//) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 PI WPI; 2005-512251/52.  
 XX GENBANK; M88483.  
 DR Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 PT Disclosure; Fig 1A-D; 34pp; English.  
 PS The invention relates to an oligonucleotide (I) consisting of: (a) the  
 XX target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 53 A; 57 C; 64 G; 64 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107  
 RESULT 56  
 AEB56804/c  
 ID AEB56804 standard; DNA; 238 BP.  
 AC AEB56804;  
 XX 22-SEP-2005 (first entry)  
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:43.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 XX US2005158710-A1.  
 XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF

XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN//) TSANG S.  
 PA (PRIC//) PRICE J A.  
 XX (HELL//) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 PI WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 43; 34pp; English.  
 CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) specifically and selectively recognizes the enterovirus genome. (I) sensitively and rapidly detects fewer than 500 copies of enteroviral genome and allows detection of broad range of enterovirus serotypes. The present sequence represents a viral 5' untranslated polynucleotide sequence given in the exemplification of the present invention.  
 XX SQ Sequence 238 BP; 48 A; 52 C; 60 G; 78 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 14; Length 238;  
 Best Local Similarity 100.0%; Pred. No. 0.049;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51  
 RESULT 57  
 ABX12451/c  
 ID ABX12451 standard; DNA; 502 BP.  
 XX AC ABX12451;  
 XX 10-MAY-2003 (first entry)  
 DT Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #6.  
 DE Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
 XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
 KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
 XX renal failure; leg amputation; ds.  
 OS Coxsackievirus.  
 XX WO2002103060-A2.  
 PN 27-DEC-2002.  
 PD 19-JUN-2002; 2002WO-IB003278.  
 PF 20-JUN-2001; 2001SE-00002198.  
 XX (INNO-) INNOVENTUS PROJECT AB.  
 PA Tuvemo HT, Frisk GE, Yin H;  
 XX

DR WPI; 2003-278229/27.  
XX Polymerase chain reaction and primers for detecting nucleic acids from  
PT the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX PS Disclosure; Page 73; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for  
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
CC P3C and P3D nucleic acids). The methods and primers are used for the  
CC detection of CBV-4 strain VD2921 which is associated with diabetes  
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
CC drugs, to prevent further loss of beta cells and severe long term  
CC consequences of diabetes including blindness, renal failure and leg  
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
CC (CBV-4) strain VD2921 associated polynucleotide  
XX  
XX Sequence 502 BP; 120 A; 132 C; 128 G; 122 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 25; DB 8; Length 502;  
Best Local Similarity 100.0%; Pred. NO. 0.053;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 452 TCCGCTGCAGAGTTGCCCGTTACGA 428  
|||||

RESULT 58  
ABX12448/C  
ID ABX12448 standard; DNA; 548 BP.  
XX  
XX AC ABX12448;  
XX  
XX DT 10-MAY-2003 (first entry)  
XX  
XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #3.  
XX  
XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
XX renal failure; leg amputation; ds.  
XX  
XX OS Coxsackievirus.  
XX  
XX PN WO2002103060-A2.  
XX  
XX PD 27-DEC-2002.  
XX  
XX PF 19-JUN-2002; 2002WO-IB003278.  
XX  
XX PR 20-JUN-2001; 2001SE-00002198.  
XX  
XX PA (INNO-) INNOVENTUS PROJECT AB.  
XX  
XX PI Tuvemo HT, Frisk GE, Yin H;  
XX  
XX PS WPI; 2003-278229/27.  
XX  
XX PT Polymerase chain reaction and primers for detecting nucleic acids from  
XX the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX PS Disclosure; Page 72; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for  
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
CC P3C and P3D nucleic acids). The methods and primers are used for the  
CC detection of CBV-4 strain VD2921 which is associated with diabetes  
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
CC

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
CC drugs, to prevent further loss of beta cells and severe long term  
CC consequences of diabetes including blindness, renal failure and leg  
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
CC (CBV-4) strain VD2921 associated polynucleotide  
XX  
XX Sequence 551 BP; 130 A; 147 C; 140 G; 134 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 25; DB 8; Length 551;  
Best Local Similarity 100.0%; Pred. NO. 0.054;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 442 TCCGCTGCAGAGTTGCCCGTTACGA 418  
|||||

RESULT 59  
ABX12453/C  
ID ABX12453 standard; DNA; 551 BP.  
XX  
XX AC ABX12453;  
XX  
XX DT 10-MAY-2003 (first entry)  
XX  
XX DE Coxsackie B virus 4 (CBV-4) strain VD2921 associated DNA #8.  
XX  
XX KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
XX strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
XX diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
XX renal failure; leg amputation; ds.  
XX  
XX OS Coxsackievirus.  
XX  
XX PN WO2002103060-A2.  
XX  
XX PD 27-DEC-2002.  
XX  
XX PF 19-JUN-2002; 2002WO-IB003278.  
XX  
XX PR 20-JUN-2001; 2001SE-00002198.  
XX  
XX PA (INNO-) INNOVENTUS PROJECT AB.  
XX  
XX PI Tuvemo HT, Frisk GE, Yin H;  
XX  
XX PS WPI; 2003-278229/27.  
XX  
XX PT Polymerase chain reaction and primers for detecting nucleic acids from  
XX the diabetogenic coxsackie B virus-4 strain VD2921.  
XX  
XX PS Disclosure; Page 74; 79pp; English.  
XX  
XX The invention describes a polymerase chain reaction (PCR) and primers for  
CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
CC P3C and P3D nucleic acids). The methods and primers are used for the  
CC detection of CBV-4 strain VD2921 which is associated with diabetes  
CC (diabetogenic enterovirus). Early detection of the diabetes e.g.  
CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
CC drugs, to prevent further loss of beta cells and severe long term  
CC consequences of diabetes including blindness, renal failure and leg  
CC amputations. This sequence represents a diabetogenic coxsackie B virus 4  
CC (CBV-4) strain VD2921 associated polynucleotide  
XX  
XX Sequence 551 BP; 130 A; 147 C; 140 G; 134 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 25; DB 8; Length 551;  
Best Local Similarity 100.0%; Pred. NO. 0.054;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE	Coxsackievirus B3 (CVB3)/CO 5' non-translated region (NTR) sequence.
XX	
KW	Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
KW	Coxsackievirus B3; CVB3; NTR; non-translated region; ds.
XX	
OS	Coxsackievirus.
XX	
XX	WO200104136-A1.
XX	
PD	18-JAN-2001.
XX	
XX	08-JUL-2000; 2000WO-US018681.
PF	
XX	09-JUL-1999; 99US-0143104P.
PR	
XX	(UYNE-) UNIV NEBRASKA.
PA	
XX	Romero JR, Bradrick SS, Dunn JJ;
PI	
XX	WPI; 2001-138310/14.
DR	
XX	
XX	Recombinant enterovirus genome for use as vector or vaccine, modified by
PT	replacing a part or all of its 5'non-translated region by 5'NTR of
PT	enterovirus genome that encodes virus modified in tropism or virulence.
XX	
XX	Example 2; Page 25; 49pp; English.
PS	
XX	The invention provides an enterovirus genome (I) for use as a vector or
CC	vaccine, modified to produce a virus (VI) having a restricted or altered
CC	species or tissue tropism, compared to an equivalent unmodified virus, or
CC	modified to produce an attenuated virus (V2), by replacing a part or all
CC	of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
CC	enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
CC	vector in targeting genes of interest to specific cells or tissues. (I)
CC	is also useful for diagnostic purposes, e.g. to identify virulent, versus
CC	nonvirulent strains of an enterovirus. The present sequence represents
CC	the 5' NTR (non-translated region) of a non-cardiovirulent enterovirus
CC	Coxsackievirus B3 (CVB3)/CO strain
XX	
SQ	Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
	Query Match 100.0%; Score 25; DB 4; Length 660;
	Best Local Similarity 100.0%; Pred. NO. 0.055;
	Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db	457 TCCGCTGCAGAGTTGCCCGTTACGA 433
RESULT 62	
AEBS56828/c	
ID	AEBS56828 standard; DNA; 660 BP.
XX	
XX	AEBS56828;
XX	
DT	22-SEP-2005 (first entry)
XX	
DE	Coxsackie virus B5 polynucleotide sequence SEQ ID NO:67.
XX	
KW	DNA detection; enteroviral detection; ds.
OS	Human coxsackievirus B5.
XX	
XX	US2005158710-A1.
PN	
XX	21-JUL-2005.
PD	
XX	
PF	16-JAN-2004; 2004US-00760048.
XX	
PR	16-JAN-2004; 2004US-00760048.
XX	
PA	(TSAN/) TSANG S.

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PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
PI Tsang S, Price JA, Hellyer TJ;
XX
DR WPI; 2005-512251/52.
DR GENBANK; AF169665.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; SEQ ID NO 67; 34pp; English.
XX
CC The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a coxsackie virus B5 polynucleotide sequence,
CC which is given in the exemplification of the present invention. Note: the
CC present sequence is designated as SEQ ID NO:67 in the Sequence Listing.
CC but corresponds with the sequence given in figure 2 designated SEQ ID
CC NO:14 in the description of the drawings.
XX
XX
SQ Sequence 660 BP; 157 A; 170 C; 166 G; 167 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 660;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 457 TCCGCTGCAGAGTTGCCCGTTACGA 433

RESULT 63
AEA00424/c
ID AEA00424 standard; DNA; 709 BP.
XX
AC AEA00424;
XX
XX
DT 28-JUL-2005 (first entry)
XX
DE Enterovirus 71 5' untranslated region internal ribosome entry site DNA.
XX
XX vector; neurological disease; ds; gene therapy;
XX internal ribosome entry site; cystic fibrosis; cns-gen.;
XX respiratory-gen.; factor VIII deficiency; hemostatic; genetic disorder;
XX factor IX deficiency; Duchenne dystrophy; muscular-gen.;
XX Becker's disease; cancer; cytostatic; neoplasm;
XX acquired immune deficiency syndrome; anti-hiv; infectious disease;
XX antimicrobial.
XX
XX Human enterovirus 71; strain TW/2086/98.
XX
XX US2005112095-A1.
XX
XX 26-MAY-2005.
XX
XX 08-JUL-2003; 2003US-00614283.
XX
XX 09-JUL-2002; 2002US-0394269P.
XX
XX (HSUT/) HSU T.

(PAUT/) WU T.
(PAUT/) LEE J.
XX
PI Hsu T, Wu T, Lee J;
XX
DR WPI; 2005-371616/38.
XX
XX New nucleic acid vector for the expression of at least two cistrons
PT comprising a nucleotide sequence comprising an internal ribosome entry
PT site (IRES) e.g. enterovirus 71 (EV71), useful for treating a patient
XX having e.g. AIDS.
XX
XX Example 2; SEQ ID NO 1; 23pp; English.
XX
CC The present invention relates to a nucleic acid vector for the expression
CC of at least two cistrons. The vector comprises a promoter operably linked
CC to a nucleotide sequence comprising at least two cistrons and at least
CC one nucleotide sequence comprising an internal ribosome entry site (IRES)
CC selected from Human enterovirus 71 (EV71), Hepatitis C virus (HCV), or
CC Encephalomyocarditis virus (EMCV). The invention also provides a method
CC for screening of anti-viral compounds using the IRES. The invention is
CC useful for the genetic treatment of patients with cystic fibrosis,
CC hemophilia A or B, Duchenne or Becker type myopathy, cancer, AIDS and
CC other bacterial or infectious diseases due to a pathogenic organism and
CC in gene therapy. The present sequence is the enterovirus 71 5'
CC untranslated region (UTR) IRES DNA.
XX
XX
SQ Sequence 709 BP; 165 A; 185 C; 172 G; 187 T; 0 U; 0 Other;
Query Match 100.0%; Score 25; DB 14; Length 709;
Best Local Similarity 100.0%; Pred. No. 0.055;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 504 TCCGCTGCAGAGTTGCCCGTTACGA 480

RESULT 64
AAC85152/c
ID AAC85152 standard; RNA; 745 BP.
XX
AC AAC85152;
XX
XX
DT 08-MAY-2001 (first entry)
XX
DE Cocksackievirus B3 (CVB3) 5' non-translated region (NTR) sequence.
XX
XX Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;
XX Cocksackievirus B3; CVB3; NTR; non-translated region; ds.
XX
XX Cocksackievirus.
XX
XX Key Location/Qualifiers
XX stem_loop 2..87
XX /*tag= d
XX /note= "Domain I"
XX stem_loop 10..34
XX /*tag= a
XX /note= "stemloop B"
XX stem_loop 35..45
XX /*tag= b
XX /note= "stemloop C"
XX stem_loop 57..70
XX /*tag= c
XX /note= "stemloop D"
XX stem_loop 105..181
XX /*tag= e
XX /note= "Domain II"
XX stem_loop 184..233
XX /*tag= f
XX /note= "Domain III"
XX stem_loop 241..444
```



```

FT      /*tag= g
FT      /note="Domain IV"
FT      stem_loop 452..560
FT      /*tag= h
FT      /note="Domain V"
FT      stem_loop 587..623
FT      /*tag= i
FT      /note="Domain VI"
FT      stem_loop 624..644
FT      /*tag= j
FT      /note="Domain VII"
FT      WO200104136-A1.
FT      18-JAN-2001.
FT      08-JUL-2000; 2000WO-US018681.
FT      09-JUL-1999; 99US-0143104P.
FT      (UYNE-) UNIV NEBRASKA.
FT      Romero JR, Bradrick SS, Dunn JJ;
FT      WPI; 2001-138310/14.
FT      Recombinant enterovirus genome for use as vector or vaccine, modified by
FT      replacing a part or all of its 5'non-translated region by 5'NTR of
FT      enterovirus genome that encodes virus modified in tropism or virulence.
FT      Disclosure; Fig 1; 49pp; English.
FT      The invention provides an enterovirus genome (I) for use as a vector or
FT      vaccine, modified to produce a virus (Vi) having a restricted or altered
FT      species or tissue tropism, compared to an equivalent unmodified virus, or
FT      modified to produce an attenuated virus (V2), by replacing a part or all
FT      of the 5'non-translated region (5'NTR) of (I) with a 5'NTR of an
FT      enterovirus genome that encodes V1 or V2. (I) is useful as vaccine or
FT      vector in targeting genes of interest to specific cells or tissues. (I)
FT      is also useful for diagnostic purposes, e.g. to identify virulent, versus
FT      nonvirulent strains of an enterovirus. The present sequence represents
FT      the enterovirus Coxsackievirus B3 (CVB3) 5' NTR (non-translated region)
FT      sequence
FT      Sequence 745 BP; 184 A; 192 C; 181 G; 1 T; 187 U; 0 Other;
FT      Query Match 100.0%; Score 25; DB 4; Length 745;
FT      Best Local Similarity 100.0%; Pred. No. 0.056;
FT      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
FT      1 TCCGCTGCAGAGTTGCCCGTTACGA 25
FT      539 TCCGCTGCAGAGTTGCCCGTTACGA 515
FT      RESULT 65
FT      ADP82873/c
FT      ID ADP82873 standard; DNA; 810 BP.
FT      AC ADP82873;
FT      XX 23-SEP-2004 (first entry)
FT      XX Human coxsackievirus B1 complete genomic DNA.
FT      XX hMPV detection; ds.
FT      XX Human coxsackievirus B1.
FT      OS WO2004057021-A2.
FT      PN 08-JUL-2004.
FT      XX

```

```

PF      19-DEC-2003; 2003WO-CA001994.
XX
PR      19-DEC-2002; 2002CA-02411264.
PR      24-JAN-2003; 2003CA-02418004.
XX
PA      (UYLA-) UNIV LAVAL.
XX
PI      Boivin G;
XX
DR      WPI; 2004-500307/47.
XX
PT      Detecting and/or quantifying human, metapneumovirus (hMPV) in a sample
PT      comprises contacting the at least one probe and/or primer with the sample
PT      to allow annealing of the probe and/or primer with the nucleic acid
PT      sequence.
XX
PS      Claim 32; SEQ ID NO 137; 158pp; English.
XX
CC      The invention relates to a novel method for detecting and/or quantifying
CC      Human metapneumovirus (hMPV) in a sample comprising providing at least
CC      one probe or primer specific for a nucleic acid sequence of hMPV,
CC      contacting the one probe and/or primer with the sample to allow annealing
CC      of the probe and/or primer with the nucleic acid sequence and detecting
CC      and/or quantifying the nucleic acid sequence using the annealed probe
CC      and/or primer. The method of the invention may be useful for detecting
CC      and/or quantifying Human metapneumovirus (hMPV) in a sample. The current
CC      sequence is that of the Human coxsackievirus B1 complete genomic DNA of
CC      the invention.
XX
SQ      Sequence 810 BP; 243 A; 180 C; 190 G; 197 T; 0 U; 0 Other;
XX
XX      Query Match 100.0%; Score 25; DB 12; Length 810;
XX      Best Local Similarity 100.0%; Pred. No. 0.056;
XX      Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX      1 TCCGCTGCAGAGTTGCCCGTTACGA 25
XX      88 TCCGCTGCAGAGTTGCCCGTTACGA 64
XX
XX      RESULT 66
XX      ADU47469/c
XX      ID ADU47469 standard; cDNA; 1560 BP.
XX
XX      AC ADU47469;
XX
XX      27-JAN-2005 (first entry)
XX      DE Enterovirus type 71 (EV71) cDNA.
XX
XX      KW Detection; enterovirus type 71; EV71; ss.
XX      OS Enterovirus.
XX
XX      Key Location/Qualifiers
XX      FT primer_bind 72..87
XX      FT /*tag= a
XX      FT /note= "f1 primer"
XX      FT primer_bind 167..187
XX      FT /*tag= b
XX      FT /note= "f2 primer"
XX      FT primer_bind 248..266
XX      FT /*tag= c
XX      FT /note= "f3 primer"
XX      FT primer_bind 423..439
XX      FT /*tag= d
XX      FT /note= "f5 primer"
XX      FT misc_binding 448..474
XX      FT /*tag= e
XX      FT /bound_moiety= "p1 probe"
XX      FT misc_binding 514..546
XX      FT /*tag= f
XX      FT /bound_moiety= "p2 probe"

```

FT misc\_binding 547. .574  
 FT /\*tag= g  
 FT /bound\_moiety= "p3 probe"  
 FT 583. .602  
 FT /\*tag= h  
 FT /note= "r2 primer"  
 FT 627. .645  
 FT /\*tag= i  
 FT /note= "r1 primer"  
 FT 1179. .1198  
 FT /\*tag= j  
 FT /note= "f7 primer"  
 FT 1344. .1373  
 FT /\*tag= k  
 FT /bound\_moiety= "16-1 probe"  
 FT 1390. .1419  
 FT /\*tag= l  
 FT /bound\_moiety= "71-2/16-2 probe"  
 FT 1454. .1481  
 FT /\*tag= m  
 FT /bound\_moiety= "71-3 probe"  
 FT 1485. .1504  
 FT /\*tag= n  
 FT /note= "r3 primer"  
 FT  
 XX US6818397-B1.  
 XX  
 XX 16-NOV-2004.  
 XX  
 XX 28-NOV-2000; 2000US-00724678.  
 XX  
 XX 28-NOV-2000; 2000US-00724678.  
 XX  
 XX (CHIP-) CHIP BIOTECHNOLOGY INC.  
 XX  
 XX Lee K, Bair C, Tseng Y, Wang Y, Wang S;  
 XX WPI; 2004-793563/78.  
 DR GENBANK; U22521.  
 XX  
 XX New kit comprising a pair of oligonucleotide primers for nucleic acid  
 FT amplification, useful in detecting and differentiating an enterovirus in  
 FT a sample.  
 XX  
 XX Disclosure; SEQ ID NO 16; 14pp; English.  
 XX  
 XX The invention provides a method and a kit for detecting and  
 CC differentiating an enterovirus type 71 (EV71) in a sample. The method  
 CC involves contacting nucleic acids in the sample with a pair of primers to  
 CC form an amplification product; contacting the amplification product with  
 CC at least one synthetic nucleotide sequence fixed on a solid substrate and  
 CC detecting hybridisation. The present sequence is the enterovirus type 71  
 CC (EV71) cDNA.  
 XX  
 XX Sequence 1560 BP; 421 A; 401 C; 346 G; 392 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 25; DB 13; Length 1560;  
 Best Local Similarity 100.0%; Pred. No. 0.061;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTCGCCGTACGA 25  
 |||||  
 Db 540 TCCGCTGCAGAGTTCGCCGTACGA 516  
 RESULT 67  
 ID ABX12440/c  
 XX ABX12440 standard; DNA; 7392 BP.  
 AC ABX12440;  
 XX  
 XX 10-MAY-2003 (first entry)  
 DT  
 XX

DE Diabetogenic coxsackie B virus 4 (CBV-4) strain VD2921 genome.  
 XX  
 KW Coxsackie virus strain VD2921; diabetogenic coxsackie B virus-4; CBV-4;  
 KW strain VD2921; VP1; VP2; VP3; VP4; P2A; P2B; P2C; P3A; P3B; P3C; P3D;  
 KW diabetes; diabetogenic enterovirus; beta cell loss; blindness;  
 XX renal failure; leg amputation; ds.  
 XX Coxsackievirus.  
 XX  
 FH Key Location/Qualifiers  
 FT misc\_feature 1. .87  
 FT /\*tag= a  
 FT /note= "Specifically claimed in claim 16"  
 FT 88. .512  
 FT /\*tag= b  
 FT /note= "Specifically claimed in claim 19"  
 FT 513. .742  
 FT /\*tag= c  
 FT /note= "Specifically claimed in claim 22"  
 FT 742  
 FT /\*tag= d  
 FT /note= "Specifically claimed in claim 25"  
 FT 743. .7303  
 FT /\*tag= f  
 FT /product= "Polyprotein"  
 FT 743. .952  
 FT /\*tag= e  
 FT /note= "Specifically claimed in claim 26"  
 FT 953. .1726  
 FT /\*tag= g  
 FT /note= "Specifically claimed in claim 29"  
 FT 1727. .2441  
 FT /\*tag= h  
 FT /note= "Specifically claimed in claim 32"  
 FT 2442. .3296  
 FT /\*tag= i  
 FT /note= "Specifically claimed in claim 35"  
 FT 3297. .3737  
 FT /\*tag= j  
 FT /note= "Specifically claimed in claim 38"  
 FT 3738. .4033  
 FT /\*tag= k  
 FT /note= "Specifically claimed in claim 41"  
 FT 4034. .5029  
 FT /\*tag= l  
 FT /note= "Specifically claimed in claim 44"  
 FT  
 XX WO2002103060-A2.  
 XX  
 XX 27-DEC-2002.  
 XX  
 XX 19-JUN-2002; 2002WO-IB003278.  
 XX  
 XX 20-JUN-2001; 2001SE-00002198.  
 XX  
 XX (INNO-) INNOVENTUS PROJECT AB.  
 XX  
 XX Tuvemo HT, Frisk GE, Yin H;  
 XX WPI; 2003-2782229/27.  
 XX P-PSDB; ABG75961.  
 XX  
 XX Polymerase chain reaction and primers for detecting nucleic acids from  
 FT the diabetogenic coxsackie B virus-4 strain VD2921.  
 XX  
 XX Example 5; Page 64-66; 79pp; English.  
 XX  
 XX The invention describes a polymerase chain reaction (PCR) and primers for  
 CC detecting nucleic acids from the diabetogenic coxsackie B virus-4 (CBV-4)  
 CC strain VD2921, (particularly VP1, VP2, VP3, VP4, P2A, P2B, P2C, P3A, P3B,  
 CC P3C and P3D nucleic acids). The methods and primers are used for the  
 CC detection of CBV-4 strain VD2921 which is associated with diabetes  
 CC (diabetogenic enterovirus). Early detection of the diabetes e.g.

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
 CC drugs, to prevent further loss of beta cells and severe long term  
 CC consequences of diabetes including blindness, renal failure and leg  
 CC amputations. This sequence represents the genome of diabetogenic  
 CC coxsackie B virus 4 (CBV-4) strain VD2921  
 XX  
 SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 8; Length 7392;  
 Best Local Similarity 100.0%; Pred. No. 0.073;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
 |||||

RESULT 68  
 AAQ11816/C  
 ID AAQ11816 standard; RNA; 7399 BP.  
 AC AAQ11816;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 05-AUG-1991 (first entry)  
 XX  
 DE RNA encoding enteroviral polypeptide.  
 XX Enteroviruses; monoclonal antibodies; myocarditis; myositis; meningitis;  
 KW encephalitis; pancreatitis; post viral fatigue syndrome; ss.  
 XX  
 OS Enterovirus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 742..7299  
 FT /\*tag= a  
 FT /product= "enteroviral polypeptide"  
 XX  
 XX DE3939200-A.  
 FN  
 PD 29-MAY-1991.  
 XX  
 PF 27-NOV-1989; 89DE-03939200.  
 XX  
 PR 27-NOV-1989; 89DE-03939200.  
 XX  
 PA (PLAC ) MAX PLANCK GES FOERDERUNG WISSENSCHAFTEN.  
 XX  
 PI Kandolf R;  
 XX  
 PI WPI; 1991-165150/23.  
 DR P-PSDB; AAR12141.  
 XX  
 XX New enteroviral polypeptide for raising group specific antibodies - for  
 PT detecting any type of enterovirus in blood or serum, also new DNA  
 PT encoding it.  
 XX  
 XX Claim 7; Page 17-21; 26pp; German.  
 PS  
 XX This RNA encodes an enteroviral polypeptide which is used to raise poly-  
 CC or monoclonal antibodies (Abs). These are useful in assays for detecting  
 CC enterovirus specific antigens, as an indication of enteroviral disease.  
 CC All 70 serotypes of the enteroviral family can be detected. Diseases such  
 CC as myocarditis, myositis, menin- gitis, encephalitis and pancreatitis can  
 CC be diagnosed using the Abs. (Updated on 25-MAR-2003 to correct PA field.)  
 XX  
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 0 T; 1740 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 2; Length 7399;  
 Best Local Similarity 100.0%; Pred. No. 0.073;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC detection of diabetogenic enteroviral RNA in peripheral mononuclear  
 CC cells, can improve prognosis by allowing treatment e.g. with antiviral  
 CC drugs, to prevent further loss of beta cells and severe long term  
 CC consequences of diabetes including blindness, renal failure and leg  
 CC amputations. This sequence represents the genome of diabetogenic  
 CC coxsackie B virus 4 (CBV-4) strain VD2921  
 XX  
 SQ Sequence 7392 BP; 2095 A; 1724 C; 1809 G; 1764 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 8; Length 7392;  
 Best Local Similarity 100.0%; Pred. No. 0.073;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
 |||||

RESULT 69  
 ABV76134/C  
 ID ABV76134 standard; DNA; 7399 BP.  
 XX  
 AC ABV76134;  
 XX  
 XX 07-MAR-2003 (first entry)  
 DT  
 XX  
 DE Coxsackievirus capsid protein VP1 nucleic acid.  
 XX  
 KW Gene therapy; vector; hepatitis B virus; cardiovascular disease; heart;  
 KW cardiant; vasotropic; antiarrhythmic; antiarteriosclerotic;  
 KW capsid protein; gene; ss.  
 XX  
 OS Coxsackievirus.  
 XX  
 PN WO200287594-A1.  
 XX  
 PD 07-NOV-2002.  
 XX  
 XX 30-APR-2002; 2002WO-US013644.  
 PF  
 XX 30-APR-2001; 2001US-0287423P.  
 PR  
 XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX Chien KR, Hoshijima M;  
 PI  
 XX WPI; 2003-111844/10.  
 DR  
 XX Novel non-viral vector comprises vesicular membrane with hepatitis B  
 PT envelope protein with cardiac targeting sequence, and nucleotide sequence  
 PT for gene therapy useful for treating, e.g., heart failure, arrhythmia and  
 PT atherosclerosis.  
 XX  
 XX Disclosure; Page 27-31; 53pp; English.  
 PS  
 XX The present sequence is that of a coxsackie virus B3 capsid protein VP1  
 CC nucleic acid. The invention provides a non-viral vesicle vector for the  
 CC delivery of nucleic acid to various cardiac cell types. The vesicle  
 CC vector contains the hepatitis B virus envelope protein in which at least  
 CC part of the liver targeting sequence is deleted and replaced with a  
 CC specific cardiac cell targeting sequence. For example, the coxsackie  
 CC virus B3, VP1 sequence can be used to target the vector to  
 CC cardiomyocytes. The vesicle vector can be delivered intravenously or  
 CC intra-arterially rather than by more invasive methods such as direct  
 CC cardiac injection. It can be used to deliver gene products to replace or  
 CC enhance expression of proteins for treatment of heart failure, or  
 CC arrhythmia, reperfusion injury, atherosclerosis, to promote angiogenesis,  
 CC etc. The vesicles are highly stable and can be produced in large  
 CC quantities, making them ideal for gene therapy  
 XX  
 SQ Sequence 7399 BP; 2128 A; 1724 C; 1807 G; 1740 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 25; DB 10; Length 7399;  
 Best Local Similarity 100.0%; Pred. No. 0.073;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
 |||||

RESULT 70  
 ADP05527  
 ID ADP05527 standard; DNA; 66 BP.  
 XX  
 AC ADP05527;

```

XX 26-AUG-2004 (first entry)
XX
XX
XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID32.
XX
XX microbe detection; microbe identification; virus; viral particle;
XX pathogenic bacterium; cellular microbe; acellular microbe;
XX clinical diagnosis; research; epidemiological surveillance;
XX bioterrorism countermeasure; environmental pathogen survey;
XX food contaminant; radioimmunoassay; ELISA; probe; ss.
XX
XX OS Viruses.
XX
XX PN WO2004045365-A2.
XX
XX PD 03-JUN-2004.
XX
XX PF 23-MAY-2003; 2003WO-US016461.
XX
XX PR 15-NOV-2002; 2002US-00295787.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX FI Jia XY, Berger MA, Tilles JG;
XX
XX DR WPI; 2004-449626/42.
XX
XX PT New (microarray) apparatus comprising a substrate with attached nucleic
XX acid probes, useful for detecting one or more microbes in a sample.
XX
XX PS Claim 16; SEQ ID NO 32; 89pp; English.
XX
XX CC This invention relates to a novel apparatus for detecting a microbe in a
XX sample which comprises a substrate having multiple microbe identification
XX sites, each having a unique address indicative of the position of that
XX microbe identification site on the substrate and groups of nucleic acid
XX probes disposed at the microbe identification sites, each group being
XX complementary to a target nucleic acid to provide a detectable signal at
XX one or more microbe identification sites. The apparatus is useful for
XX detecting the presence of one or more microbes in a sample, such as virus
XX or viral particle, (non-)pathogenic bacteria, or cellular or acellular
XX microbe. The apparatus is particularly useful for clinical diagnosis,
XX research, epidemiological surveillance, bioterrorism countermeasures,
XX environmental pathogen surveys, and monitoring food contaminants. Current
XX testing procedures or devices, such as radioimmunoassays and ELISA, are
XX difficult to implement, time consuming, expensive, outdated, and
XX typically rely on the use of agents that recognise and bind to membrane
XX bound proteins or carbohydrates of the pathogen. These further cannot
XX assay multiple pathogens. The new apparatus or device for detecting
XX microbes overcomes these disadvantages. The apparatus is compact,
XX sensitive, and quick to detect the presence of any of a number of
XX pathogens present in a sample. The present sequence is that of an
XX oligonucleotide probe which is related to the microbe detection apparatus
XX of the invention.
XX
XX SQ Sequence 66 BP; 13 A; 19 C; 19 G; 15 T; 0 U; 0 Other;
XX
XX Query Match 96.0%; Score 24; DB 12; Length 66;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
XX |||||||
XX Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24
XX
XX RESULT 71
XX ADP05501
XX ID ADP05501 standard; DNA; 70 BP.
XX
XX AC ADP05501;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID19.

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XX Novel microbe detection apparatus-related oligonucleotide probe SeqID6.
XX
XX microbe detection; microbe identification; virus; viral particle;
XX pathogenic bacterium; cellular microbe; acellular microbe;
XX clinical diagnosis; research; epidemiological surveillance;
XX bioterrorism countermeasure; environmental pathogen survey;
XX food contaminant; radioimmunoassay; ELISA; probe; ss.
XX
XX OS Viruses.
XX
XX PN WO2004045365-A2.
XX
XX PD 03-JUN-2004.
XX
XX PF 23-MAY-2003; 2003WO-US016461.
XX
XX PR 15-NOV-2002; 2002US-00295787.
XX
XX PA (REGC ) UNIV CALIFORNIA.
XX
XX FI Jia XY, Berger MA, Tilles JG;
XX
XX DR WPI; 2004-449626/42.
XX
XX PT New (microarray) apparatus comprising a substrate with attached nucleic
XX acid probes, useful for detecting one or more microbes in a sample.
XX
XX PS Claim 16; SEQ ID NO 6; 89pp; English.
XX
XX CC This invention relates to a novel apparatus for detecting a microbe in a
XX sample which comprises a substrate having multiple microbe identification
XX sites, each having a unique address indicative of the position of that
XX microbe identification site on the substrate and groups of nucleic acid
XX probes disposed at the microbe identification sites, each group being
XX complementary to a target nucleic acid to provide a detectable signal at
XX one or more microbe identification sites. The apparatus is useful for
XX detecting the presence of one or more microbes in a sample, such as virus
XX or viral particle, (non-)pathogenic bacteria, or cellular or acellular
XX microbe. The apparatus is particularly useful for clinical diagnosis,
XX research, epidemiological surveillance, bioterrorism countermeasures,
XX environmental pathogen surveys, and monitoring food contaminants. Current
XX testing procedures or devices, such as radioimmunoassays and ELISA, are
XX difficult to implement, time consuming, expensive, outdated, and
XX typically rely on the use of agents that recognise and bind to membrane
XX bound proteins or carbohydrates of the pathogen. These further cannot
XX assay multiple pathogens. The new apparatus or device for detecting
XX microbes overcomes these disadvantages. The apparatus is compact,
XX sensitive, and quick to detect the presence of any of a number of
XX pathogens present in a sample. The present sequence is that of an
XX oligonucleotide probe which is related to the microbe detection apparatus
XX of the invention.
XX
XX SQ Sequence 70 BP; 13 A; 20 C; 19 G; 18 T; 0 U; 0 Other;
XX
XX Query Match 96.0%; Score 24; DB 12; Length 70;
XX Best Local Similarity 100.0%; Pred. No. 0.13;
XX Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX Qy 2 CCGCTGCAGAGTTGCCCGTTACGA 25
XX |||||||
XX Db 1 CCGCTGCAGAGTTGCCCGTTACGA 24
XX
XX RESULT 72
XX ADP05514
XX ID ADP05514 standard; DNA; 70 BP.
XX
XX AC ADP05514;
XX
XX DT 26-AUG-2004 (first entry)
XX
XX DE Novel microbe detection apparatus-related oligonucleotide probe SeqID19.

```

XX microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 XX Viruses.  
 OS  
 XX WO2004045365-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 23-MAY-2003; 2003WO-US016461.  
 XX  
 XX 15-NOV-2002; 2002US-00295787.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Jia XY, Berger MA, Tilles JG;  
 XX WPI; 2004-449626/42.  
 XX  
 XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 PT  
 XX  
 XX Claim 16; SEQ ID NO 19; 89pp; English.  
 XX  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX  
 XX Sequence 70 BP; 13 A; 19 C; 20 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 96.0%; Score 24; DB 12; Length 70;  
 Best Local Similarity 100.0%; Pred. No. 0.13;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 2 CCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 1 CCGCTGCAGAGTTGCCCGTTACGA 24  
 RESULT 73  
 ADP05512  
 ID ADP05512 standard; DNA; 70 BP.  
 XX  
 XX ADP05512;  
 AC  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX  
 XX Novel microbe detection apparatus-related oligonucleotide probe SeqID17.  
 DE  
 XX microbe detection; microbe identification; virus; viral particle;  
 KW

KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW bioterrorism countermeasure; environmental pathogen survey;  
 KW food contaminant; radioimmunoassay; ELISA; probe; ss.  
 OS Viruses.  
 XX  
 XX WO2004045365-A2.  
 XX  
 XX 03-JUN-2004.  
 XX  
 XX 23-MAY-2003; 2003WO-US016461.  
 XX  
 XX 15-NOV-2002; 2002US-00295787.  
 XX  
 XX (REGC ) UNIV CALIFORNIA.  
 XX  
 XX Jia XY, Berger MA, Tilles JG;  
 XX WPI; 2004-449626/42.  
 XX  
 XX New (microarray) apparatus comprising a substrate with attached nucleic  
 PT acid probes, useful for detecting one or more microbes in a sample.  
 PT  
 XX  
 XX Claim 16; SEQ ID NO 17; 89pp; English.  
 XX  
 XX This invention relates to a novel apparatus for detecting a microbe in a  
 CC sample which comprises a substrate having multiple microbe identification  
 CC sites, each having a unique address indicative of the position of that  
 CC microbe identification site on the substrate and groups of nucleic acid  
 CC probes disposed at the microbe identification sites, each group being  
 CC complementary to a target nucleic acid to provide a detectable signal at  
 CC one or more microbe identification sites. The apparatus is useful for  
 CC detecting the presence of one or more microbes in a sample, such as virus  
 CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular  
 CC microbe. The apparatus is particularly useful for clinical diagnosis,  
 CC research, epidemiological surveillance, bioterrorism countermeasures,  
 CC environmental pathogen surveys, and monitoring food contaminants. Current  
 CC testing procedures or devices, such as radioimmunoassays and ELISA, are  
 CC difficult to implement, time consuming, expensive, outdated, and  
 CC typically rely on the use of agents that recognise and bind to membrane  
 CC bound proteins or carbohydrates of the pathogen. These further cannot  
 CC assay multiple pathogens. The new apparatus or device for detecting  
 CC microbes overcomes these disadvantages. The apparatus is compact,  
 CC sensitive, and quick to detect the presence of any of a number of  
 CC pathogens present in a sample. The present sequence is that of an  
 CC oligonucleotide probe which is related to the microbe detection apparatus  
 CC of the invention.  
 XX  
 XX Sequence 70 BP; 9 A; 20 C; 23 G; 18 T; 0 U; 0 Other;  
 SQ  
 Query Match 93.6%; Score 23.4; DB 12; Length 70;  
 Best Local Similarity 96.0%; Pred. No. 0.25;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 DB 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 RESULT 74  
 ADP05530  
 ID ADP05530 standard; DNA; 70 BP.  
 XX  
 XX ADP05530;  
 AC  
 XX 26-AUG-2004 (first entry)  
 DT  
 XX  
 XX Novel microbe detection apparatus-related oligonucleotide probe SeqID35.  
 DE  
 XX microbe detection; microbe identification; virus; viral particle;  
 KW pathogenic bacterium; cellular microbe; acellular microbe;  
 KW clinical diagnosis; research; epidemiological surveillance;  
 KW

bioterrorism countermeasure; environmental pathogen survey;  
food contaminant; radioimmunoassay; ELISA; probe; ss.

Viruses.

WO2004045365-A2.

03-JUN-2004.

23-MAY-2003; 2003WO-US016461.

15-NOV-2002; 2002US-00295787.

(REGC ) UNIV CALIFORNIA.

Jia XY, Berger MA, Tilles JG;

WPI; 2004-449626/42.

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 35; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 12 A; 21 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 12; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCGCTGCAGAGTTCGCCGTTACGA 25

1 TCCGCTGCAGAGTTCGCCGTTACGA 25

RESULT 75

ADP05506

ID ADP05506 standard; DNA; 70 BP.

ADP05506;

26-AUG-2004 (first entry)

Novel microbe detection apparatus-related oligonucleotide probe SeqID11.

microbe detection; microbe identification; virus; viral particle;  
pathogenic bacterium; cellular microbe; acellular microbe;  
clinical diagnosis; research; epidemiological surveillance;  
bioterrorism countermeasure; environmental pathogen survey;  
food contaminant; radioimmunoassay; ELISA; probe; ss.

Viruses.

WO2004045365-A2.

03-JUN-2004.

23-MAY-2003; 2003WO-US016461.

15-NOV-2002; 2002US-00295787.

(REGC ) UNIV CALIFORNIA.

Jia XY, Berger MA, Tilles JG;

WPI; 2004-449626/42.

New (microarray) apparatus comprising a substrate with attached nucleic acid probes, useful for detecting one or more microbes in a sample.

Claim 16; SEQ ID NO 11; 89pp; English.

This invention relates to a novel apparatus for detecting a microbe in a sample which comprises a substrate having multiple microbe identification sites, each having a unique address indicative of the position of that microbe identification site on the substrate and groups of nucleic acid probes disposed at the microbe identification sites, each group being complementary to a target nucleic acid to provide a detectable signal at one or more microbe identification sites. The apparatus is useful for detecting the presence of one or more microbes in a sample, such as virus or viral particle, (non-)pathogenic bacteria, or cellular or acellular microbe. The apparatus is particularly useful for clinical diagnosis, research, epidemiological surveillance, bioterrorism countermeasures, environmental pathogen surveys, and monitoring food contaminants. Current testing procedures or devices, such as radioimmunoassays and ELISA, are difficult to implement, time consuming, expensive, outdated, and typically rely on the use of agents that recognise and bind to membrane bound proteins or carbohydrates of the pathogen. These further cannot assay multiple pathogens. The new apparatus or device for detecting microbes overcomes these disadvantages. The apparatus is compact, sensitive, and quick to detect the presence of any of a number of pathogens present in a sample. The present sequence is that of an oligonucleotide probe which is related to the microbe detection apparatus of the invention.

Sequence 70 BP; 13 A; 20 C; 18 G; 19 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 12; Length 70;  
Best Local Similarity 96.0%; Pred. No. 0.25;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 TCCGCTGCAGAGTTCGCCGTTACGA 25

1 TCCGCTGCAGAGTTCGCCGTTACGA 25

RESULT 76

ADP05522

ID ADP05522 standard; DNA; 70 BP.

ADP05522;

26-AUG-2004 (first entry)

Novel microbe detection apparatus-related oligonucleotide probe SeqID27.

microbe detection; microbe identification; virus; viral particle;  
pathogenic bacterium; cellular microbe; acellular microbe;  
clinical diagnosis; research; epidemiological surveillance;  
bioterrorism countermeasure; environmental pathogen survey;  
food contaminant; radioimmunoassay; ELISA; probe; ss.

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XX WO2004045365-A2.
PN
XX
XX
PD 03-JUN-2004.
XX
XX
XX 23-MAY-2003; 2003WO-US016461.
XX
XX
XX 15-NOV-2002; 2002US-00295787.
XX
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX
XX Jia XY, Berger MA, Tilles JG;
PI
XX
XX WPI; 2004-449626/42.
DR
XX
XX New (microarray) apparatus comprising a substrate with attached nucleic
PT acid probes, useful for detecting one or more microbes in a sample.
XX
XX Claim 16; SEQ ID NO 27; 89pp; English.
PS
XX
XX This invention relates to a novel apparatus for detecting a microbe in a
CC sample which comprises a substrate having multiple microbe identification
CC sites, each having a unique address indicative of the position of that
CC microbe identification site on the substrate and groups of nucleic acid
CC probes disposed at the microbe identification sites, each group being
CC complementary to a target nucleic acid to provide a detectable signal at
CC one or more microbe identification sites. The apparatus is useful for
CC detecting the presence of one or more microbes in a sample, such as virus
CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
CC microbe. The apparatus is particularly useful for clinical diagnosis,
CC research, epidemiological surveillance, bioterrorism countermeasures,
CC environmental pathogen surveys, and monitoring food contaminants. Current
CC testing procedures or devices, such as radioimmunoassays and ELISA, are
CC difficult to implement, time consuming, expensive, outdated, and
CC typically rely on the use of agents that recognise and bind to membrane
CC bound proteins or carbohydrates of the pathogen. These further cannot
CC assay multiple pathogens. The new apparatus or device for detecting
CC microbes overcomes these disadvantages. The apparatus is compact,
CC sensitive, and quick to detect the presence of any of a number of
CC pathogens present in a sample. The present sequence is that of an
CC oligonucleotide probe which is related to the microbe detection apparatus
CC of the invention.
XX
XX Sequence 70 BP; 13 A; 20 C; 18 G; 19 T; 0 U; 0 Other;
SQ
Query Match 93.6%; Score 23.4; DB 12; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25
Db 1 TCCGCTGCAGAGTTACCGGTTACGA 25
RESULT 77
ADP05520
ID ADP05520 standard; DNA; 70 BP.
XX
XX
XX ADP05520;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Novel microbe detection apparatus-related oligonucleotide probe SeqID25.
DE
XX
XX microbe detection; microbe identification; virus; viral particle;
KW pathogenic bacterium; cellular microbe; acellular microbe;
KW clinical diagnosis; research; epidemiological surveillance;
KW bioterrorism countermeasure; environmental pathogen survey;
KW food contaminant; radioimmunoassay; ELISA; probe; ss.
XX
XX Viruses.
OS
XX
XX WO2004045365-A2.
PN
XX
XX 03-JUN-2004.
PD
```

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XX 03-JUN-2004.
PD
XX
XX 23-MAY-2003; 2003WO-US016461.
XX
XX
XX 15-NOV-2002; 2002US-00295787.
XX
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX
XX Jia XY, Berger MA, Tilles JG;
PI
XX
XX WPI; 2004-449626/42.
DR
XX
XX New (microarray) apparatus comprising a substrate with attached nucleic
PT acid probes, useful for detecting one or more microbes in a sample.
XX
XX Claim 16; SEQ ID NO 25; 89pp; English.
PS
XX
XX This invention relates to a novel apparatus for detecting a microbe in a
CC sample which comprises a substrate having multiple microbe identification
CC sites, each having a unique address indicative of the position of that
CC microbe identification site on the substrate and groups of nucleic acid
CC probes disposed at the microbe identification sites, each group being
CC complementary to a target nucleic acid to provide a detectable signal at
CC one or more microbe identification sites. The apparatus is useful for
CC detecting the presence of one or more microbes in a sample, such as virus
CC or viral particle, (non-)pathogenic bacteria, or cellular or acellular
CC microbe. The apparatus is particularly useful for clinical diagnosis,
CC research, epidemiological surveillance, bioterrorism countermeasures,
CC environmental pathogen surveys, and monitoring food contaminants. Current
CC testing procedures or devices, such as radioimmunoassays and ELISA, are
CC difficult to implement, time consuming, expensive, outdated, and
CC typically rely on the use of agents that recognise and bind to membrane
CC bound proteins or carbohydrates of the pathogen. These further cannot
CC assay multiple pathogens. The new apparatus or device for detecting
CC microbes overcomes these disadvantages. The apparatus is compact,
CC sensitive, and quick to detect the presence of any of a number of
CC pathogens present in a sample. The present sequence is that of an
CC oligonucleotide probe which is related to the microbe detection apparatus
CC of the invention.
XX
XX Sequence 70 BP; 14 A; 21 C; 18 G; 17 T; 0 U; 0 Other;
SQ
Query Match 93.6%; Score 23.4; DB 12; Length 70;
Best Local Similarity 96.0%; Pred. No. 0.25;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCCGCTGCAGAGTTCCCGTTACGA 25
Db 1 TCCGCTGCAGAGTTGCCGTTACGA 25
RESULT 78
ADP05516
ID ADP05516 standard; DNA; 71 BP.
XX
XX
XX ADP05516;
AC
XX
XX 26-AUG-2004 (first entry)
DT
XX
XX Novel microbe detection apparatus-related oligonucleotide probe SeqID21.
DE
XX
XX microbe detection; microbe identification; virus; viral particle;
KW pathogenic bacterium; cellular microbe; acellular microbe;
KW clinical diagnosis; research; epidemiological surveillance;
KW bioterrorism countermeasure; environmental pathogen survey;
KW food contaminant; radioimmunoassay; ELISA; probe; ss.
XX
XX Viruses.
OS
XX
XX WO2004045365-A2.
PN
XX
XX 03-JUN-2004.
PD
```





PS Disclosure; SEQ ID NO 40; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX SQ Sequence 117 BP; 25 A; 33 C; 28 G; 31 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 117;

Best Local Similarity 96.0%; Pred. No. 0.27;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 81

AEB56856/c

ID AEB56856 standard; DNA; 173 BP.

XX AC AEB56856;

XX 22-SEP-2005 (first entry)

XX Human echovirus 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

KW Human echovirus 5.

OS US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; AF188359.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX SQ Sequence 117 BP; 25 A; 33 C; 28 G; 31 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 117;

Best Local Similarity 96.0%; Pred. No. 0.27;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

DB 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 82

AEB56855/c

ID AEB56855 standard; DNA; 173 BP.

XX AC AEB56855;

XX 22-SEP-2005 (first entry)

XX Human echovirus 5' untranslated polynucleotide sequence.

DE DNA detection; enteroviral detection; ds.

KW Human echovirus 5.

OS US2005158710-A1.

XX 21-JUL-2005.

XX 16-JAN-2004; 2004US-00760048.

XX 16-JAN-2004; 2004US-00760048.

XX (TSAN/) TSANG S.

XX (PRIC/) PRICE J A.

XX (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;

XX WPI; 2005-512251/52.

XX GENBANK; AF188359.

XX Novel oligonucleotide comprising sequences for binding and amplifying or

PT detecting target, useful for detecting enterovirus nucleic acids.

XX Disclosure; Fig 1A-D; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the

CC target binding sequence of an oligonucleotide chosen from any one of the

CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for

CC selected amplification or detection reaction. Also described: (1) a kit

CC (K1) comprising (I), and one or more container that contains (I); and (2)

CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying

CC the target sequence using first amplification primer having a sequence

CC consisting essentially of target binding sequence of any one of AEB56764

CC to AEB56771 and optionally a sequence required for selected amplification

CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and

CC (K1) are useful for detecting enterovirus target sequences. (I)

CC specifically and selectively recognizes the enterovirus genome. (I)

CC sensitively and rapidly detects fewer than 500 copies of enteroviral

CC genome and allows detection of broad range of enterovirus serotypes. The

CC present sequence represents a viral 5' untranslated polynucleotide

CC sequence given in the exemplification of the present invention.

XX SQ Sequence 173 BP; 36 A; 44 C; 45 G; 48 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 173;

Best Local Similarity 96.0%; Pred. No. 0.28;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25

DB 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

```
XX SQ Sequence 173 BP; 36 A; 45 C; 45 G; 47 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 173;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
Db 131 TCCGCTGCAGAGTTGCCGTTACGA 107

RESULT 83
AEB56865/c
ID AEB56865 standard; DNA; 198 BP.
XX AC AEB56865;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 12 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 12.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11706.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 41 A; 49 C; 50 G; 58 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 198;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
XX 131 TCCGCTGCAGAGTTGCCGTTACGA 107
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Db 91 TCCGCTGCAGAGTTGCCGTTACGA 67

RESULT 84
AEB56853/c
ID AEB56853 standard; DNA; 198 BP.
XX AC AEB56853;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 2 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 2.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11707.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
Query Match 93.6%; Score 23.4; DB 14; Length 198;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCGTTACGA 25
    |||||
Db 91 TCCGCTGCAGAGTTGCCGTTACGA 67

RESULT 85
AEB56860/c
ID AEB56860 standard; DNA; 198 BP.
XX AC AEB56860;
XX DT 22-SEP-2005 (first entry)
XX DE Human echovirus 2 5' untranslated polynucleotide sequence.
XX KW DNA detection; enteroviral detection; ds.
XX OS Human echovirus 2.
XX PN US2005158710-A1.
XX PD 21-JUL-2005.
XX PF 16-JAN-2004; 2004US-00760048.
XX PR 16-JAN-2004; 2004US-00760048.
XX PA (TSAN/) TSANG S.
XX PA (PRIC/) PRICE J A.
XX PA (HELL/) HELLYER T J.
XX PI Tsang S, Price JA, Hellyer TJ;
XX WPI; 2005-512251/52.
XX GENBANK; U11707.
XX Novel oligonucleotide comprising sequences for binding and amplifying or
XX detecting target, useful for detecting enterovirus nucleic acids.
XX Disclosure; Fig 1A-D; 34pp; English.
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
XX target binding sequence of an oligonucleotide chosen from any one of the
XX 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
XX selected amplification or detection reaction. Also described: (1) a kit
XX (K1) comprising (I), and one or more container that contains (I); and (2)
XX detecting (M1) an enterovirus target sequence, involving: (a) amplifying
XX the target sequence using first amplification primer having a sequence
XX consisting essentially of target binding sequence of any one of AEB56764
XX to AEB56771 and optionally a sequence required for selected amplification
XX reaction; and (b) detecting the amplified target sequences. (I), (M1) and
XX (K1) are useful for detecting enterovirus target sequences. (I)
XX specifically and selectively recognizes the enterovirus genome. (I)
XX sensitively and rapidly detects fewer than 500 copies of enteroviral
XX genome and allows detection of broad range of enterovirus serotypes. The
XX present sequence represents a viral 5' untranslated polynucleotide
XX sequence given in the exemplification of the present invention.
XX SQ Sequence 198 BP; 42 A; 53 C; 51 G; 52 T; 0 U; 0 Other;
```

DT 22-SEP-2005 (first entry)  
 XX Human echovirus 9 5' untranslated polynucleotide sequence.  
 DE DNA detection; enteroviral detection; ds.  
 KW Human echovirus 9.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 PN 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 PI WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 PS Disclosure; Fig 1A-D; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 198 BP; 39 A; 49 C; 52 G; 58 T; 0 U; 0 Other;  
 SQ Query Match 93.6%; Score 23.4; DB 14; Length 198;  
 Best Local Similarity 96.0%; Pred. No. 0.29;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTCGCCGTACGA 25  
 DB 91 TCCGCTGCAGAGTTCGCCGTACGA 67  
 RESULT 86  
 AEB56811/c  
 ID AEB56811 standard; DNA; 236 BP.  
 XX AEB56811;  
 AC AEB56811;  
 XX 22-SEP-2005 (first entry)  
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:50.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 OS US2005158710-A1.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 XX 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.  
 XX Tsang S, Price JA, Hellyer TJ;  
 PI WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 PT detecting target, useful for detecting enterovirus nucleic acids.  
 PS Disclosure; SEQ ID NO 50; 34pp; English.  
 XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (K1) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC consisting essentially of target binding sequence of any one of AEB56764  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequence. (I) and  
 CC (K1) are useful for detecting enterovirus target sequences. (I) and  
 CC specifically and selectively recognizes the enterovirus genome. (I)  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.  
 XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;  
 SQ Query Match 93.6%; Score 23.4; DB 14; Length 236;  
 Best Local Similarity 96.0%; Pred. No. 0.29;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 TCCGCTGCAGAGTTCGCCGTACGA 25  
 DB 75 TCCGCTGCAGAGTTCGCCGTACGA 51  
 RESULT 87  
 AEB56810/c  
 ID AEB56810 standard; DNA; 236 BP.  
 XX AEB56810;  
 AC AEB56810;  
 XX 22-SEP-2005 (first entry)  
 DT Viral 5' untranslated polynucleotide sequence SEQ ID NO:49.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 OS US2005158710-A1.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 PA (HELL/) HELLYER T J.

XX Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 49; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically  
 CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;  
 SQ

Query Match 93.6%; Score 23.4; DB 14; Length 236;  
 Best Local Similarity 96.0%; Pred. No. 0.29;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 88  
 AEB56812/c  
 ID AEB56812 standard; DNA; 236 BP.  
 AC AEB56812;  
 DT 22-SEP-2005 (first entry)  
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:51.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 51; 34pp; English.

CC The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically  
 CC sensitively and rapidly recognizes the enterovirus genome. (I)  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.

XX Sequence 236 BP; 60 A; 52 C; 51 G; 73 T; 0 U; 0 Other;  
 SQ

Query Match 93.6%; Score 23.4; DB 14; Length 236;  
 Best Local Similarity 96.0%; Pred. No. 0.29;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 Db 75 TCCGCTGCAGAGTTGCCCGTTACGA 51

RESULT 89  
 AEB56798/c  
 ID AEB56798 standard; DNA; 236 BP.  
 XX AEB56798;  
 AC AEB56798;  
 DT 22-SEP-2005 (first entry)  
 XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:37.  
 DE DNA detection; enteroviral detection; ds.  
 KW Unidentified.  
 OS US2005158710-A1.  
 XX 21-JUL-2005.  
 PD 16-JAN-2004; 2004US-00760048.  
 PF 16-JAN-2004; 2004US-00760048.  
 XX (TSAN/) TSANG S.  
 PA (PRIC/) PRICE J A.  
 XX (HELL/) HELLYER T J.  
 PI Tsang S, Price JA, Hellyer TJ;  
 XX WPI; 2005-512251/52.  
 XX Novel oligonucleotide comprising sequences for binding and amplifying or  
 XX detecting target, useful for detecting enterovirus nucleic acids.  
 XX Disclosure; SEQ ID NO 37; 34pp; English.

XX The invention relates to an oligonucleotide (I) consisting of: (a) the  
 CC target binding sequence of an oligonucleotide chosen from any one of the  
 CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for  
 CC selected amplification or detection reaction. Also described: (1) a kit  
 CC (KI) comprising (I), and one or more container that contains (I); and (2)  
 CC detecting (MI) an enterovirus target sequence, involving: (a) amplifying  
 CC the target sequence using first amplification primer having a sequence  
 CC to AEB56771 and optionally a sequence required for selected amplification  
 CC reaction; and (b) detecting the amplified target sequences. (I), (MI) and  
 CC (KI) are useful for detecting enterovirus target sequences. (I) specifically  
 CC sensitively and rapidly recognizes the enterovirus genome. (I)  
 CC genome and allows detection of broad range of enterovirus serotypes. The  
 CC present sequence represents a viral 5' untranslated polynucleotide  
 CC sequence given in the exemplification of the present invention.



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ID AEB56861 standard; DNA; 237 BP.
XX
AC AEB56861;
XX
XX 22-SEP-2005 (first entry)
XX
DE Human echovirus 9 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
OS Human echovirus 9.
XX
PN US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX (TSAN/) TSANG S.
PA (PRIC/) PRICE J A.
PA (HELL/) HELLYER T J.
XX
XX Tsang S, Price JA, Hellyer TJ;
PI WPI; 2005-512251/52.
XX
XX GENBANK; X84981.
XX
XX Novel oligonucleotide comprising sequences for binding and amplifying or
PT detecting target, useful for detecting enterovirus nucleic acids.
XX
XX Disclosure; Fig 1A-D; 34pp; English.
XX
XX The invention relates to an oligonucleotide (I) consisting of: (a) the
CC target binding sequence of an oligonucleotide chosen from any one of the
CC 10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
CC selected amplification or detection reaction. Also described: (1) a kit
CC (K1) comprising (I), and one or more container that contains (I); and (2)
CC detecting (M1) an enterovirus target sequence, involving: (a) amplifying
CC the target sequence using first amplification primer having a sequence
CC consisting essentially of target binding sequence of any one of AEB56764
CC to AEB56771 and optionally a sequence required for selected amplification
CC reaction; and (b) detecting the amplified target sequences. (I), (M1) and
CC (K1) are useful for detecting enterovirus target sequences. (I)
CC specifically and selectively recognizes the enterovirus genome. (I)
CC sensitively and rapidly detects fewer than 500 copies of enteroviral
CC genome and allows detection of broad range of enterovirus serotypes. The
CC present sequence represents a viral 5' untranslated polynucleotide
CC sequence given in the exemplification of the present invention.
XX
SQ Sequence 237 BP; 48 A; 54 C; 65 G; 70 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 237;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 130 TCCGCTGCAGAGTTGCCCGTTACGA 106

RESULT 93
AEB56849/c
ID AEB56849 standard; DNA; 238 BP.
XX
XX AC AEB56849;
XX
XX 22-SEP-2005 (first entry)
XX
XX Human coxsackievirus B5 5' untranslated polynucleotide sequence.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX

ID AEB56794 standard; DNA; 238 BP.
XX
XX AC AEB56794;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:33.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
XX

Human coxsackievirus B5.
US2005158710-A1.
21-JUL-2005.
16-JAN-2004; 2004US-00760048.
16-JAN-2004; 2004US-00760048.
(TSAN/) TSANG S.
(PRIC/) PRICE J A.
(HELL/) HELLYER T J.
Tsang S, Price JA, Hellyer TJ;
WPI; 2005-512251/52.
GENBANK; X67706.
Novel oligonucleotide comprising sequences for binding and amplifying or
detecting target, useful for detecting enterovirus nucleic acids.
Disclosure; Fig 1A-D; 34pp; English.
The invention relates to an oligonucleotide (I) consisting of: (a) the
target binding sequence of an oligonucleotide chosen from any one of the
10 sequence of AEB56762 to AEB56771; and (b) a sequence required for
selected amplification or detection reaction. Also described: (1) a kit
(K1) comprising (I), and one or more container that contains (I); and (2)
detecting (M1) an enterovirus target sequence, involving: (a) amplifying
the target sequence using first amplification primer having a sequence
consisting essentially of target binding sequence of any one of AEB56764
to AEB56771 and optionally a sequence required for selected amplification
reaction; and (b) detecting the amplified target sequences. (I), (M1) and
(K1) are useful for detecting enterovirus target sequences. (I)
specifically and selectively recognizes the enterovirus genome. (I)
sensitively and rapidly detects fewer than 500 copies of enteroviral
genome and allows detection of broad range of enterovirus serotypes. The
present sequence represents a viral 5' untranslated polynucleotide
sequence given in the exemplification of the present invention.
Sequence 238 BP; 53 A; 57 C; 61 G; 67 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 238;
Best Local Similarity 96.0%; Pred. No. 0.29;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 94
AEB56794/c
ID AEB56794 standard; DNA; 238 BP.
XX
XX AC AEB56794;
XX
XX 22-SEP-2005 (first entry)
XX
XX Viral 5' untranslated polynucleotide sequence SEQ ID NO:33.
XX
XX DNA detection; enteroviral detection; ds.
XX
XX Unidentified.
XX
XX US2005158710-A1.
XX
XX 21-JUL-2005.
XX
XX 16-JAN-2004; 2004US-00760048.
XX
```



CC selected amplification or detection reaction. Also described: (1) a kit  
CC (K1) comprising (I), and one or more container that contains (I); and (2)  
CC detecting (MI) an enterovirus target sequence, involving; (a) amplifying  
CC the target sequence using first amplification primer having a sequence  
CC consisting essentially of target binding sequence of any one of ABB56764  
CC to ABB56771 and optionally a sequence required for selected amplification  
CC reaction; and (b) detecting the amplified target sequence. (I), (M1) and  
CC (K1) are useful for detecting enterovirus target sequences. (I)  
CC specifically and selectively recognizes the enterovirus genome. (I)  
CC sensitively and rapidly detects fewer than 500 copies of enteroviral  
CC genome and allows detection of broad range of enterovirus serotypes. The  
CC present sequence represents a viral 5' untranslated polynucleotide  
CC sequence given in the exemplification of the present invention.

XX SQ Sequence 238 BP; 50 A; 55 C; 64 G; 69 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 14; Length 238;  
Best Local Similarity 96.0%; Pred. No. 0.29;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 131 TCCGCTGCAGAGTTGCCCGTTACGA 107

RESULT 97  
ABL53113/C  
ID ABL53113 standard; DNA; 525 BP.

XX AC ABL53113;

XX DT 07-AUG-2003 (revised)  
XX DT 25-JUN-2002 (first entry)

XX DE Micro-organism detection probe #55.

XX KW Probe; microorganism detection; microbiological quality;  
XX KW water purification; ss.

XX OS Echovirus sp.

XX FN WO200202811-A2.

XX PD 10-JAN-2002.

XX PF 06-JUL-2001; 2001WO-FR002191.

XX PR 06-JUL-2000; 2000FR-00008839.

XX PA (INNR ) BIO MERIEUX.

XX PI Renaud P, Guillot E, Mabilat C, Vachon C, Lacroix B, Vernet G;  
XX PI Armand M, Laffaire P;

XX DR WPI; 2002-148021/19.

XX PT Monitoring microbiological quality of water, useful particularly for  
XX PT controlling water purification, uses oligonucleotide probes to detect at  
XX PT least three representative microbes.

XX PS Claim 24; Page 76; 85pp; French.

XX CC The present invention relates to a method for monitoring microbiological  
XX CC quality of an aqueous environmental medium that potentially contains many  
XX CC different microorganisms. A reference set of at least three  
XX CC microorganisms is chosen that, separately or collectively, represent  
XX CC microbiological quality. The test medium is treated, then any  
XX CC microorganisms, or their fragments, in the treated medium is contacted  
XX CC with a set of at least three probes for specific identification and  
XX CC multiple determination of selected microorganisms. This determination  
XX CC represents the level of microbiological quality. The method is useful for  
XX CC identifying and quantifying microorganisms in water and provides results  
XX CC that are used to control water purification/production processes. The

CC present sequence is a probe which was used to illustrate the invention.  
CC (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 525 BP; 117 A; 142 C; 135 G; 131 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 6; Length 525;  
Best Local Similarity 96.0%; Pred. No. 0.32;  
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
Db 475 TCCGCTGCAGAGTTGCCCGTTACGA 451

RESULT 98

AAC85153/C

ID AAC85153 standard; RNA; 646 BP.

XX ID AAC85153;

XX AC AAC85153;

XX DT 08-MAY-2001 (first entry)

XX DE Echo virus (ECV12) 5' non-translated region (NTR) sequence.

XX KW Gene therapy; enterovirus; vaccine; diagnostic; RT-PCR; primer;

XX KW Cocksackievirus B3; CVB3; NTR; non-translated region; echo virus; ds.

XX OS Echo virus.

XX FH Key Location/Qualifiers

XX FT stem\_loop 2..87

XX FT /tag= a

XX FT /note= "Domain I"

XX FT 103..180

XX FT /tag= b

XX FT /note= "Domain II"

XX FT 183..232

XX FT /tag= c

XX FT /note= "Domain III"

XX FT 240..443

XX FT /tag= d

XX FT /note= "Domain IV"

XX FT 451..559

XX FT /tag= e

XX FT /note= "Domain V"

XX FT 586..622

XX FT /tag= f

XX FT /note= "Domain VI"

XX FT 623..643

XX FT /tag= g

XX FT /note= "Domain VII"

XX WO200104136-A1.

XX PD 18-JAN-2001.

XX PF 08-JUL-2000; 2000WO-US018681.

XX PR 09-JUL-1999; 99US-0143104P.

XX PA (UYNE-) UNIV NEBRASKA.

XX PI Romero JR, Bradrick SS, Dunn JJ;

XX DR WPI; 2001-138310/14.

XX CC Recombinant enterovirus genome for use as vector or vaccine, modified by  
XX CC replacing a part or all of its 5' non-translated region by 5'NTR of  
XX CC enterovirus genome that encodes virus modified in tropism or virulence.

XX PS Disclosure; Fig 2; 49pp; English.

XX CC The invention provides an enterovirus genome (I) for use as a vector or



CC vaccine, modified to produce a virus (V1) having a restricted or altered  
 CC species or tissue tropism, compared to an equivalent unmodified virus, or  
 CC modified to produce an attenuated virus (V2), by replacing a part or all  
 CC of the 5' non-translated region (5'NTR) of (1) with a 5'NTR of an  
 CC enterovirus genome that encodes V1 or V2. (1) is useful as vaccine or  
 CC vector in targeting genes of interest to specific cells or tissues. (1)  
 CC is also useful for diagnostic purposes, e.g. to identify virulent, versus  
 CC nonvirulent strains of an enterovirus. The present sequence represents  
 CC the 5' NTR (non-translated region) sequence of echo virus (BCV12)  
 XX

SQ Sequence 646 BP; 145 A; 176 C; 163 G; 0 T; 162 U; 0 Other;  
 Query Match 93.6%; Score 23.4; DB 4; Length 646;  
 Best Local Similarity 96.0%; Pred. No. 0.33;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
 |||||

RESULT 99  
 AAZ98719/c  
 ID AAZ98719 standard; cDNA; 7400 BP.  
 XX  
 AC AAZ98719;  
 XX  
 DT 20-JUN-2000 (first entry)  
 XX  
 DE Swine vesicular disease virus (SVDV) N3 mutant strain gene sequence.  
 XX  
 KW Swine vesicular disease virus; SVDV; swine vesicular disease;  
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 KW differentiation; vaccine; prevent; ss.  
 XX  
 OS Swine vesicular disease virus.

FH Key Location/Qualifiers  
 FT misc\_feature 2693..2710  
 FT /\*tag= a  
 FT /note= "Nucleotides in this position replace the wild-  
 FT type nucleotide sequence of strain Taiwan Yu-Li (see  
 FT AAZ98717)"  
 XX

PN EP982403-A1.  
 XX  
 XX 01-MAR-2000.  
 XX  
 PF 14-AUG-1998; 98EP-00306486.  
 XX  
 PR 14-AUG-1998; 98EP-00306486.  
 XX  
 XX (BIOT-) DEV CENT BIOTECHNOLOGY.  
 PA  
 XX  
 PI Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;  
 DR WPI; 2000-258616/23.  
 XX  
 DR Mutant strains of swine vesicular disease virus (SVDV) used in vaccines  
 PT to prevent swine vesicular disease.  
 XX  
 PS Claim 4; Page: 65pp; English.

XX  
 CC This sequence represents the full length Swine vesicular disease virus  
 CC (SVDV) gene sequence from the SVDV strain N3. SVDV is the causative agent  
 CC of swine vesicular disease, which is very similar to foot and mouth  
 CC disease. The invention relates to the wild-type Taiwan Yu-Li strain cDNA  
 CC sequence, and the gene sequences of the mutant SVDV strains N3, H21 and  
 CC SP7. The mutant SVDV nucleotide sequence can be used in a vaccine for the  
 CC prophylaxis of swine vesicular disease. The invention also includes a  
 CC method for differentiating the mutant SVDV nucleotide sequences from the  
 CC wild type strain of SVDV, coxsackie virus and foot-and-mouth disease  
 CC virus through the use of polymerase chain reaction. Note: This sequence

CC is not present in the specification, but has been derived from the wild-  
 CC type Taiwan Yu-Li strain SVDV gene sequence (see AAZ98717) shown on pages  
 CC 34-38 of the specification  
 XX

SQ Sequence 7400 BP; 2084 A; 1786 C; 1862 G; 1668 T; 0 U; 0 Other;  
 Query Match 93.6%; Score 23.4; DB 3; Length 7400;  
 Best Local Similarity 96.0%; Pred. No. 0.43;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
 |||||

RESULT 100  
 AAZ98717/c  
 ID AAZ98717 standard; cDNA; 7400 BP.  
 XX

AC AAZ98717;  
 XX  
 DT 20-JUN-2000 (first entry)  
 XX  
 DE Swine vesicular disease virus (SVDV) gene sequence.  
 XX

KW Swine vesicular disease virus; SVDV; swine vesicular disease;  
 KW Taiwan Yu-Li strain; foot and mouth disease; coxsackie virus;  
 KW differentiation; vaccine; prevent; ss.

OS Swine vesicular disease virus.

XX EP982403-A1.

PN 01-MAR-2000.

PF 14-AUG-1998; 98EP-00306486.

PR 14-AUG-1998; 98EP-00306486.

XX (BIOT-) DEV CENT BIOTECHNOLOGY.

XX Hwong CL, Lo C, Yang Y, Jeng K, Chang EL;

XX WPI; 2000-258616/23.

XX Mutant strains of swine vesicular disease virus (SVDV) used in vaccines  
 PT to prevent swine vesicular disease.

XX Claim 1; Page 34-38; 65pp; English.

XX This sequence represents the full length Swine vesicular disease virus  
 CC (SVDV) gene sequence from the SVDV strain Taiwan Yu-Li. SVDV is the  
 CC causative agent of swine vesicular disease, which is very similar to foot  
 CC and mouth disease. The invention relates to the wild-type Taiwan Yu-Li  
 CC strain cDNA sequence, and the gene sequences of the mutant SVDV strains  
 CC N3, H21 and SP7. The mutant SVDV nucleotide sequence can be used in a  
 CC vaccine for the prophylaxis of swine vesicular disease. The invention  
 CC also includes a method for differentiating the mutant SVDV nucleotide  
 CC sequences from the wild type strain of SVDV, coxsackie virus and foot-and-  
 CC mouth disease virus through the use of polymerase chain reaction

SQ Sequence 7400 BP; 2082 A; 1786 C; 1862 G; 1670 T; 0 U; 0 Other;

Query Match 93.6%; Score 23.4; DB 3; Length 7400;  
 Best Local Similarity 96.0%; Pred. No. 0.43;  
 Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 TCCGCTGCAGAGTTGCCCGTTACGA 25  
 |||||  
 DB 538 TCCGCTGCAGAGTTGCCCGTTACGA 514  
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Search completed: March 9, 2006, 00:30:40

Job time : 264.485 secs

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